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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 16, 2005, 08:21:21; Search time 11.2069 Seconds (without alignments) 111.611 Million cell updates/sec

US-09-648-816B-6 65 1 ARYRKFKNKILKS 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

22893 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
4: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

S	Description	hypothetical prote	hypothetical prote	hypothetical prote	٦	Rch1 protein - mou	hypothetical prote	30S ribosomal prot	rleukin-3	53K protein - chic	\mathbf{H}	30S ribosomal prot	-		hypothetical prote	ribosomal protein	degenerate transpo	hypothetical prote			7	ъ	hypothetical prote	_		hypothetical prote	hypothetical prote	hypothetical prote	pro	beta-endorphin - A
SUMMARIES	ΩI	E70239	G81343	D89806	JU0329	862116	H64442	H81379	I57554	A41669	BGMS	AE2050	C72262	AH1876	B85569	E64251	H98038	B70225	G64002	T18150	C82724	I46593	G90010	AG1829	T12949	D69384	G69058	AB0406	S62570	OECMB
	DB	7	7	~	~	~	7	~	~	7	~	~	7	~	~	~	~	7	7	7	~	~	7	0	~	7	~	~	~	Н
	Length	34	61	20	37	43	65	70	74	41	52	58	69	41	44	48	53	57	63	69	69	36	21	54	58	62	67	68	74	31
de	Query Match	53.8	52.3	50.8		49.2	49.2	49.2	49.2	47.7	47.7	47.7	47.7	46.2	46.2	46.2	46.2	46.2	46.2	•	46.2	44.6	44.6		•	•	44.6	44.6	44.6	43.1
	Score	35	34	33	32	32	32	32	32	31	31	31	31	30	30	30	30	30	30	30	30	29	29	29		29		29	53	28
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hypothetical prote ATP synthase chain	30S ribosomal prot ribosomal protein	ribosomal protein 30S ribosomal prot	30S ribosomal prot	type i restriction acanthophin d - de	hypothetical prote	nypouneticai prote acyltransferase (E	hypothetical prote	probable NADPH-fer	hypothetical prote	hypothetical prote
E95226 T11313	F89938 H97058	S48688 H90020	F86885	D82933 A60518	A70195	PQ0049	S13571	T06541	G64036	G71716
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37	28 28	60	61	9 V	37	47	48	20	20	20
43.1	43.1	43.1	43.1	43.1 43.1	5.1.5	41.5	41.5	41.5	41.5	41.5
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30 31	33 33	ი ი 4 ი	96.	38	36	4 4 0 1	42	43	44	45

ALIGNMENTS

RESULT 1 E70339 hypothetical protein C;Species: Borrelia C;Date: 13-Feb-1998 C;Accession: E70239 R;Fraser, C.M.; Casj Son, D.; Peterson, J; Bowan, C.; Garlan Nature 390, 580-586, A;Authors: Smith, H.	RESULT 1 E70239 Chypotherical protein BBH39 - Lyme disease spirochete plasmid H/lp28-3 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Species: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004, C;Accession: E70239 E75 Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004, C;Accession: Journal S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, FS E75 Feb-1997 FS E75 Feb-1997 FS E75 Feb-1997 FS E75 Feb-1998 FS FS E75 Feb-1998 FS FS E75 Feb-1998 FS
A; It.E: Genomic Seques A; Reference number: A7 A; Accession: E70239 A; Status: preliminary; A; Molecule type: DNA A; Residues: 1-34 «KLE> A; Coss-references: UN A; Experimental source: C; Genetics: A; Genetics: A; Genetics:	A):Reference number: A70100; MUID:98065943; PMID:9403685 A):Reference number: A70100; MUID:98065943; PMID:9403685 A):Recession: B70239 A):Resture: pre-liminary; nucleic acid sequence not shown; translation not shown A):Rolecule type: DNA A):R
Query Match Best Local Similarity Matches 5; Conservat	S3.8%; Score 35; DB 2; Length 34; Similarity 50.0%; Pred. No. 21; 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
, e	3 YRKFKNKILK 12

8 8

3 YRKFKNKILK 12 |:| ||:::| 10 YKKIKNELIK 19

hypothetical protein Cj0724 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Date: J. Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C:W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrelj
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Title: The genome sequence of the food-borne pathogen
A;Tocesion: GB134
A;Tocesion: GB134
A;Tocesion: GB134
A;Molecule type: DNA
A;Residues: 1-61 <PAR>A;Molecule type: DNA
A;Residues: 1-61 <PAR>A;Coss-references: UNIPROT:Q9PP13; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB72998
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:

Query Match

52.3%; Score 34; DB 2; Length 61;

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Gaps

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Indels

Length 43

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CjAccession: H6442

R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Pleischmann, R.D.; Sutton, G.G.; Blake, i. Reich, C.I.; White, O.; Olsen, G.J.; Zhou, L.; Pleischmann, R.D.; Sutton, G.G.; Blake, A.; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ston, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Atuthors: Kaine, B.P.; Boxodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A; Tille: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. A; Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accesion: H81379
C;W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
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A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT: Q58545; GB: U67557; GB: L77117; NID: 91591777; PIDN: AAB99155.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein MJ1145 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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C;Superfamily: Escherichia coli ribosomal protein S21
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                                                                                                                                                                Score 32; DB 2;
Pred. No. 85;
1; Mismatches 2
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                                                                                                                                                                   49.2%;
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                                                                                                                                                                                                                                                                                                                                    12 ARLINEFKINK 20
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16 YRKFKKQV 23
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Best Local Similarity
Matches 8; Conserva
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Matches 6; Conserv
                                                                                                               C; Superfamily: pendulin
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A;Molecule type: DNA
A;Residues: 1-70 <PAR>
                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-43 <CUO>
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     A, Accession: S62116
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C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JU0329
R;Diaz, E.; Garcia, J.L.
R;Diaz, E.; Garcia, J.L.
A;Title: Characterization of the transcription unit encoding the major pneumococcal auto
                                                                                                                                                                                                                                                                                                                                                              C;Accession: D89806
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Obta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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Proc. Natl. Acad. Sci. U.S.A. 91, 6156-6160, 1994
A,Title: Rchl, a protein that specifically interacts with the RAG-1 recombination-activa
A,Reference number: 138606; MUID:94286596; PMID:8016130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q99WI4; GB:BA000018; PID:g13700309; PIDN:BAB41607.1; GSPDB:d
A;Experimental source: strain N315
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A;Experimental source: strain M31
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                                                                                                                                                                                                                                                                                  hypothetical protein SAS012 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                            C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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C;Specise: Mus musculus (house mouse)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 29-Jan-1999
C;Accession: S62116
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Pred. No. 66;
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Pred. No. 74;
  ed. No. 53;
Mismatches
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Matches 7; Conservative
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27 RLCKFKNKVQK 37
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22 AKFKPFKNRI 31
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Best Local Similarity
Matches 5; Conserv
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Residues: 1-37 <DIA>
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A, Residues: 1-50 < KUR>
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Gaps

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Gaps

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1; Indels

Length 70;

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A; Accession: JS0038

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-55 «KLE>
A;Cross-references: EMBL:X12521; NID:g54850; PIDN:CAA31039.1; PID:g54851
C;Comment: This protein replaces histones and is replaced by other transition proteins on
C;Goment: G;Goment: This protein in transition protein 1
A;Introns: 47/1
C;Superfamily: spermatid transition protein 1
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
C;Keywords: DNA binding transition protein 1 #status predicted <a href="MAI">MAI</a>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT: QBYVM0; GB:BA000019; PIDN:BAB73654.1; PID:g17131045; GSPDB:GPA;Experimental source: strain PCC 7120
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seque A;Atele: commenter and action from genome seque any accession: C72262

A;Accession: C72262

A;Status: preliminary
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A;Residues: 1-69 <ARN>
A;Cross-references: UNIPROT:09X1A6; GB:AE001791; GB:AE000512; NID:g4981929; PIDN:AAD36456
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1386
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: C7:262
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30S ribosomal protein S21 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
S;Note: Nostoc sp. ptc 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2050
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Pred. No. 1.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                               47.7%; Score 31; DB 1; Length 55; 50.0%; Pred. No. 1.6e+02; tive 3; Mismatches 2; Indels
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C,Superfamily: Escherichia coli ribosomal protein S21
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Best Local Similarity
Matches 6; Conserv
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Matches 5; Conserv
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A; Residues: 1-58 < KUR>
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A; Status: preliminary
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A;Molecule type: mRNA
A;Residues: 1-74 RRBS-
A;Kesidues: 1-74 RRBS-
A;Conserreferences: UNIPROT: Q64130; GB:S78451; NID:998544; PIDN:AAB34209.1; PID:998545
C;Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor H
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C;Date: 05-Jun-1992 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Date: 05-Jun-1992 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A40561; JS0038
R;Yelick, P.C.; Kozak, C.; Kwon, Y.K.; Seldin, M.F.; Hecht, N.B.
Genomics 11, 687-694, 1991
A;Title: The mouse transition protein 1 gene contains a B1 repetitive element and is loc
A;Reference number: A40561; MJID:92128951; PMID:1685480
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                                                                                                                                   C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 157554
R;Hannemann, J: Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
Mol. Cell. Biol. 15, 2402-2412, 1995
A;Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-sequence number: 157554; MUID:92257920; PMID:7739524
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A11669
A11669
S1X protein - chicken (fragments)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 30-Unn-1992 #sequence_revision 30-Jun-1992 #text_change 03-May-1996
C;Accession: A1669
R;Bassuk, J.A.; Berg, R.A.
J. Blol. Chem. 266, 23132-23738, 1991
A;Title: A novel 53-kDa polypeptide from chicken embryo.
A;Title: A novel 53-kDa polypeptide from chicken embryo.
A;Reference number: A41669; MUID:92084663; PMID:1660884
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Pred. No. 1.2e+02;
2; Mismatches 2; Indels
                                                                                                           interleukin-3 receptor beta subunit - mouse (fragment)
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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A,Residues: 1-41 <BAS>
C,Superfamily: calreticulin
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67 YRKWKEKI 74
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-55 <YEL>
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46.2%;
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Conservative
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50.0%;
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Best Local Similarity
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Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-53 <KUR>
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B8556
B;Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A88480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:Q8YZB8, GB:BA000019, PIDN:BAB72519.1, PID:g17129906, GSPDB:G
A,Experimental source: strain PCC 7120
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                                                                                                                                                                                                                          hypothetical protein as10561 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH1876
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Pred. No. 1.9e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 41;
  Length 69;
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Pred. No. 1.8e+02;
DB 2;
2e+02;
                                          3; Mismatches
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    Score 31;
Pred. No. 2
47.7%;
50.0%;
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50.0%;
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Best Local Similarity 50.0°
                                          5; Conservative
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                                                                                   3 YRKFKNKILK 12
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54 YERFKNELEK 63
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34 WRRFNNKLI 42
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Best Local Similarity
                       Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-44 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-41 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: as10561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: 20840
    Query Match
                                          Matches
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CyAccession: E64251

RyFraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.N.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MulD:96026346; PMID:7569993
A;Accession: E64251
A;Accession: E64251
A;Actures preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-48 < TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Streptococcus pheumoniae
C; Date: 22-Oct-2001 #text_change 09-Jul-2004
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C; Accession: H98038
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
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Circlesion. B10225

Circlesion. B10226

Circlesion. B10226

Circlesion. B10226

Circlesion. B10226

Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Son, D.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Atthors: Smith, H.O.; Venter, J.C.

A;Atthors: A70100; MUID:98065943; PMID:9403685

A;Accession: B70225

A;Status: preliminary; nucleic acid sequence not shown: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P47704; GB:U39733; GB:L43967; NID:g3845054; PIDN:AAC72486.1; A;Experimental source: strain G-37 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      j. Bacteriol. 183, 5709-5717, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A,Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A,Reference number: A97872; MUID:21429245; PMID:11544234
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
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Pred. No. 2.3e+02;
2; Mismatches 4; Indels
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82724
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc Nature 406, 151-157, 200
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A85515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                             Ajaccession: C82724
Ajstatus: preliminary
Ajstolecule type: DNA
Ajstesiduse: 1-69 <SIM>
Ajstoss-references: UNIPROT:Q9PEE0; GB:AE003945; GB:AE003849; NID:g9106036; PIDN:AAFB3898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Algebraimental gource: strain 9a5c

Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al Briones, M.R.S.; Buenco, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Barbeto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
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A.Authors: Ferreira, A.J.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigre chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, B.C.; Miyaki, C.Y.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Sawasaki, A.G.R.; Santelli, R.V.; Sawasaki, A.R.B.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze A.Contents: annotation
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Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A;Title: Identification and overlapping expression of multiple unconventional myosin gene
A;Reference number: A55758; MUID: 94294418; PMID: 8022818
A;Status: 146593
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-36 < BEM>
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C'Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C'Accession: 690010
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:Q29059; GB:L29128; NID:9457338; PIDN:AAA20913.1; PID:9531144 C;Superfamily: brush border myosin heavy chain I; myosin motor domain homology
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
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Pred. No. 2.4e+02;
2: Mismatches 5; IndelB
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Pred. No. 2.9e+02;
2; Mismatches 3; Indels
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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nes 6; Conserve

    pig (fragment)

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                                   A;Cross-references: UNIPROT:050703; GB:AE000785; NID:g2689951; PIDN:AAC66041.1; PID:g268
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: P43953; GB:U32701; GB:L42023; NID:g3212182; PIDN:AAC21830.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CiSpecies: Harmophilus influenzae
CiSpecies: Harmophilus influenzae
CiDate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
CiDate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
CiAccession: G64002
R.P.; Anithor, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: G64002
A;Accession: G74002

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A;Experimental source: specific host Chlorella strain NC64A
C;Genetics: A;Note: a648L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein a648L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Accession: T18150
A;Reference number: Z18806
A;Reference number: Z18806
A;Reference number: T18150
A;Reference number: T18150
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                     Gaps
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C82724
hypothetical protein XF1088 [imported] - Xylella fastidiosa (strain 9a5c)
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G64002
hypothetical protein HI0149 - Haemophilus influenzae (strain Rd KW20)
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                                                                                                                                                                                                                           46.2%; Score 30; DB 2; Length 57; 55.6%; Pred. No. 2.5e+02;
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100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0;
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Best Local Similarity 50.0
Matches 4; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                     5; Conservative
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14 KYMNKIIKN 22
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52 YRRYKQKV 59
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A;Residues: 1-57 <KLE>
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Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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RKFKEVLIKA 26
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Best Local Similarity
Matches 5; Conserv
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T12949
hypothetical protein yotN - Bacillus subtilis phage SPBC2
C;Species: Bacillus subtilis phage SPBC2
C;Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Date: 13-Aug-1949; #69929
R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D. submitted to the EMBL Data Library, August 1997
A;Referrence number: 217583
A;Referrence number: 217583
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
Nak Res. 8, 205-213, 200
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A; Residues: 1-58 «LAZ»
A; Crossidues: 1-58 «LAZ»
B; Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Brilich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8Z0B5; GB:BA000019; PIDN:BAB77707.1; PID:g17135161; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:Q99SA4; GB:BA000018; PID:g13701956; PIDN:BAB43248.1; GSPDB:q
      C.; Sekimizu, K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein asr0183 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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                                                                                    A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUD:21311952; PMID:11418146 A;Accession: G90010 A;Azcession: G9010 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, (Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. 257, 1225-1240, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 2; Pred. No. 3.3e+02;
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A;Accession: T12949
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 6; Conserv
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Matches 5; Conserv
                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-51 <KUR>
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lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laudinois, A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mandua, S.; Maucel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Perk, S.H.; Parro, V.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekwaska, A.; Seror, A.; Muthors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekwaska, A.; Seror, T.; Winters, P.; Winters, P.; Winters, P.; Voshida, K.; Yasumoto, H.; Yasumoto, K.; Yasumoto, V.; Uchiyama, T.; Winters, P.; Winters, P.; Yoshikawa, H.; Janchin, A.; Togato, V.; Uchiyama, A.; Reference number: A65880; MulD:98044033; PMID:9384377
A, Accession: H69229
A, Status: nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Residues: 1-58 - KUN>
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Space: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69384
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250, MuID:98049343; PMID:9389475
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I publy, Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Tilla: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functil A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Reference number: A69009
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A,Experimental source: strain 168
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A;Molecule type: DNA
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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Pred. No. 3.7e+02;
2; Mismatches 4; Indels
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Pred. No. 4e+02;
3; Mismatches 2; Indels
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Rili, C.H.; Chung, D.
Proc. Natl. Acad. Sci. U.S.A. 73, 1145-1148, 1976
A;Tille: Isolation and structure of an untriakontapeptide with opiate activity from camel
A;Reference number: A01468; MUID:76176450; PMID:1063395
A;Accession: A01468
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Cispeciaes: Sispeciaes: Sisp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein SP1938 [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                              Deta-endorphin - Arabian camel
N;Contains: Met-enkephalin
C;Species: Camelus dromedarius (Arabian camel)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01468
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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          Score 29; DB 2; Leusur
Pred. No. 4.7e+02;
3; Indels
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Pred. No. 3.1e+02;
2; Mismatches 1; Indels
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C,Superfamily: corticotropin-lipotropin
C;Keywords: hormone, neuropeide, opioid peptide
F;1-5/Product: Met-enkephalin #status experimental <MEK>
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ATP synthase chain 8 - Pedinomonas minor mitochondrion
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Pred. No. 3.6e+02;
1; Mismatches 3
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                             44.6%;
50.0%;
                         Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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23 ARVKKNQNKAVK 34
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18 FKNAIIKN 25
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YRDCKNILLK
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Matches 6; Conserv
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A; Residues: 1-37 < KUR>
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A;Residues: 1-68 <KUR>
A;Cross-references: UNIPROT:Q8ZBR3; GB:AL590842; PIDN:CAC92574.1; PID:g15981271; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C'Species: Yersinia pestis
C'Species: Versinia pestis
C'Date: O'S.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C'Accession: AB0406
R'Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Geno-Tararaga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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                  A;Cross-references: UNIPROT:027489; GB:AE000905; GB:AE000666; NID:g2622541; PIDN:AAB8591
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1440
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A,Experimental source: strain 972h-; cosmid c30D11
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NyAlternate names: protein SPAC30D11.1
C.Species: Schizosaccharomyces pombe
C.Species: O6-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                        Score 29; DB 2; Length 67;
Pred. No. 4.3e+02;
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Pred. No. 4.3e+02;
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A;Introns: 1/3; 64/1
C;Superfamily: rat ribosomal protein L38
C;Keywords: cytosol; protein biosynthesis; ribosome
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                                                                                                                                                                                                                                     Best_Local Similarity 62.5
Matches 5; Conservative
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50 FKKIKNKFIE 59
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A; Accession: T38587
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13 QFLKFKNK 20
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Matches 4; Conserv
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A; Residues: 1-74 < PEA>
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A;Residues: 1-74 <PE2>
A;Residues: 1-67 <MTH>
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A; Gene: YPO3344

C; Genetics:

Query Match

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Genetics:

Gene: atp8 Genetics:

Matches

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C;Species: Bacillus stearothermophilus
C;Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Dates: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48688; S59054
C;Accession: S48688; S59054
C;Accession: S48688
C;Accession: S48688
C;Accession: S48688
C;Accession: S48688
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A; Residues: 1-60 <-HER>
R; VI slub, H: Xruft, V.; Bischof, O.; Mueller, E.C.; Wittmann-Liebold, B.
EMBO J. 14, 4578-4588, 1995
A; Title: Protein-rRNA binding features and their structural and functional implications i
A; Reference number: S59051; MUID: 96003638; PMID: 7556101
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A;Tille: Whole genome sequencing of meticillin-resistant Stanvlococcus
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A;Experimental source: strain N315
         A;Cross-references: UNIPROT:Q97JJ2; GB:AE001437; PIDN:AAK79259.1; PID:g15024217; GSPDB:Gr
A;Experimental source: Clostridium acetobutylicum ATCC824
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Jate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
Accession: H90020
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F;1-60/Product: ribosomal protein S14 #status experimental <MAT>
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                                                                                                                                                         Score 28; DB 2; Length 58;
Pred. No. 5.5e+02;
0; Mismatches 1; Indels
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Superfamily: Escherichia coli ribosomal protein S14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribosomal protein $14 - Bacillus stearothermophilus
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                                                                                                                                                               43.1%;
85.7%;
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Matches 5; Conservative
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                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserva
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A;Residues: 1-61 <KUR>
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                                                                   C;Genetics:
A;Gene: CAC1288
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H97058
ribosomal protein S21 [imported] - Clostridium acetobutylicum
ribosomal protein S21 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97058
R;Ohling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J; Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J; Batteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H97058
A;Accession: H97058
A;Accession: preliminary
A;Residues: 1-58 cKUR>
                                                         C,Accession: T11313
R,Turmel, M.; Lemieux, C.; Burger, G.; Lang, B.F.; Otis, C.; Plante, I.; Gray, M.W.
R,Dubmitted to the EMBL Data Library, December 1998
A,Description: The complete mitochondrial DNA sequences of Nephroselmis olivacea and Ped A,Reference number: 217261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30S ribosomal protein S21 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Bate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89938
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                            Cross-references: UNIPROT: Q92Y29; EMBL: AF116775; NID: 9437876; PID: 94378767; PIDN: AAD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT: Q99TS1; GB: BA000018; PID: 913701373; PIDN: BAB42667.1; GSPDB: G
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Species: mitochondrion Pedinomonas minor
Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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C;Superfamily: Escherichia coli ribosomal protein S21
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2; Mismatches 3
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Pred. No. 5.5e+02;
0; Mismatches 1
                                                                                                                                                                                                                      A,Accession: T11313
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-48 <TUR>
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Pred. No. 4.6e+02
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Best Local Similarity
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Best Local Similarity
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A; Residues: 1-58 < KUR>
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Comp. Biochem. Physiol. B 95, 45-50, 1990
A,Title: The complete amino acid sequence of a post-synaptic neurotoxin isolated from the
A,Reference number: A60518; MUID:90235556; PMID:2158871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Rosatiuse: 1.37 (KLES-
A;Cross-references: UNIPROT: 051703; GB:AE001176; GB:AE000783; NID:g2688699; PIDN:AAC67111;
A;Experimental source: strain B31
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A; Residues: 1-38 <KLE>
A; Cross-references: UNIPROT:051479; GB: AE001154; GB: AE000783; NID: 92688431; PIDN: AAC6689;
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Rills: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Rraser, C.M.; Casjens, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
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                                                                                 A,Accession: A60518
A,Molecule type: protein
A,Rolecule type: 1-74 <SHEs-
A,Cross-references: UNIPROT:P34073
A,Cross-references: UNIPROT:P34073
C,Superfamily: snake toxin
C;Keywords: disulfied bond; monomer; postsynaptic neurotoxin
P;3-21,14-42,27-31,46-57,58-63/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                              Score 28; DB 2; Length 74;
Pred. No. 7e+02;
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Pred. No. 5.4e+02;
2; Mismatches 3; Indels
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 50.0°
Matches 4; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
*Residues: 1-61 -STO>
A;Cross-references: UNIPROT:Q9CDX5; GB:AE005176; PID:g12725139; PIDN:AAK06184.1; GSPDB:G
A;Experimental source: strain IL1403
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A;Molecule type: DNA
A;Residues: 1-69 GGLA>
A;Cross-references: GB:AE002110; GB:AP222894; NID:g6899051; PIDN:AAF30503.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
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type I restriction enzyme S protein, truncated homolog UU097 [imported] - Ureaplasma ure
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82933
C;Accession: User Complete sequence of Ureaplasma urealyticum: Alternate views of a A;Accession: D82933
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N;Alternate names: post-synaptic neurotoxin
C;Species: Acanthophis antarcticus (death adder)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accesion: A60518
R;Sheumack, D.D.; Spence, I.; Tyler, M.I.; Howden, M.E.H.
   Gaps
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      Indels
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C,Superfamily: Escherichia coli ribosomal protein S14
   Mismatches
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                                                         3 YRKFK 7
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A,Gene: hsdS-2; UU097
A,Genetic code: SGC3
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C;Genetics:
A;Note: PSC450R1
C;Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprot
C;Keywords: flavoprotein; NADP; oxidoreductase
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R;Pelsischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A. Brielschmann, R.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

Science 269, 496-51
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Experimental source: strain Madrid E
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A,Residues: 1-50 <TIGR>
A,Cross-references: UNIPROT:P44258; GB:U32831; GB:L42023; NID:g1574407; PIDN:AAC23223.1;
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C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: G71716
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: G77716
A;Status: presliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-50 <AND>
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C.Species: Haemophilus influenzae
C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
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A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                            Query Match 41.5%; Score 27; DB 2; Length 50; Best Local Similarity 45.5%; Pred. No. 7.2e+02; Matches 5; Conservative 3; Mismatches 3; Indels
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A; Experimental source: cv. Greenfeast
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31 FRRIKDKELK 40
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Matches 5; Conserva
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Matches 5; Conserva
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Gene: RP080
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C.Species: Pisum sativum (garden pea)
C.Species: Pisum sativum (garden pea)
C.Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C.Accession: T06541
R.Strid, A.; Brosche, M.
R.Strid, A.; Brosche, M.
R.Strid, A.; Brosche, M.
A.Reference number: 215748
A.Accession: T06541
A.Accession: Freliminary; translated from GB/EMBL/DDBJ
A.Accession: Joseph RNA
A.Accession: A.Accession: Brosche RNA
A.Accession: Brosch RNA
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A.Accession: T06541
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A.Accession: T06441
A.Accessi
                                                                                                                                                                                                                                                                                                                                                                          acyltransferase (EC 2.3.1.-) - Photobacterium leiognathi (fragment)
C;Species: Photobacterium leiognathi
C;Species: Photobacterium leiognathi
C;Species: Photobacterium leiognathi
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: PQ0049
R;Illarionov, B.A.; Blinov, V.M.; Donchenko, A.P.; Protopopova, M.V.; Karginov, V.A.; Me Gene 86, 89-94, 1990
A;Tile: Isolation of bioluminescent functions from Photobacterium leiognathi: analysis A;Accession: PQ0049; MUID:90185252; PMID:2311938
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A;Residues: 1-47 <ILLi>
A;Crose-references: UNIPROT:P21309; GB:X08036; GB:M34564; GB:M38298; NID:g45589; PIDN:CA
C;Superfamily: acyltransferase (EC 2.3.1.-) luxD
C;Keywords: acyltransferase
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R;Huang, D.C.; Novel, M.; Novel, G.
FEMS Microbiol. Lett. 77, 101-106, 1991
A;Title: A transposon-like element on the lactose plasmid of Lactococcus lactis subsp.
A;Reference number: S1356
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A, Accession: S13571 A, Status: nucleic acid sequence not shown

A; Molecule type: DNA

A; Mobile element: insertion sequence 1076

6; Conservative 1 ARYRKFKNKILK 12 :|: || ||| 35 SROKTLKNIILK 46

Best Local Similarity

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Query Match Matches

1; Mismatches

Best Local Similarity 71.4 Matches 5; Conservative

Query Match

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Q8f2z2 leptospira
Q6h148 bacillus th
Q65x13 oryza sativ
Q63dm5 bacillus ii
Q6064 borrealia bu
Q9684 rhocrealia bu
Q9687 rhocrealia bu
Q99pi3 campylobact
Q99pi3 campylobact
Q90pi3 campylococ
Q9073 plasmodium
Q90v0 bacillus st
Q73v9 bacillus st
Q73v9 bacillus st
Q73v9 bacillus an
Q54v9 thermoanaer
Q61sv brachydanio
Q8x1c3 clostridium
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Q8x1c3 clostridium
Q8x3p thermoanaer
Q54s9 thermoanaer
Q58s413 mus sp. int
Q9ps63 gallus gaillus ce
Q4130 mus point
Q9ps63 gallus ce
Q4629 jointvillea
Q7um50 rhodopirell
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                                                                   May 16, 2005, 08:21:21; Search time 54.8017 Seconds (without alignments) 121.475 Million cell updates/sec
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Q9a016
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                     1612378 seqs, 512079187 residues
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Q54890
Q9EXLC3
Q8XLC3
Q8XLC3
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Q64529
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Q71MSO
STP1_MOUSE
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Listing first 45 summaries
                                                - protein search, using sw model
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Q6HL48
Q65WT3
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O50694
Q9G8W3
Q8CL39
Q9PP13
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Q7A7I0
Q9U7G3
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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65
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Match Length
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[1] SEQUENCE FROM N.A. STRAIN=97-27;

		(e)		E =	Leptospira ; 64;	ngth 55; Indels 0;		e) cillus.
MENTS	55 AA.			rrhagiae / Se. OI=10.1038/na R., Miao YG R., Jiang HI Cai Z., Sheng IL., Qian Z. OC., Quo X. n YM., Shi I	features of 1 sequencing." 6870E93F5 CRC	, 2,		NY; PRT; 67 AA. 1. 27, Created) 1. 27, Last sequence update) 1. 27, Last annotation update) 1. 27, Last some annotation update) 1. 28, Last some annotation update) 1. 28, Sales annotation update) 2. 3 (subsp. konkukian). 3. 4 Sales Bacillus Bacillales; Bacillus
ALIGN	PRT;	Created) Last seq Last ann	rochaetal	terohaemo 712204; D 3., Zeng 70., 9 YQ., Huang H Q., Xia	athogenic le-genome r. CB125F8	Score 4 Pred. N 2; Mism		OGHI48 PRELIMINARY; PRT; OGHI48; PRT; OGHI48; CHI48; CHI48; CHI48; COS-UUL-2004 (TrEMBLrel. 27, Last seq 05-UUL-2004 (TrEMBLrel. 27, Last ann Hypothetical protein yphs. Name-yphs; OrderedLocusNames=BT9727 Bacillus thuringiensis (subsp. konku Bacteria; Firmicutes; Bacillales; Ba
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	RESULT 1 Q8F2Z2 ID Q8F2Z	01-MP 01-MP 01-MP 01-MP 01-MP	Lepto Bacte NCBI	(1) SEQUE STRAI MEDLI Ren S Zhang Zhang Yao Z	Xu J. "Uniq inter Natur EMBL; Compl	ery Ma st Loc tches		RESULT 2 GEHL48 1D 06HL48 AC 06HL48; DT 05-JUL-; DT
	ALIGNMENTS	ALIGNMENTS 1 9P2Z2 PRELIMINARY; PRT; 55	ALIGNMENTS 1 8F2Z2 PRELIMINARY; PRT; 55 ; 8F2Z2; TYRR-2003 (TrEMBLrel. 23, Created) 1-MAR-2003 (TrEMBLrel. 23, Last sequence 1-MAR-2003 (TrEMBLrel. 23, Last sequence received to the sequence rec	ALIGNMENTS 1. 8F2Z2 PRELIMINARY; PRT; 55 AA. 8F2Z2; 1-WAR-2003 (TrEMBLrel. 23, Last sequence up. 1-MAR-2003 (TrEMBLrel. 23, Last sequence up. 1-MAR-2003 (TrEMBLrel. 23, Last annotation rderedLocusNames=LA2619; eptospira interrogans. eptospira interrogans. eptospira interrogans. egtospira interrogans. egtospira interrogans.	ALIGNMENTS 11 18F2Z2 1-MAR-2003 (TrEMBLrel. 23, Created) 1-MAR-2003 (TrEMBLrel. 23, Last sequence update) 1-MAR-2003 (TrEMBLrel. 23, Last annotation update) 1-MAR-2003 (TrEMBLrel.) 1-MAR-2003 (TrEMBRELLEL.) 1-MAR-2003 (TrEMBLRel.) 1-MAR-2003 (TrEMBREL.) 1-MAR-2	ALIGNMENTS 1. RELIMINARY; PRT; 55 AA. 8F2Z2; PRELIMINARY; PRT; 55 AA. 1-MAR-2003 (TrEMBLrel. 23, Last sequence update) 1-MAR-2003 (TrEMBLrel. 23, Last annotation update) 1-MAR-2003 (TrEMBLrel. 23, Last sequence update) 1-MAR-2003 (TrEMBLrel. 23, Last sequencing H H Yin H Y Yin H	ALIGNMENTS BFZZZ BFRELIMINARY; PRT; 55 AA. BFZZZ; 1-MAR-2003 (TrEMBLrel. 23, Last sequence update) 1-MAR-2003 (TrEMBLrel. 23, Last sequence in Leptospira. 1-MAR-2003 (TrEMBLrel. 23, Last sequence and Leptospira. 1-MAR-2003 (TrEMBLrel. 23, Last sequence and Leptospira. 1-MAR-2003 (TrEMBLrel. 23, Last sequence sequencing.", Mang Y. C. X. X. X. X. X. X. Y. X. M. H. Y. X. Mang Y. C. X. X. X. X. X. X. Y. X. M. M. X.	ALIGNMENTS 1 8F2Z2 BF2Z2; 1-MAR-2003 (TrEMBLrel. 23, Created) 1-MAR-2003 (TrEMBLrel. 23, Last sequence update) 1-MAR-2003 (TrEMBLrel. 23, Last sequences is bettersopins 2-GE-TAXID=173; 1-MAR-2003 (TrEMBLrel. 23, Last sequences is Leptospira. 1-MAR-2003 (TrEMBLrel. 23, Last sequencing. 13, March 14, March 18, March 14, March 14, March 18, March 1

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licheniformis and comparisons with closely related Bacillus species."; Genome Biol. 5:R77-R77(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 14580;
Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky I Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Bhrlich S.D., Berka R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;

Ehrenreich A., Gottschalk G.;

"The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential.";

J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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SEQUENCE 67 AA; 7608 MW; 39EB25334EF4B59C CRC64;
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OrderediocusNames=BBH39;
Borrelia burgdorferi (Lyme disease spirochete)
Plasmid 1p28-3.
                                                                                                A8D438EE2183E8E6
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Pred. No. 86;
2; Mismatches
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Pred. No. 86
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   Submitted (JUL-2004) to the EMBL, CP000001; AAU18859.1; Hypothetical protein. SEQUENCE 67 AA; 7418 MW;
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                                                                                                                                                                                                                                                                                   1 ARYRKFKNKILK 12
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Best Local Similarity
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PubMed=15383718;
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Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chen Y.-T., Cheng C.-H., Chung C.-I., Han S.-Y., Heisen S.-H.,
Heiung J.-N., Heu C.-H., Hang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.,
"Oryza sativa PAC P0615D12 genomic sequence:",
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin E., Tice H.,
"Complete genome sequence of Bacillus cereus ZK.";
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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R. Richardson P., Rubin E., Tice H.; Longmire J., Lucas S., Okinaka R. "Complete genome sequence of Bacillus thuringiensis 97-27."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, ABCH7355; ART62720.1; Complete proteome; Hypotherical protein. SEQUENCE 67 AA; 7418 MW; 30F9C43E2183E8F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
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                                                                                                                                                                                                                                                                                   56.2%; Score 36.5; 175.0%; Pred. No. 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Name=yphE; ORFNames=BTZK1389;
Bacillus cereus ZK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.4%;
                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 63.0
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             1 ARYRKFKNKILK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRY-KIKNKILK 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 YRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 WRKFRVKILKN 62
                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=288681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknow protein.
Name=P0615D12.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
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Matches
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Q65WT3
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DOI=10.1128/JB.184.16.4601-4611.2002;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Schustz D.C., Fetherston J.D., Lindler L.B., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitchead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae, Campylobacter.
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                                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 60;
Pred. No. 1.5e+02;
1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 2; Length 61;
Pred. No. 1.5e+02;
1; Mismatches 3; Indel8
                                                                                                                                                                                                        PIR; G81343; G81343.
Complete proteome; Hypothetical protein.
SEQUENCE 61 AA; 7176 MW; 4D4970AD1C1B0EF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Cj0/24.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                 SEQUENCE FROM N.A.
STRAIN-KIMS / Biovar Mediaevalis;
MEDLINE-22137863; PubMed-12142430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL139076; CAB72998.1; -.
Enterobacteriaceae, Yersinia.
NCBI_TaxID=632;
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(TrEMBLrel. 16, I
(TrEMBLrel. 24, I
                                                                                                                                                                                                                                                                                                                  52.3%;
85.7%;
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63.6%;
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Best Local Similarity 85.70,
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       5 KPKNKIL 11
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01-MAR-2001
01-JUN-2003
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Q9G887;
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ID AC
DT O02
DT O01
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                                             MEDLINE=8065943; PubMed=9403685; DOI=10.1038/37551;
MEDLINE=8065943; PubMed=9403685; DOI=10.1038/37551;
Prager C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
Artiach P., Bowman C., Garland S.A., Puji C., Cotton M.D., Horst K.,
Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP288090; AAG17734.1; -.
EMBL; AC005739; C:mitochondrion; IEA.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 2; Length 72;
Pred. No. 1.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 2; Length 34; Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
NCBI_TaxID=52970;
                                                                                                                                                                                                                                                                                                                                    Complete proteome; Hypothetical protein; Plasmid. SEQUENCE 34 AA; 4081 MW; PD687CA065B19056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AA; 8959 MW; 221456EB5D4B7179 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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                                                                                                                                                                                                                                                               Nature 390:580-586(1997).
EMBL; AE000784; AAC66012.1; -.
PIR; E70239; E70239.
                                                                                                                                                                                                                                                                                                                                                                                       53.8%;
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.0
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10 YKKIKNELIK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 YRKFKNKILK 12
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62 KKFRNKFLK 70
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Mitochondrion.
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                              SEQUENCE FROM N.A.
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 NCBI_TaxID=139;
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Q8CL39;
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RESULT 7

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RESULT 8

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protein SAS012.
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                                                                                                                                                                                                                                                                                                    1 ARYRKFKNKI 10
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                                                                   SEQUENCE FROM N.A.
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01-MAY-2000 (
01-MAY-2000 (
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Q9U7G3
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STRAIR=Muso / ATCC 700699;

STRAIR=Muso / ATCC 700699;

MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                       Gaps
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                                                                                                   Burger G., O'Kelly C.J., Gray W.M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF295546; AAG13666.1; -.
GO, GO:0005739; C:mitochondrion; IEA.
GO; CO:0007735; F:structural constituent of ribosome; IEA.
Mitochondrion; Ribosomal protein.
SEQUENCE 74 AA; 8878 MW; 4F3D3328F424C79E CRC64;
                                                                                                                                                                                                Length 74;
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Pred. No. 1.8e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                               Score 34; DB 2; Length 74;
Pred. No. 1.8e+02;
3; Mismatches 2; Indels
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PIR; D89806; D89806.
Complete protecome; Hypothetical protein.
SEQUENCE 50 AA; 5699 MW; 056461C216F9EBEA CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus (strain Mu50 / ATCC 700699)
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                            50 AA.
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                                         Eukaryota; Malawimonadidae; Malawimonas.
NCBI_TaxID=136089;
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                     Malawimonas jakobiformis
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                                                                                                                                                                                                                                             3 YRKFKNKILKS 13
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22 AKFKPFKNRI 31
 Ribosomal protein L20
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                                                                              SEQUENCE FROM N.A. STRAIN=ATCC 50310;
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=158878
                                    Mitochondrion.
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05-JUL-2004
05-JUL-2004
05-JUL-2004
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Q99WI4;
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Q7A710
ID Q7A71
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NCBI_TaxID=5833;
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Pred. No. 2e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 2; Length 50;
Pred. No. 1.8e+02;
4; Mismatches 1; Indels
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EMBL, AP001130; BAB41607.1; -.
Complete proteome.
SEQUENCE 50 AA; 5699 MW; 056461C216F9E8EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Erythrocyte membrane protein 1 SD128B (Fragment).
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Last annotation update)
Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158879;
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01-MAR-2001 (TrEMBLrel. 16, Last seque
01-MAR-2003 (TrEMBLrel. 23, Last annot
NNA polymerase beta subunit (Fragment)
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Best Local Similarity 62.5°,
Best S; Conservative
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Best Local Similarity 50...
S; Conservative
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MEDLINE-2260844; PubMed=1271629; DOI=10.1038/nature01586;

Read T.D., Peterson S.N., Tourasse N.J., Bailla L.W., Paulsen I.T.,

Read T.D., Peterson S.N., Tourasse N.J., Bailla L.W., Paulsen I.T.,

Read T.D., Peterson S.N., Tourasse N.J., Bailla L.W., Paulsen I.T.,

Read T.D., Peterson D.E., Reisen J.A., Gill S.R.,

Kolonay J.F., Beanan M.J., Dodson R.J., Brinkec L.M., Gwinn M.L.,

Beboy R.T., Madpu R., Dodson R.J., Brinkec L.M., Gwinn M.L.,

Bencon W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

A Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

A Hanna P.C., Kolsece A.-B., Fraser C.M.;

The genome sequence of Bacillus anthracis Ames and comparison to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.; Submirted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AR017028; AAP25465-1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Fed Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L., Fraser C.M.; "Bacillus anthracis comparative genomics."; submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 3.1e+02;
1; Mismatches 2; Indels
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SEQUENCE 67 AA; 7466 MW; A97F38EE2183E8F7 CRC64;
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                                                           isolate Porton;
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66.7%;
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STRAIN=Ames / isolate 0581;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                     DOI=10.1128/JB.182.21.6114-6122.2000;
Krasny L., Vacik T., Fucik V., Jonak J.;
"Cloning and characterization of the str operon and elongation factor Tu expression in Bacillus stearothermophilus.";
J. Bacteriol. 182:6114-6122(2000).
EMBL; AJ249558; CAC09925.1;
HSSP; P04050; 1150.
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PubMed=14960714; DOI=10.1093/nar/gkh258;
Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angluoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.; reveals metabolic "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXOI."; Nucleic Acids Res. 32:977-988(2004).
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                               Firmicutes; Bacillales; Bacillaceae; Geobacillus.
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Pred. No. 2.6e+02;
1; Mismatches 4; Indels
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NCBI_TaxID=1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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SEQUENCE 67 AA; 7466 MW; A97F38EE2183E8F7 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 3.1e+02;
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OrderedLocusNames=BA1528, BAS1417, GBAA1528;
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                                                                                                                                               STRAIN=CCM 2184;
MEDLINE=20485563; PubMed=11029432;
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58.3%;
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66.7%;
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Bacillus stearothermophilus
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nes 8; Conservative
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                                                                                                                   SEQUENCE FROM N.A.
                               Bacteria, Firmic
NCBI_TaxID=1422;
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Q73AY8

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Q81SW6
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AC Q81SW
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49.2%;
70.0%;
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45 RYRLEEIKNQILES 58
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                            Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                               6 KKLKNKILWS 15
                                                                                                                                                       4 RKFKNKILKS 13
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Q58545;
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Q8R998
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Diaz E., Garcia J.L.;
"Characterization of the transcription unit encoding the major pneumococcal autolysin.";
Gene 90:157-162(1990).
EMBL: M13812: AAAA5916.1; --
PIRI: JU0329; JU0329; JU0329
ERQUENCE 37 AA; 4390 MW; 555D75C4CBC3DCCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 2; Length 42;
Pred. No. 2.3e+02;
2; Mismatches 2; Indels
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Pred. No. 2.1e+02;
1; Mismatches 3; Indels
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Zhao Q., Collodi P.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF342953; AAK07664.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149239B02EA68314 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CPE1119.
OrderedLocusNames=CPE1119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Fibronectin fn2 (Fragment).
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EMBL; AP003189; BAB80825.1; -.
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Best Local Similarity
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01-JUN-2001
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Firzderald L.M., Clayton R.A., Gocayne J.D.,
Karlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klonk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
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                                                                Gaps
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MBCLIRES-192816; PubMed=11997336; DOI=10.1101/gr.219302;

Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Wang J., Yu J., Yang H.;

Genome Res. 12:689-700(2002).

BML; ABO13126; AAM24919.1; -.

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Bacteria, Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacter.
Thermoanaerobacteriaceae; Thermoanaerobacter.
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Pred. No. 3.4e+02;
Score 32; DB 2; Length 57;
Pred. No. 3.2e+02;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
OrderedLocusNames=TTE1719;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-UUL-2004 (Rel. 44, Last annotation update)
Hypothetical protein MJ1145 precursor.
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                                                                1; Mismatches
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AL-1 / DSM 2661 / ATCC 43067;
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Best Local Similarity
Matches 5; Conserv
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01-JUN-2003
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Q64130;
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1099563
AC 099866
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BRBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=NTCI 1168;
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
MELLINE=20150912; Mindall K.L., Ketley J.M., Churcher C.M., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagham D., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.,
The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacieria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Campylobacteraceae, Campylobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein MJ1145.
1DD7EF92E847F51F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
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PIR; H81379; H81379.
HAMAP; MF_00158; -; 1.
InterPro; IFR001911; Ribosomal S21.
Pfam; PF01165; Ribosomal S21; 1.
PRINTS; PR00976; RIBOSOMĀLS21.
PRODOM; PR005521; RIBOSOMĀLS21; 1.
PROSITE; PS01181; RIBOSOMĀL S21; 1.
PROSITE; PS01181; RIBOSOMĀL S21; PALSE NEG.
COMPLETE PS01181; RIBOSOMĀL S21; PALSE NEG.
SEQUENCE 70 AA; 8673 MW; A26FA2317333E0F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 1; Length
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                      TIGR; MJ1145; -.
Complete proteome; Hypothetical protein; Signal.
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Nature 403:665-668(2000).
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                                                                                                                                                                                                                                                                                                             EMBL; U67557; AAB99155.1; -. PIR; H64442; H64442.
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34 ARIKKRKEKNLKS 46
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09PID2:
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RS21_CAMJB
INCLUMENT SERVICAND
DT 16-OCT-DT 25-OCT-DDE 30S x11
ON Name-TI
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RN NELLIN
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"Sequential mutations in the interleukin-3 (IL3)/granulocyte-
"Sequential mutations in the interleukin-3 (IL3)/granulocyte-
macrophage colony-stimulating factor/IL5 receptor beta-subunit genes
are necessary for the complete conversion to growth autonomy mediated
by a truncated beta C subunit.";
Mol. Cell. Biol. 15:2402-2412(1995).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PDI-like 53 kDa polypetide (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                      Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE-95257920; PubMed-7739524;
Hannemann J., Hara T., Kawai M., Miyajima A., Ostertag W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 2; Length 74;
Pred. No. 4.2e+02;
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Score 32; DB 1; Length 70;
Pred. No. 4e+02;
                                                      Indels
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                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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"A novel 53-kDa polypeptide from chicken embryo.";
J. Biol. Chem. 266:23732-23738(1991).
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Interleukin-3 receptor beta subunit (Fragment)
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GO; GO:0004872; F:receptor activity; IEA
                                                                                                                                                                                                                                                                                                                  Created)
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MEDLINE=92084663; PubMed=1660884;
         49.2%;
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                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 01,
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                                                      5; Conservative
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                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                16 YRKFKKQV 23
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Matches 6; Conserv
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8 RYRKNSSGILK 18

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RKFKNKILKS 13

RESULT 25

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MEDLINE=92128951; PubMed=1685480; Yelick P.C., Kozak C., Kwon Y.K., Seldin M.F., Hecht N.B., Yelick P.C., Kozak C., Kwon Y.K., Seldin M.F., Hecht N.B., Yelick P.C., Kozak C., Kwon Y.K., Seldin M.F., Hecht N.B., Glemons of transition protein 1 gene contains a B1 repetitive element and is located on chromosome 1."; Genomics 11:687-694(1991).

-!- FUNCTION: In the elongating spermatids of mammals, the conversion of nucleosomal chromatin to the compact, nonnucleosomal form found in the sperm nucleus is associated with the appearance of a small set of basic chromosomal transition proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kleene K.C., Borzorgzadeh A., Flynn J.F., Yelick P.C., Hecht N.B.; "Nucleotide sequence of a cDNA clone encoding mouse transition protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88252150; PubMed=3382664; DOI=10.1016/0167-4781(88)90013-9;
                                                                                                                                                                                                                                                                                                                MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp. strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                 Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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EMBL, BX294148; CAD76067.1; -.
InterPro; FR8000977; DNA ligase.
PROSITE; PS00697; DNA LIGASE Al; UNKNOWN_1.
COMPLETE Proceeme; Hypothetical protein.
SEQUENCE 48 AA; 5454 MW; 3E11BD14AC2BE151 CRC64;
                                                                                                          Last sequence update)
Last annotation update)
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Pred. No. 4.1e+02;
3; Mismatches 1;
                                                     48 AA.
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                                                                                          Created)
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Best Local Similarity 55.6%;
                                                                                       01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                            Hypothetical protein.
OrderedLocusNames=RB9072;
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                                                     PRELIMINARY;
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7 RVRRFKSKV 15
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TISSUE=Testis;
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Matches
               RESULT 27
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PubMcall 4960714; DOI=10.1093/nar/gkh258;
Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shorses K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1.";
Nucleic Acids Res. 32:977-988(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.8e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                     Hypothetical protein.
OrderedLocusNames=BCE1494;
Bacillus cereus (strain ATCC 10987).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barker N.P., Linder H.P., Harley E.H.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBU, AF001864 AAB93964.1;
GO, GO:0009507; C:chloroplast; IEA.
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33 33 33
33 AA, 3824 MW, 21202A8E659ECE61 CRC64;
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                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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Pred. No. 2.6e+02;
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Best Local Similarity 63.6
Matches 7; Conservative
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15 KYRTLKNAMLHS 26
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                                                                                                          PRELIMINARY;
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RLFKNALLKN 18
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SEQUENCE FROM N.A.
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Matches

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Gaps

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or send an email to license@isb-sib.ch)
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Testis.
-!- SIMILARITY: Belongs to the nuclear transition protein 1 family.
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MBEDLINE=2222144; PubMed=12240834;
MARAMINE T2222144; PubMed=12240834;
MARAMINE X., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N.,
Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB 1; Length 54;
Pred. No. 4.6e+02;
3; Mismatches 2; Indels
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103 GO:0000786; C:nucleosome; ISS.
104; GO:0003677; F:DNA binding; ISS.
105; GO:000542; P:DNA binding; ISS.
105; GO:000556; P:fertilization; ISS.
105; GO:000012; P:nucleosome disassembly; ISS.
106; GO:000012; P:single strand break repair; ISS.
107; GO:000012; P:single strand break repair; ISS.
108; GO:000012; P:sperm motility; ISS.
109; GO:0001290; P:spermatid nuclear elongation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=rps0; Synonyms=rps21; OrderedLocusNames=t810038; Synechococcus elongatus (Thermosynechococcus elongatus Bacteria; Cyanobacteria; Chrococccales; Synechococcus
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54 AA; 6276 MW; 333C139969BA02CF CRC64;
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10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                  EMBL; S80846; AAB21244.2; -. EMBL; X12521; CAA31039.1; -. PIR; A40561; BGMS.
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ProDom; PD010292; TP1; 1.
PROSITE; PS00541; TP1; 1.
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Best Local Similarity
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MGD;
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DNA Res. 8:205-213(2001).
-1- SIMILARITY: Belongs to the ribosomal protein S21P family.
                                                                                                                                                                                                                                                                                                      Score 31; DB 1; Length 57; Pred. No. 4.9e+02; 2; Mismatches 2; Indels
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Pred. No. 5e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-CT-2004 (Rel. 45, Last annotation update)
310S ribosomal protein 31 C.
Name=rpsU3; Synonyms=rps21; OrderedLocusNames=asr1955;
                                                                                                                                                                                                                    Complete protecome; Ribosomal protein.
SEQUENCE 57 AA; 6910 MW; 1678D3AE92682664 CRC64;
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3B8220EB8FD23963 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 AA.
                       HAMAP; MF 00358; -; I.
InterPro; IRR01911; Ribosomal S21.
Pfam; PP01165; Ribosomal S21; I.
PRINTS; PR00976; RIBOSOMĀLS21.
ProDom; PD005521; RIBOSOMĀLS21.
TIGRFAMS; TIGR0030; S21p; I.
PROSITE; PS01181; RIBOSOMĀL S21; I.
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ProDom; PD005521; Ribosomal S21; 1.
TIGRFAMs; TICR00030; S21p; 1.
PROSITE; PS01181; RIBOSOWAL S21; 1.
Complete protecome; Ribosomal protei
SEQUENCE 58 AA; 6846 MW; 3B8220
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HAMAP; MF 00358; -; 1.
ILITE-FO-; IPR001911; Ribosomal S21.
Pfam; PF01165; Ribosomal S21; 7.
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EMBL; AP005369; BAC07591.1; -.
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17 RRFKKKIOKA 26
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Best Local Similarity
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RRFKKKIOKA 26

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09A016

RESULT 31 Q9A016

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STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ZK,
Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin E., Tice H.;
"Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=288681;
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                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Hypothetical protein.
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Q01-UTN-2003 (TFEMBLrel. 24, Created)
01-UTN-2003 (TFEMBLrel. 24, Last sequence update)
25-OCT-2004 (TFEMBLrel. 28, Last annotation update)
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                                                                                                                                                                  PRT;
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Best Local Similarity 63.6
Matches 7; Conservative
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|:| |||:
48 YQKIXNKL 55
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25-OCT-2004
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Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., McLaughlin H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
EMBL, ARC196544, AAK13881.1; -..
Complete proteome; Hypothetical protein.
SEQUENCE 59 AA; 7070 MW; 25B521C3EAC45A0C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 5.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31, DB 2; Length 59;
Pred, No. 5.1e+02;
2; Mismatches 1; Indels
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Streptococcus pyogenes (Serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JOCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein SPy0976.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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EMBL; AE010050; AAL97880.1; -.
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CHARTAGE FROM A.A.
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Matches 5; Conservative
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                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus.
NCBI_TaxID=1314;
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RESULT 32 **Q7CN57**

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STRAIN=MSBB / DSM 3109 / ATCC 43589;

MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;

Melson K.E., Clayton R.A., Gill B.R., Gwinn M.L., Dodon R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,

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"Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotoga maritima.";

Mature 399:323-329(1999).

PIRI, C72262; C72262.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUB-Cancerous endometrium;
MEDLINE=21641524; PubMed=11783137;
Meng Y., Wei L., Li C.,
Application of manA differential display technique in screening related gene of endometrial carcinoma.";
Zhonghua Fu Chan Ke Za Zhi 36:364-367(2001).
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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SEQUENCE 69 AA; 8037 MW; AE7243AA781F36CF CRC64;
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Last annotation update)
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Endometrial cancer-related protein (Fragment)
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01-MAR-2001 (TEMBLEEL 16,
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54 YERFKNELEK
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"Complete genome sequence of Bacillus thuringiensis 97-27.";

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AEQUISS, AATG2845.1;

COMPLETE PROTECOME: HYPORTETIAL

EXEQUENCE 66 AA; 7996 MW; CDCCCDBI2D88A9E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                          ., Hill K.,
Okinaka R.
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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                                                                                                                                                                Score 31; DB 2; Length 66;
Pred. No. 5.7e+02;
0; Mismatches 4; Indels
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       "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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Bacillus thuringiensis (Subsp. konkukian).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; GBAA4456; -.
Complete proteome; Hypothetical protein.
SEQUENCE 66 AA; 7992 MW; CDCCCDB1252AB9E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 63.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                              STRAIN=Sterne;
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AC 06HD71
DT 05-JU
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MEDLINE=94174282; PubMed=8128227;
Jansson A., Gillin F.D., Kagardt U., Hagblom P.;
"Coding of hemolysins within the ribosomal RNA repeat on a plasmid in Entamoeba histolytica.";
Science 263:1440-14431(1994).
EMBL; Z29969; CAA82857.1; -:
SEQUENCE 38 AA; 4824 MW; 87ECBF27E5F7B76C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
STRAIN=21074935; Pubmed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunketf G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                           As10561 protein.
OrderedLocusNames=as10561;
Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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Pred. No. 5.3e+02;
3; Mismatches 3; Indels
                                                                                                                                      Score 30; DB 2; Length 38. Pred. No. 4.9e+02;
                                                                                                                                                                         2; Indels
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SEQUENCE 41 AA; 5016 MW; 5B5145D43C65EA2F CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                                                                                                                                         3; Mismatches
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NCBI_TaxID=83334;
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                                                                                                                                      46.2%;
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50.0%;
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Best Local Similarity 50.v.
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                                                                                                                                         Query Match 46.2
Best Local Similarity 50.0
Matches 5; Conservative
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OrderedLocusNames=z0840;
                                                                                                                                                                                                        3 YRKFKNKILK 12
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13 FRRFSHSILK 22
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Q8X421;
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Q8YZB8
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        Rasko D.A., Ravel J., Osktad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Favel J., Osktad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.; "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and alarge plasmid related to Bacillus anthracis pXOI."; Nucleic Acids Res. 32:977-988 (2004).

FIRBL; BCB3171; -.
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Saccharomycetales, Saccharomycetaceae, Dekkera.
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                                                                                                                                                                                                        Score 30; DB 2; Length 31;
Pred. No. 4e+02;
3; Mismatches 1; Indels
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Pred. No. 4.8e+02;
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Roberts I.N.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y11919; CAA72677.1;
                                                                                                                                                                         75256BAC07C0EEFC CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Reverse transcriptase (Fragment).
Brettanomyces anomalus (Yeast).
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Last annotation update)
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Pfam; PF00078; RVT 1; 1.
RNA-directed DNA polymerase; Transferase.
PubMed=14960714; DOI=10.1093/nar/gkh258;
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NCBI_TaxID=5759;
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                                                                                                                                                                         31 AA; 3572 MW;
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01-NOV-1998 (TrEMBLrel.
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12 ATFQKFMNNVL 22
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21 KKYANKIVK 29
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                                                                                                                                                         Complete proteome. SEQUENCE 31 AA;
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SEQUENCE FROM N.A.
STRAIN=HMI;
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44 AA; 5246 MW; F5EE98B8FE54BCE5 CRC64;
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            Virology 314:471-487(2003).
EMBL; AJ410483; CAC85002.1; -.
Hypothetical protein.
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31 EFKNVILKT 39
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31 EFKNVILKT 39
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SEQUENCE
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MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
BIBSER A., Thurau M., Wittmann S., Fickenscher H.;
"The genome of herpesvirus saimiri C488 which is capable of transforming human T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIARE 22218177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5; Ensser A., Thurau M., Wittmann S., Fickenscher H.; The genome of herpesvirus saimiri C488 which is capable of transforming human T cells."; Virology 314:471-487(200). EMBL; AJ410485; CAC85008.1; -.. Hypothetical protein.
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Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller D., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
EMBL; ABG05247; AAGS5014.1; -.
EMBL; B85569; B85569.
Complete proteome.
SEQUENCE 44 AA; 5185 MW; 9587668BBCBD5338 CRC64;
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Pred. No. 5.7e+02;
4; Mismatches 1; Indels
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Pred. No. 5.7e+02;
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Gammaherpesvirinae; Rhadinovirus.
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
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                                                                                                                                                                                                                                                                                             Best Local Similarity 44.4
Matches 4; Conservative
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Matches 6; Conservative
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SEQUENCE FROM N.A.
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01-JUN-2003 (
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080806
1D 008080
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DT 01-JU
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DE HYPOT
OC Gamma
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SAIMI
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Q80BJ3
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STRAIN=A5147;

WEDLINE=22918177; PubMed=145540777; DOI=10.1016/S0042-6822(03)00449-5;

BRBSER A., Thurau M., Wittmann S., Fickenscher H.;

"The genome of herpesvirus saimiri C488 which is capable of transforming human T cells.";

Virology 314:471-487(2003).

EMBL; AJ410482; CAC84996.1; -.

Hypothetical protein.

NOW TER

44

84

SEQÜENCE 44 AA; 5232 MW; F5FE42D8FE54BCE5 CRC64;
                                                                                                                                            Gaps
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Pred. No. 5.7e+02;
2; Mismatches 1; Indels
Score 30; DB 2; Length 44;
Pred. No. 5.7e+02;
2; Mismatches 1; Indels
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Q80BK1; Q80BK1
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Best Local Similarity 66.7
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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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protein search, using sw model OM protein - May 16, 2005, 08:21:21; Search time 58.2931 Seconds (without alignments) 92.887 Million cell updates/sec Run on:

US-09-648-816B-8 74 Title: Perfect score:

1 KLYKKWKKKLLKLK 14 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay57470 Antimicro	Abg69894 Rabbit pl	Aay57467 Antimicro	Abg69891 Rabbit pl	Antimic	Abg69895 Rabbit pl	Abr00883 Bioactive	Abr00882 Bioactive	Aay57472 Antimicro	Abg69896 Rabbit pl	Aay57500 Antimicro		Abg69924 Rabbit pl	Rabbit	Aay57501 Antimicro	Aay57499 Antimicro	_	Abg69925 Rabbit pl	Aay57502 Antimicro	Abg69926 Rabbit pl	Antimic		Peptide	Aay57497 Antimicro	Abg69921 Rabbit pl
ID	AAY57470	ABG69894	AAY57467	ABG69891	AAY57471	ABG69895	ABR00883	ABR00882	AAY57472	ABG69896	AAY57500	AAY57465	ABG69924	ABG69889	AAY57501	AAY57499	ABG69923	ABG69925	AAY57502	ABG69926	AAY57496	ABG69920	ADL70275	AAY57497	ABG69921
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ADL70276 ADL70277 ADG69990 ABG69992 ARG69992 ARX57466 ARX57503 AXX57504 AXX57504 AXX57509	ADL90041 ADL45055 ADP43801 ADL72804 AAW65895 AAX49957 ADE34633
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ALIGNMENTS

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. (HARB-) HARBOR-UCLA RES & EDUCATION INST. Antimicrobial peptide RP-6 SEQ ID NO:8. AAY57470 standard; peptide; 14 AA 99WO-US003350. 98US-00025319. (first entry) Synthetic. Oryctolagus cuniculus. Shen AJ; WPI; 1999-527417/44. 18-FEB-1998; 17-FEB-1999; WO9942119-A1 25-FEB-2000 26-AUG-1999. Yeaman MR, AAY57470; AAY57470

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure, Page 109; 166pp; English.

activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXEXB and its derivatives selected from XZBBZBXEXB, BXZXZB, XBBXZXBX and BBXZBBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, BBXZXBX, XBBXZBB, and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, BBXZXBX, BXXBXXB, XBBXZBB, and XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X = at least one aromatic amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of The present invention describes an antimicrobial peptide (AP) for direct

been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, reteaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid core sequence (derived from 150 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance, potentiate or restore efficacy of functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rabbit platelet microbicidal protein, PMP-2, based peptide #6.
                                                                                                                         100.0%; Score 74; DB 2; Length 14; 100.0%; Pred. No. 0.0018; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                      ABG69894 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple antibiotic resistance
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                                                                                                                                                                                                                                         1 KLYKKWKKKLLKLK 14
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                                                                                                                                             Local Similarity 100.
nes 14; Conservative
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                                                                                   Sequence 14 AA;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXENSB and its derivatives selected from XZBBZBXENSB, BXZXZB, XBBXZXBB and its derivatives selected from the group consisting of XBBXBBX, XBBXXENS, XBBXZXBB, and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXENSB, BXXBBXB, ABBXZBBX; and (b) a separated and acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal confections. The peptides leffect cellular disruption and rapid apoptosis of microbial cells. ANSTAGS to AANSTAST represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                  ö
                                                                                                                                                                    Length 14;
                                                                                                                                                                                                 0; Indels
                                                                                                                                                                    100.0%; Score 74; DB 5; 100.0%; Pred. No. 0.0018;
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide RP-3 SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 108; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                      AAY57467 standard; peptide; 14
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                                                                                                                                                                                                                                                   1 KLYKKWKKKLLKLK 14
                                                                                                                                                                                                                               1 KLYKKWKKKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus.
                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                       Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                       AAY57467;
                                                                                                                                                                                                                                                                                                             RESULT 3
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The invention trainers to an antimutional peptide comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,

truncations, extensions, combinations, fusions and their derivatives. The
possible structures are fully described in the specification. Also

cricleded are (1) an antimicrobial peptide composition for direct activity

or for potentiating antimicrobial agents active against organisms such as
bacteria and fungi comprising a peptide of 13-74 containing an amino acid

core sequence selected from truncations of the peptides described above,
and retromers, extensions, combinations and fungion and activity of
antimicrobial peptides for potentiating antimicrobial agents,
antimicrobial peptides are useful as individual antimicrobial agents,
cantimicrobial peptides are useful as individual antimicrobial agents

cantimicrobial peptides are useful as individual antimicrobial agents,
conventional antimicrobials, agents that enhance the antimicrobial

conventions of leukocytes, as disinfectants or preservatives for use in

conventions of leukocytes, as disinfectants or preservatives for use in

consequence and cosmetics and as agents to improve efficiency of foods and cosmetics and as agents to improve efficiency of molecular

conventions of leukocytes, as disinfectants or preservatives for use in

conventions of leukocytes, as disinfectants or preservatives for use in

considered to have undesirable toxicity, immunogenicity and short

considered to have undesirable toxicity, immunogenicity and short

convention and ural antimicrobial peptides that have generally

convention and retains pathogens exhibiting multiple antibiotic

cresistance. They exhibit lower inherent mammalian cell toxicities and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial infection, fungal infection, fungicide, disinfectant,
preservative; foods, cosmetic, multiple antibiotic resistance; rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an antimicrobial peptide composition for use
                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabbit platelet microbicidal protein, PMP-2, based peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
   Length 14;
                                                                         1; Indels
DB 2;
0.5;
                                                                     2; Mismatches
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Score 56;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                        ABG69891 standard; peptide; 14 AA.
75.7%;
78.6%;
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                                                                                                                                               1 KLYKKWKKKLLKLK 14
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                                                                         11; Conservative
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                                  Local Similarity
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                   Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                   75.7%; Score 56; DB 5; Length 14; 78.6%; Pred. No. 0.5;
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                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                              Antimicrobial peptide RP-7 SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 110; 166pp; English.
                                                                                                                                                                                            AAY57471 standard; peptide; 13 AA.
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                                                                                                               1 KLYKKWKKKLLKLK 14
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|KLYRKFKNKLLKLK 14
                                                                                                                                                                                                                                       (first entry)
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                                                                                          11; Conservative
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Matches 10; Conserv
                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 AA;
                                             Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                    Query Match
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The invention features to an antimatical peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from peptide and peptide). Also and peptides composition, and extoners, truncations, extensions, combinations, funions and their derivatives. The possible structures are fully described in the specification. Also concluded are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungi. The entimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, agents useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular conventional antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic creatstance. They exhibit lower inherent mammallan cell toxicities and companies of toxicity, immunogenicity, and schotterial and companies of toxicity, immunogenicity, and schotterial and companies of toxicity, immunogenicity, and schotterial and companies of coxicity, immunogenicity, and schotterial and companies of coxicity, immunogenicity, and schotterial or resistence or preserve 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                 Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
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                                                                                                                                   ABG69895 standard; peptide; 13 AA.
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(HARB-) HARBOR-UCLA RES
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Synthetic.
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Sequence 13 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated peptide for treating cancer, cystic fibrosis, wounds or acne, inhibiting growth of microbial cells, or promoting proliferation of cells, comprises phenylalanine, leucine, alanine or lysine residues.
                                                                                                                                                                                                                                                        Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis; acne; attimicrobial; human fibroblast; human lymphocyte; wound healing; bioactive.
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DB 5; Length 13;
0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                             1; Indels
                                                                                                                                                                                                                                           Bioactive synthetic peptide Modelin-1-CO2H.
                             0, Mismatches
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Score 55;
Pred. No.
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                                                                                                                                                        ABR00883 standard; peptide; 16 AA.
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28-MAR-2001; 2001US-0279505P.
74.3%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX BIOMEDIX INC.
                                                                                                                                                                                                               (first entry)
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                           10; Conservative
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                                                         2 LYKKWKKKLLK
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             Synthetic.
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Matches
                           Matches
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organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXXB and its derivatives selected from XZBBZBXXBX. BXZXZBX XBBXXZBXB and its derivatives selected from XZBBZBXXBX BXZXBX BXXZXBX XBBXXBBX and BBXZBBXZ; and (b) as second peptide template XBBXXXBX XBXXBXXB and BBXZBBXZ; and (b) XZBZXBBXXZBBX; where B = at least one positively charged amino acid; and where B, X and Z may be separated by one or more other amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal netrophials. The peptides overall effect cellular disruption and rapid appoptosis of microbial cells. AAY57463 to AAX57557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                    Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rabbit platelet microbicidal protein, PMP-2, based peptide #8.
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Pred. No. 3;
0; Mismatches 1; Indels
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                                                                                                                                                                                                          (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 111; 166pp; English.
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                                                                                                                                                                   98US-00025319.
                                                                                                                                                                                                                                                                                                                                                          against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLYKKWKKKL 10
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Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus.
                                                                                                                                                                                                                                                   (eaman MR, Shen AJ
                                                                                                                                                                                                                                                                                             WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
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                                         WO9942119-A1
                                                                                                                       17-FEB-1999;
                                                                                  26-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG6989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel isolated peptide which is 5-23 amino acids in length, and comprising phenylalanine, leucine, alanine or lysine residues, or contains at least 50 % of the residues. The peptides of the invention have antibacterial, fungicide, cytostatic, and vulnerary activity. The peptides are useful in treating cancer, cystic fibrosis or and/or proliferation of human fibroblasts and lymphocytes, promoting we stimulation and/or proliferation of human fibroblasts and lymphocytes, promoting wound healing, and in enhancing the activity of a therapeutic agent. The sequences shown in ABR00759-ABR00923 represent the bioactive peptides of
                                                                                                      Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis; acne; antimicrobial; human fibroblast; human lymphocyte; wound healing; bioactive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated peptide for treating cancer, cystic fibrosis, wounds or acne, inhibiting growth of microbial cells, or promoting proliferation of cells, comprises phenylalanine, leucine, alanine or lysine residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial, metapeptide, PMP-2; platelet microbicidal protein, antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 6; Length 17; Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                             /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptide RP-8 SEQ ID NO:10.
                                                                                  Bioactive synthetic peptide Modelin-1.
                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 8; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY57472 standard; peptide; 18 AA
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76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2002; 2002WO-US009534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2001; 2001US-00820053
28-MAR-2001; 2001US-0279505P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX BIOMEDIX INC.
                                       03-APR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-221247/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                      WO200279408-A2
                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention
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                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2002.
                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
ABR00882;
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Matches

Š 셤 RESULT 9 AAY57472

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99WO-US003350.
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LYKKFKKKLLK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus.
                                                                                                                                                                                         Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                           WPI; 1999-527417/44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                           17-FEB-1999;
                                                                                18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
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  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fundi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,

truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also concluded are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial apents active against organisms such as bacteria and fundi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fundion; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents.

Ceres separations are thance, potentiate or restore efficiacy of antimicrobial peptides are useful as individual antimicrobial agents.

Conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in fooder and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in the loop techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic or resistence. They exhibit lower inherent mammalian cell toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                antimicrobial peptide composition for the prevention and treatment of setions caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                           to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial, metapeptide, PMP-2; platelet microbicidal protein, antibiotic, infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                    (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                   Disclosure; Page 130; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57500 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                  multiple antibiotic resistance.
25-AUG-2000; 2000US-00648816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.9%;
90.0%;
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                                                                                                         Shen AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLYKKWKNKL
                                                                                                                                                           WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
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                                                                                                         Yeaman MR,
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Matches

ઠ g RESULT 11

26-AUG-1999.

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZENENE and its derivatives selected from XZBENENENE, BXZXEB, XBENZXEBS and its derivatives a second peptide template XBEXX BENZXEBS and their derivatives selected from the group consisting of XBBXEBS, BXZASEB, BXZASEB, and XBBZXXBENZYEBES, where B = at least one positively charged amino acid; X = at least one aromatic amino acid; and where B, X and Z amay be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAX57557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                    Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                             HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial peptide RP-1 SEQ ID NO:3.
                                                                                                                                                                                                                                                               Disclosure, Page 58; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY57465 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.6%;
98US-00025319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 67.6
Best Local Similarity 90.9
Matches 10; Conservative
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24-AUG-2001; 2001WO-US041877 21-OCT-2002 (first entry) ABG69924; RESULT 13 ABG69924 ઠે 셤

peptides for potentiating antimicrobial agents active against bacteria and fungi.

Claim 17; Page 106; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting eslected from XEBERMENE, MEXEXTSHE, KEBEXTSHER and BEXEBEX; and (b) a second peptide template XEBERMENE, MEXEXTSHE, ABEXERMEN, THE SECOND CONSISTING A SECOND CONSISTING A SECOND CONSISTING A SERVENCE AND ACCOUNTY ACCO

Sequence 18 AA;

Score 50; DB 2; Length 18; Pred. No. 4.1; 1; Mismatches 0; Indels Best Local Similarity 90.9 Matches 10, Conservative 2 LYKKWKKKLLK 12 2 LYKKFKKKLLK 12 Query Match

ABG69924 standard; peptide; 18 AA.

Rabbit platelet microbicidal protein, PMP-2, based peptide #36.

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.

Oryctolagus cuniculus Synthetic.

WO200255554-A2

18-JUL-2002.

25-AUG-2000; 2000US-00648816

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 2002-590659/63.

New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance

Example; Page 72; 221pp; English

The invention relates to an antimicrobial peptide composition for use

against organisms such as bacteria and fungi comprising a peptide of 5150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino sextensions, combinations and their derivatives. The
151 possible structures are fully described in the specification. Also
152 core included are (1) an antimicrobial agents active against organisms such as
153 core sequence selected from truncations of the peptides described above,
154 core sequence selected from truncations and fulsions; and (2)
155 antimicrobial peptides for potentiating antimicrobial activity of
156 antimicrobial peptides are useful as individual antimicrobial agents
157 conventional antimicrobials, agents that enhance the antimicrobial agents
158 conventional antimicrobials, agents that enhance the antimicrobial
158 conventional antimicrobials, agents to improve efficiency of molecular
159 techniques. Antimicrobial peptides of prior art have generally
158 considered to have undesirable toxicity, immunogenicity and short
159 considered to bave undesirable toxicity, immunogenicity and short
159 controm of the partial antimicrobial peptides of the present invention
150 considered to bave undesirable toxicity, immunogenicity and short
150 controm problems of toxicity, immunogenicity, and short considered problems of toxicity, immunogenicity, and short considered problems of toxicity, immunogenicity, and short considered problems of toxicity immunogenicity, and short considered problems of toxicity immunogenicity, and short considered problems of toxicity immunogenicity, and short in the peptides of farming and and antimicrobial antimicro of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

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Sequence 18 AA;

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Gaps

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Gaps ö 67.6%; Score 50; DB 5; Length 18; 90.9%; Pred. No. 4.1; Indels ö 1; Mismatches 90.08; 10, Conservative Query Match Best Local Similarity Best Loca Matches

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RESULT 14 ABG69889

ABG69889 standard; peptide; 18 AA.

ABG69889;

21-OCT-2002 (first entry)

Rabbit platelet microbicidal protein, PMP-2, based peptide #1

Antimicrobial, platelet microbiocidal protein; PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant; preservative, foods, cosmetic, multiple antibiotic resistance, rabbit.

Oryctolagus cuniculus.

WO200255554-A2

18-JUL-2002.

24-AUG-2001; 2001WO-US041877

25-AUG-2000; 2000US-00648816

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR,

WPI; 2002-590659/63.

New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

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against bacteria and fungi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                              distriction relaters to an antimitational peptide comparishing and the internation for large and the peptide comparishing and the peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retroacers,
truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also considered are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial agents, combinations and funsions; and (2) antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial for the functions of leukocytes, as disinfectants or preservatives for use in those and cosmetics and as agents to improve efficiency of conventions of leukocytes, as disinfectants or preservatives for use in those and cosmetics and as agents to improve efficiency of conventions and endeal and as a second or preservative for use in those phen conventions are not as agents to improve efficiency of biology techniques. Antimicrobial peptides of prior art have generally been conventions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                     The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Claim 24; Page 71; 221pp; English
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2 LYKKFKKGLLK 12
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Antimicrobial peptides for potentiating antimicrobial agents active

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                                                              activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBAZKABB and its derivatives selected from XZBBZBXBKB, BXZXXB, XBBXZXBBX and BBXZBBXZ; and (b) as second peptide template XBBXXXBXX XBBXXBBX and BBXZBBXZ; and (b) group consisting of XBBXBBX, RBXXBXXB, XBBXXXBB, and ABBZXXBBXXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophials. The peptides overall effect callular disruption and rapid appotests of microbial cells. ANY57463 to AAY57557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBARNENE and its derivatives selected from XZBABSKEX, BAZZAB, XBAZZABNZ and BBXZBBXZ; and (b)
                                               invention describes an antimicrobial peptide (AP) for direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.6%; Score 50; DB 2; Length 19; 90.9%; Pred. No. 4.3; 1ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         used in the exemplification of the present invention
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Disclosure; Page 59; 166pp; English.
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 AA;
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a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and XBBZXXBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid, Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
                                                                                                                                                                                                                                                             neutrophile. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences used in the exemplification of the present invention
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ABG69923
XX ABG69
XX ABG69
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antimicrobial peptides are useful as individual antimicrobial agents,

specifically against bacteria and fungi, agents in combination with other
artimicrobials, agents that enhance, potentiate or restore efficacy of
conventional antimicrobials, agents that enhance the antimicrobial

functions of leukocytes, as disinfectants or preservatives for use in

cods and comedites and as agents to improve efficiency of molecular

biology techniques. Antimicrobial peptides of prior art have generally

been considered to have undesirable toxicity, immunogenicity and short

considered to have undesirable toxicity, immunogenicity and short

are based upon natural antimicrobial peptides that have potent and broad

spectrum activity against pathogens exhibiting multiple antibiotic

cresistance. They exhibit lower inherent mammalian cell toxicities and

overcome problems of toxicity, immunogenicity, and shortness of durantion

of effectiveness due to biodegradation, retaining activity in plasma and

serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabbit platelet microbicidal protein, PMP-2, based peptide #37.
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Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                       67.6%;
90.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG69925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 18
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        8X33333333333333333
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a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXBBB, and SEBZXBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7463 to AAYS7557 represent sequences used in the exemplification of the present invention

88666666666888

Sequence 20 AA;

bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and artimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of leukocytes against bacteria as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agants that enhance the antimicrobial agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular bloodsy techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic cresistants and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of sourcent problems expended antimic Gaps Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. ö 67.6%; Score 50; DB 5; Length 19; 90.9%; Pred. No. 4.3; 0; Indels Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40. 1; Mismatches AAY57502 standard; peptide; 20 AA (first entry) Local Similarity 90.9 2 LYKKWKKKLLK 12 2 LYKKFKKKLLK 12 Oryctolagus cuniculus. Sequence 19 AA; WO9942119-A1 25-FEB-2000 Synthetic. AAY57502; Query Match Matches RESULT 19 ઠે 8888888888888888888888888888888 셤

The invention relates to an antimicrobial peptide composition for use (HARB-) HARBOR-UCLA RES & EDUCATION INST. Example; Page 72; 221pp; English. 25-AUG-2000; 2000US-00648816. Yeaman MR, Shen AJ; WPI; 2002-590659/63.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXB, BXZXZB, XBBXZXBBX and BBXZBBXZ; and (b)

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure; Page 59; 166pp; English.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Shen AJ;

Yeaman MR,

WPI; 1999-527417/44.

99WO-US003350 98US-00025319

17-FEB-1999; 18-FEB-1998;

26-AUG-1999.

ö against organisms such as bacteria and fungi comprising a peptide of 5150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino sextensions, combinations, fusions and their derivatives. The
150 possible structures are fully described in the specification. Also
150 included are (1) an antimicrobial peptide composition for direct activity
151 or potentiating antimicrobial agents acitive against organisms such as
152 bacteria and fungi comprising a peptide of 13-74 containing an amino acid
153 core sequence selected from truncations of the peptides described above,
154 antimicrobial peptides for potentiating antimicrobial activity of
155 antimicrobial peptides for potentiating antimicrobial activity of
156 leukocytes against organisms such as bacteria and fungi. The New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance. Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungiçide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; Gaps ; 0 Rabbit platelet microbicidal protein, PMP-2, based peptide #38. Score 50; DB 2; Length 20; Pred. No. 4.5; 1; Mismatches 0; Indels ABG69926 standard; peptide; 20 AA. 67.6%; 24-AUG-2001; 2001WO-US041877. (first entry) Local Similarity 90.9 nes 10; Conservative 2 LYKKWKKKLLK 12 3 LYKKFKKKLLK 13 Oryctolagus cuniculus. mutant; mutein. WO200255554-A2. 21-OCT-2002 18-JUL-2002 Synthetic. ABG69926; Query Match Matches RESULT 20 ABG69921 엄 ઠે

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specifically against bacteria and fungi, agents in combination with other attimicrobial against bacteria and fungi, agents in combination with other artimicrobials, agents that enhance bestore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and comercies and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short care based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of durantion of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBENEXEB and its derivatives selected from XZBEZEBEXEXB, BXZXZE, XBEXZEBEX and BEXZBEXZ; and (b) a second peptide template XBEXX and their derivatives selected from the group consisting of XBEXBEX XBEXXEBS, BXZEXEB, and XBEXXEBX; where B = at least one positively charged amino acid; X = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 5; Length 20;
Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY57496 standard; peptide; 25 AA.
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90.98;
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.6
Best Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LYKKWKKKLLK 12
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                                                                                                                                                                                                                                                                                                                                           Sequence 20 AA;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid corre sequence (derived from 150 amino acids containing a 7-13 amino acid corre sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also concluded are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents.

Corresponded are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial control foods and cosmetics and as disinfectants or preservatives for use in foods and cosmetics and a gents that to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally
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amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7463 to AAXS7557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection; fungicide, disinfectant; preservative, foods, cosmetic, multiple antibiotic resistance, rabbit.
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rabbit platelet microbicidal protein, PMP-2, based peptide #32.
                                                                                                                                                                      DB 2; Length 25;
                                                                                                                                                                                                              0; Indels
                                                                                                                                                                    Score 50; DB 2;
Pred. No. 5.5;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      ABG69920 standard; peptide; 25 AA.
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                                                                                                                                                                                                              1;
                                                                                                                                                                      67.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-2001; 2001WO-US041877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                       2 LYKKWKKKLLK 12
                                                                                                                                                                                                                                                                               2 LYKKFKKKLLK 12
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                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                               Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200255554-A2
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ID ABG6
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been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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Sequence 25 AA;

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                     Gaps
                   ö
Length 25;
                   0; Indels
Score 50; DB 5;
Pred. No. 5.5;
                     Mismatches
 67.68;
                     10; Conservative
Query Match
Best Local Similarity
                     Matches
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2 LYKKWKKKLLK 12

|||||:|||||| . LYKKFKKKLLK 12

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ADL70275 standard; peptide; 33 AA. ADL70275;

20-MAY-2004 (first entry)

Peptide antibiotide PT-1.

Protide; antibiotide; antimicrobial; interleukin-8; Staphylococcus; infection.

Synthetic.

15. .16
/note= "Cleaved by V8 protease" Location/Qualifiers Cleavage-site

WO2004017985-A1

04-MAR-2004.

20-AUG-2003; 2003WO-US026405

20-AUG-2002; 2002US-00225562

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Brass EP; Yount NY, Edwards JE, Yeaman MR,

WPI; 2004-226740/21

New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition

Claim 1; SEQ ID NO 1; 103pp; English.

The present sequence is that of Protide-1 (PT-1), a peptide antibiotide with distinct effector and activator domains. PT-1 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for staphylococcus VB protease. PT-1 was designed to be cleaved into 2 distinct effectors in the presence of VB protease. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of VB protease produced by Staphylococcus aureus. Thus, PT-1 was synthesised by solidal activity in the context of infections due to staphylococcal cells elaborating the virulence factor VB protease. PT-1 was synthesised by solid-phase synthesis. It is an example of context-activated procides of the invention that have 2 or more effectors with individual distinct biological functions and one or ADIJO2755

ID ADIJO27575

XXX ADIJO200-1XXX
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more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad
                                                                                                                                             Gaps
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0
                                                                                                              Length 33
                                                                                                                                           0; Indels
                                                                                                              DB 8;
                                                                                                            Score 50; DB 8
Pred. No. 7.1;
1; Mismatches
                                                 range of pathological conditions.
                                                                                                              67.6%;
                                                                                                                                              10; Conservative
                                                                                                                                                                          2 LYKKWKKKLLK 12
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17 LYKKFKKKLLK 27
                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                Sequence 33 AA;
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RESULT 24 AAY5749

AAY57497 standard; peptide; 35 AA.

AAY57497;

(first entry) 25-FEB-2000

Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

Oryctolagus cuniculus. Synthetic

WO9942119-A1

26-AUG-1999

99WO-US003350 17-FEB-1999; (HARB-) HARBOR-UCLA RES & EDUCATION INST.

Teaman MR, Shen AJ;

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi

Disclosure; Page 126; 166pp; English

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against conganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZEXEBE and its derivatives selected from XZBEZEREBE BEZZEREBE BEZZEREBE AND BEZZEREBE A neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences apoptogis of microbial cells. AAY57463 to AAY57557 reused in the exemplification of the present invention

Sequence 35 AA;

ö Gaps ö 67.6%; Score 50; DB 2; Length 35; 90.9%; Pred. No. 7.5; ive 1; Mismatches 0; Indels Best Local Similarity 90.9 Matches 10; Conservative Query Match

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-

(150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids composition), and retromers, truncations, extensions, combinations, funcions and their derivatives. The possible structures are fully described in the specification. Also or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising, a peptide of 13-74 containing an amino acid antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial against bacteria and fungi, agents in combination with other specifically against bacteria and fungi, agents in combination with other conventional antimicrobials, agents that enhance the antimicrobial activity of functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular conventional antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic or esistence. They exhibit lower inherent mammalian cell toxicity and overcome problems of toxicity, immunogenicity, and schotterial and companient or resistence from pathogens are abbit pymp based antimicrobial peptide or esistence is a rabbit pymp based antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide composition for the prevention and treatment
by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                     Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                             Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
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                                                                                                                                                         ABG69921 standard; peptide; 35 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               multiple antibiotic resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-AUG-2000; 2000US-00648816
                                                                                                                                                                                                                                              21-OCT-2002 (first entry)
                       2 LYKKFKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antimicrobial per
ections caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-590659/63
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The present sequence is that of Protide-2 (PT-2), a peptide antibiotide with distinct effector and activator domains. PT-2 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (Interleukin-8 domain) and an activator site specific contextase, a complement fixing protease. PT-2 is cleaved into 2 for C3 convertase, in the presence of C3 convertase. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of C3 convertase. Thus, PT-2 was designed to exert optimal antimicrobial activity in the complement pathways that make up the complement system, which is part of the innate immune response to antigen exposure. PT-2 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                 Gaps
                                 ö
 Length 35;
                                 Indels
                                                                                                                                                                                                                                                                                                           Protide; antibiotide; antimicrobial; interleukin-8.
                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Cleaved by C3 convertage"
Score 50; DB 5;
Pred. No. 7.5;
1; Mismatches C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 16. .17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edwards JE,
                                                                                                                                                                             ADL70276 standard; peptide; 36 AA.
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   67.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2002; 2002US-00225562
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                           Peptide antibiotide PT-2.
                                 Conservative
                                                                 2 LYKKWKKKLLK 12
                                                                                               2 LYKKFKKKLLK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-226740/21.
                  Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004017985-A1
                                                                                                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeaman MR,
                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 condition.
                                                                                                                                                                                                             ADL70276;
   Query Match
                  Best Loc
Matches
                                                                                                                                              RESULT 26
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Gaps ö

Score 50; DB 8; Length 36; Pred. No. 7.7; 0; Indels

67.6**%**; 90.9**%**;

Query Match Best Local Similarity 90.9 Matches 10; Conservative

2 LYKKWKKKLLK 12

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range of pathological conditions

Sequence 36 AA;

Protide; antibiotide; antimicrobial; interleukin-8; cytostatic.

/note= "Cleaved by MMP-9"

WO2004017985-A1.

20-AUG-2003; 2003WO-US026405. 20-AUG-2002; 2002US-00225562

18. .19
/note= "Cleaved by thrombin"

Location/Qualifiers

Location/Qualifiers 17. .18

Cleavage-site

Synthetic.

ADL70278 standard; peptide; 39 AA.

(first entry)

20-MAY-2004

ADL70278;

Peptide antibiotide PT-4.

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New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                   Protide; antibiotide; antimicrobial; interleukin-8.
                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                      Claim 1, SEQ ID NO 3, 103pp; English.
                                          ADL70277 standard; peptide; 37 AA.
                                                                                                                                                                                      20-AUG-2003; 2003WO-US026405
                                                                                                                                                                                                   20-AUG-2002; 2002US-00225562.
                                                                       20-MAY-2004 (first entry)
                                                                                     Peptide antibiotide PT-3.
|||||:||||||
LYKKFKKKLLK 30
                                                                                                                                                                                                                               Yount NY,
                                                                                                                                                                                                                                            WPI; 2004-226740/21
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37 AA;
                                                                                                                                                          WO2004017985-A1
                                                                                                                                     Cleavage-site
                                                                                                                                                                        04-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                   conditions
                                                                                                                                                                                                                               Yeaman MR,
                                                                                                                 Synthetic
                                                         ADL70277;
        20
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Brass EP;

Edwards JE,

The present sequence is that of Protide-3 (PT-3), a peptide antibiotide with distinct effector and activator domains. PT-3 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (RP-1), and an activator site specific for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors in the presence of thrombin. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of thrombin, but equivalent to or exceeding that of RP-1 in the presence of thrombin. Thus, PT-3 exerts optimal antimicrobial activity in the context of thrombin as would be present in the setting of vascular injury or infection. PT-3 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological ö Gaps .; 0 Score 50; DB 8; Length 37; Pred. No. 7.9; 1; Mismatches 0; Indels 67.68; 186.06 Best Local Similarity 90.8 Matches 10; Conservative Query Match

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                                             22 LYKKFKKKLLK 32
                                    2 LYKKWKKKLLK 12
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RESULT 28 ADL70278

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The present sequence is that of Protide-4 (PT-4), a peptide antibiotide with distinct effector and activator domains. PT-4 concains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like antimicrobial peptide effector (Interleukin-8 domain) and an activator site specific for matrix metalloproteinase MMP-9, which is produced to dissolve the tissue in front of the growing blood vessel tip to allow for its continued tissue invasion. PT-4 was designed to be cleaved into 2 distinct effectors in the presence of MMP-9. In particular, PT-4 exerts antimeoplastic and/or antimicrobial activity less than that of RP-1 in the presence of MMP-9, but equivalent to or exceeding that of RP-1 in the presence of MMP-9, the context of new blood vessel formation. PT-4 exerts of an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one cor more effectors with individual distinct biological functions and one cor more corresponding activator sites that can each initiate or amplify the protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50; DB 8; Length 39;
Pred. No. 8.3;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Brass EP
                                                                                                                                                                                                                                                                                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Yeaman MR, Yount NY, Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG69990 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 90.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LYKKWKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-226740/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG69990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ABG69990
BXXXE
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acide core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents.

CC antimicrobial peptides are useful as individual antimicrobial agents (antimicrobial peptides are useful as individual antimicrobial activity of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short or are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic considered to have undesirable toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, relationing activity in plasma and commander or each of effectiveness due to biodegradation, retaining activity in plasma and commanderics.

CC enterstance. They exhibit lower inherent mammallan cell toxicity, in plasma and contributed to biodegradation, retaining activity in plasma and commanderics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                     Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                       Rabbit platelet microbicidal protein, PMP-2, based peptide #102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 67; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2001; 2001WO-US041877
                                                                                                                                                                                                                                                                                                                                                                                                                      25-AUG-2000; 2000US-00648816
                                                                                                                                                                                               Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-590659/63.
                                                                                                                                               mutant; mutein.
                                                                                                                                                                                                                                                                       WO200255554-A2.
                                                                                                                                                                                                                                                                                                                     18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeaman MR,
                                                                                                                                                                                                                         Synthetic
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ö Score 50; DB 5; Length 40; Pred. No. 8.5; 1; Mismatches 0; Indels 67.6%; 90.9%; 10; Conservative 2 LYKKWKKKLLK 12 Query Match Best Local Similarity Sequence 40 AA; Matches

Gaps

2 LYKKFKKKLLK 12

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RESULT 30 ABG69992

Rabbit platelet microbicidal protein, PMP-2, based peptide #104. ABG69992 standard; peptide; 40 AA. (first entry) 21-OCT-2002 ABG69992;

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;

Oryctolagus cuniculus. mutant; mutein.

Synthetic.

WO200255554-A2.

18-JUL-2002.

24-AUG-2001; 2001WO-US041877.

25-AUG-2000; 2000US-00648816.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 2002-590659/63.

å New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

Example; Page 67; 221pp; English

The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-10 amino acid core sequence (derived from 150 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and retromers. The protein structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial antimicrobials, agents that enhance the antimicrobial for and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular belongy techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides exhibiting multiple antibicitic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

ö 67.6%; Score 50; DB 5; Length 40; 90.9%; Pred. No. 8.5; 1, Mismatches 0; Indels Local Similarity 90.9 nes 10; Conservative Query Match Matches

Sequence 40 AA;

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Gaps

2 LYKKWKKKLLK 12 <u>..</u>

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2 LYKKFKKKLLK 12

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against occanishms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBBX and its derivatives selected from the group consisting a second peptide template XZBZXBXBX XBBXXBBX and BBXZBBXZ; and (b) a second peptide template XBBXXXBX, XBBXXBBX, ABBXZXBBX; and (b) group consisting of XBBXBBX, and their derivatives selected from the group consisting of XBBXBBX, BXXXBXB, XBBXXBB, and XBBZXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one anomatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.2%; Score 46; DB 2; Length 13; 90.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                         Antimicrobial peptide RP-2 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 107; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69890 standard; peptide; 13 AA.
                                                                         AAY57466 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00025319
                                                                                                                                                                                                                      25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 YKKWKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||:||||||
3 YKKFKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeaman MR, Shen AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6-AUG-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                AAY57466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG69890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 32
ABG69890
ID ABG69
XX
AC ABG69
XX
DT 21-OC
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AAY57466
AAY57466
AAY57466
AAY57466
AAY57466
AAY57AA
AAY57466
AAY57AA
AAY57AB

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide corts sequence (derived from 150 amino acide containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbioidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial activity of attimicrobial peptides are useful as individual antimicrobial agents or specifically against pacteria and fungi, agents in combination with other antimicrobial peptides are useful as individual antimicrobial agents that enhance the antimicrobial conventional antimicrobials, agents to improve efficiency of conventional antimicrobials, agents to improve efficiency of functions of leukocytes, as disinfectants or preservatives for use in foods and commercis and as agents to improve efficiency of conventional antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic creatstance. They exhibit lower inherent mammalian cell toxicits and and concerned problems of toxicity, immunogenicity, and schotness of defectiveness defences a rabbit pMP based antimicrobial peptides or the present sequence is a rabbit pMP based antimicrobial peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting
                                                               Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                    Rabbit platelet microbicidal protein, PMP-2, based peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 128; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                              24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                              25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                            Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-590659/63
                                                                                                                                              mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13 AA;
                                                                                                                                                                                                                                                                   WO200255554-A2.
                                                                                                                                                                                                                                                                                                                18-JUL-2002.
                                                                                                                                                                                                                  Synthetic
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Gaps

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Score 46; DB 5; Length 13; Pred. No. 11; 1; Mismatches 0; Indels

62.2%; 90.0%;

Query Match Best Local Similarity

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Gaps

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0; Indels

9; Conservative

Matches

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RESULT 33 AAY57503

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Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
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                                           WO9942119-A1.
                                                                                                            18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-2000
                                                                 26-AUG-1999
            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB22991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB22991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, XBBXZXBX and BBXZBBXZ; and (b) a second peptide template XBBXXXB, XBBXXXBX, BXBBXXB, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and Consisting of XBBXBBX, XBBXXBBX, BXXBXXB, ABBZXXBB, and Consisting of XBBZXBBX, XBBXXXB, BXXBXXB, ABBZXXBB, and consisting of XBBZABBX and their derivatives cone aromatic amino acid, and where B, X and Z man acid; Z = A least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of apoptosis of microbial cells. AANS7463 to AANS7757 represent sequences to sed in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                              Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                      Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 2; Length 18;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptide RP-1-10F SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                Antimicrobial peptide RP-1-2R SEQ ID NO:41.
                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57504 standard; peptide; 18 AA.
 AAY57503 standard; peptide; 18 AA
                                                                                                                                                                                                  99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.2%;
90.0%;
                                                                                                                                                                                                                        98US-00025319
                                                                                                                                                                                                                                                                                                                          against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000 (first entry)
                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 YKKWKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YKKFKKKLLK 12
                                                                                                                                 Oryctolagus cuniculus
                                                                                                                                                                                                                                                                    Shen AJ;
                                                                                                                                                                                                                                                                                         WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
                                           25-FEB-2000
                                                                                                                                                                                                  17-FEB-1999;
                                                                                                                                                                                                                        .8-FEB-1998;
                                                                                                                                                       WO9942119-A1
                                                                                                                                                                            26-AUG-1999.
                                                                                                                                                                                                                                                                    Yeaman MR,
                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY57504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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organisms such as pacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting sessentially of a first peptide template XZBZZBXBR and its derivatives selected to xZBBZBRXB. BXZXSB, BXZXZBBX and BBXZBBZZ; and (b) a second peptide template XBBXXB, BXZXXB, XBBZXBBX and BBXZBBZZ; and (b) a second peptide template XBBXXB and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXZBXXB, and XBBZXXBBX, WBBZXBBX, where B = at least one positively charged amino acid; X at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect callular disruption and rapid apoptosis of microbial cells. ANYS7463 to ANYS7557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amphipathic cationic peptide used in a novel gene delivery method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic peptide; nucleic acid delivery; intravascular delivery; parenchymal cell; nuclease degradation; DNA condensation; tissue targetting; membrane attachment; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.2%; Score 46; DB 2; Length 18; 81.8%; Pred. No. 14; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in the exemplification of the present invention
                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 59; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB22991 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2000; 2000WO-US004521.
98US-00025319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LYKKWKKKLLK 12
                                                                                                                                                                         Yeaman MR, Shen AJ;
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The invention relates to a process for delivering a polynucleotide complexed with a compound into a parenchymal cell of a mammal comprising inserting the polynucleotide into a mammalian blood vessel and increasing the permeability of the vessel into an embodiment of the invention, the permeability of the vessel into me embodiment of the invention.

The polycations used include polycationic proteins such as histones and protamines, and synthetic polycationic proteins such as histones and protamines, and synthetic polycationic peptides such as polylysine. The polycations which may be important for gene delivery in vivo.

Additionally they allow attachnent of DNA to the target cell surface, and they can be used to attach specific receptors or ligands to the DNA, so that DNA/polycation complexes can be targetted to specific cell types. It was found that gene delivery and expression was most efficient when the overall net charge of the DNA/polycation complexes was negative (i.e., DNA negative charge > polycation positive charge), in contrast to prior att methods. The process of the invention is useful for delivering therepay of diseases not specified). The present sequence represents an emphipathic cationic peptide used in an exemplification of the invention.
                                                                                                                                                                                                                                      Delivering a polynucleotide complexed with a compound into a parenchymal cell of a mammal comprising inserting the polynucleotide into a mammalian vessel and increasing its permeability, useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This peptide was complexed with a luciferase reporter plasmid (pCILuc) and injected into the tail veins of ICR mice. After 24 hours, the mice were killed, the livers were removed and assayed for luciferase
                                                                                                                      Hagstrom JE, Slattum PM,
                                                                                                                                                                                                                                                                                                                                      Example; Page 32; 38pp; English
99US-0121730P
                                                                                                                      Monahan SD,
                                                                                                                                                                                            WPI; 2000-572096/53
                                                                       (MIRU-) MIRUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
26-FEB-1999;
30-JUL-1999;
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                                                                                                                                               DB;
                                                                                                                 Wolff JA,
                                                                                                                                                  Rozema
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Gaps ; Score 46; DB 3; Length 18; Pred. No. 14; 4; Indels 0; Mismatches 62.2%; 71.4%; 10; Conservative Best Local Similarity Query Match Matches ò

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ABG69928 standard; peptide; 18 AA. 21-OCT-2002 (first entry) ABG69928; RESULT 36

Rabbit platelet microbicidal protein, PMP-2, based peptide #40.

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein

Oryctolagus cuniculus.

WO200255554-A2.

18-JUL-2002.

24-AUG-2001; 2001WO-US041877.

25-AUG-2000; 2000US-00648816.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

Budker VG;

New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance. WPI; 2002-590659/63

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Example; Page 72; 221pp; English.

The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5150 amino acids containing a 7-13 amino acid core sequence (derived from the name PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,

truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial apents active against organisms such as and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents of sentence that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents to manage that enhance the antimicrobial reforms and cosmetics and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in the foods and cosmetics and as agents to improve efficiency of molecular conventions and an adent of segment in a peptides of the present invention are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides of the present and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibite lower inherent mammalian cell toxicities and and and antimicrobial and and antimicrobial and and antimicrobial and and antimicrobial antimicrobial and and antimicrobial and and and anti overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide The invention relates to an antimicrobial peptide composition for use

Sequence 18 AA;

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Gaps . 0 Score 46; DB 5; Length 18; Pred. No. 14; 1; Mismatches 1; Indels 62.2%; 81.8%; Query Match
Best Local Similarity 81.0

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2 LYKKFKKKFLK 12 2 LYKKWKKKLLK 12 ò g

RESULT 37 ABG69927

ABG69927 standard; peptide; 18 AA.

ABG69927;

21-OCT-2002 (first entry)

Rabbit platelet microbicidal protein, PMP-2, based peptide #39

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.

Oryctolagus cuniculus. Synthetic.

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glutaric dialdehyde-poly-glutamic acid copolymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004019007-A1.
                                                                                                                                                            29-NOV-1999;
                                                                                                                                                                                                                                                                                                      Monahan SD,
Slattum PM;
                                                                                                04-SEP-2003
                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AD145055;
                                                                                                                                                                                                          (WOLF/)
(HAGS/)
(BUDK/)
(ROZE/)
(SLAT/)
                                                                                                                                                                                           MONA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD145055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                             The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide contentining a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers.

Truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungion and (2) antimicrobial peptides for potentiating antimicrobial agents or general and fungi, agents in combination with other antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficiant antimicrobials, agents the inhance the antimicrobial for conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular companients and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistence. They exhibite lower inherent mammalian cell toxicity immunogenicity and short inherent mammalian cell definition of toxicity immunogenicity and short inherity against pathogens exhibiting and experimental and and an agent inherent mammalian cell definition of toxicity immunogenicity and short inherent mammalian cell definition and and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                        New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide complex delivery method associated peptide segid 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            extravascular muscle cell; polynucleotide-polymer complex; zeta potential; blood vessel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.2%; Score 46; DB 5; Length 18; 90.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                             (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL90041 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                       Example; Page 72; 221pp; English
                                                                                                                                                                                                                                                                          multiple antibiotic resistance.
                                                                              24-AUG-2001; 2001WO-US041877
                                                                                                             25-AUG-2000; 2000US-00648816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 90.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YKKWKKKLLK 12
                                                                                                                                                                           feaman MR, Shen AJ;
                                                                                                                                                                                                          WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
                WO200255554-A2
                                                18-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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The invention describes a polynucleotide complexed with a compound and delivered into the extravascular muscle cell of a mammal. The method comprises forming a polynucleotide-polymer complex having a zeta potential that is not positive; inserting the polynucleotide into a mammalian blood vessel. The method is useful for delivering a polynucleotide complexed with a compound into an extravascular muscle cell of a mammalian blood vessel in biologic systems. The inventive method allows the delivery of a polynucleotide to a cell to express an expension of an endogenous nucleotide sequence, to inhibit, eliminate, augment, or alter expression of an endogenous nucleotide sequence, or to express a specific physiological characteristic not naturally associated with the cell. The polynucleotides may be coded to express a whole or partial protein, or may be anti-sense. This is the amino acid sequence of a cationic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delivery of polynucleotide complexed with compound into extravascular muscle cell of mammal, involves inserting polynucleotide in mammalian blood vessel in vivo, and increasing permeability of blood vessel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 14;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in the creation of a copolymer of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hagstrom JE, Budker VG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 2; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI45055 standard; peptide; 18 AA.
                                                                                                                                            27-FEB-2002; 2002US-00085378.
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Best Local Similarity 71.4
Marches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolff JA,
                                                                                                                                                                                                                                                                                                                           WOLFF J A.
HAGSTROM J E.
BUDKER V G.
ROZEMA D B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-874921/81.
                                                                                                                                                                                                                                                                                         MONAHAN S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLATTUM P M
US2003166280-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 AA;
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30-JUN-2003; 2003US-00609938.

03-JUN-2004

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The present invention relates to a method for transfecting genetic material into a mammalian cell. The method comprises designing the genetic material for transfection, inserting the genetic material into a mammalian blood vessel, increasing permeability of the blood vessel, delivering the genetic material to the mammalian cell, and altering delivering the genetic material to the mammalian cell, and altering conjourning properties of the cell. Also disclosed is a method for delivering a polymucleotide complexed with a compound into a parenchymal cell of a mammal. This method involves making the polymucleotide-compound compound is chosen from amphipathic compounds, polymers and non-viral vectors, inserting the polymucleotide into a mammalian vessel, increasing the permeability of the vessel, and cell is increased by increasing pressure against vessel walls. The plood vessel consists of a tail vein. The parenchymal cell is chosen from liver cells, pance cells, heart cells, fairey cells, prostate cells, skin cells, testis cells, pancreas cells, thymus cells and lung cells. Diadder cells, brain cells, pancreas cells, thymus cells and lung cells. The present actionic peptide into a mammalian cell. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                    Transfecting genetic material into a mammalian cell, by designing genetic material, inserting genetic material into a blood vessel, increasing the permeability of blood vessel, delivering genetic material to cell.
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                                                                                                                                                                                                                         Budker VG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 8; Length 18;
Pred. No. 14;
7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cationic peptide; gene delivery.
                                                                                                                                                                                                                         Slattum PM, Hagstrom JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic peptide used in gene delivery
                                                                                                                                                                                                                                                                                                                                                                   Example; SEQ ID NO 1; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP43801 standard; peptide; 18 AA.
                               20-JUN-2003; 2003US-00600290.
                                                             99US-00391260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.2%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KLLKLWKKLLKKLK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLYKKWKKKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
                                                                                                                                                                                                                       Monahan SD, Wolff JA,
                                                                                                        MONAHAN S D.
WOLFF J A.
SLATTUM P M.
HAGSTROM J E.
BUDKER V G.
ROZEMA D B.
                                                                                                                                                                                                                                                                       WPI; 2004-122084/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biological system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                               07-SEP-1999;
                                                                            23-NOV-1999;
                                                                                                                                                                                                                                      Rozema DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP43801;
                                                                                                                                         (SLAT/)
(HAGS/)
(BUDK/)
                                                                                                           (MONA/)
                                                                                                                                                                                        (ROZE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
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US2004106567-A1

Unidentified

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a process for inhibiting expression of a gene in an extravascular mammalian cell. The process involves delivering a naked polymuclectide to an extravascular cell outside of the blood vessel via the increased permeability. The method is useful in biological systems, e.g. for inhibiting expression of a gene in an extravascular mammalian cell. It is useful for inhibiting, eliminating, augmenting, or altering expression of an endogenous nucleotide sequence, or to express a specific physiological characteristic not naturally associated with the cell. The present sequence is a cationic peptide used in gene delivery. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting expression of a gene in an extravascular mammalian cell, useful for inhibiting, eliminating, or altering expression of endogenous nucleotide, comprises delivering polynucleotide to extravascular cell via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA delivery; protein delivery; muscle tissue; ischaemic; blood flow; blood vessel; muscle cell; angiogenic factor; vascular endothelial growth factor; VBGF; fibroblast growth factor; FGF; angiogenesis; heart muscle; skeletal muscle; cardiac function; peripheral vascular disease; peripheral arterial occlusive disease; peripheral deficient vascular disease; myocardial ischaemia; occlusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monahan SD, Rozema DB, Budker VG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 8; Length 18;
Pred. No. 14;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic cationic peptide used in DNA delivery method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; SEQ ID NO 2; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL72804 standard; peptide; 18 AA.
                                                                                                                 99US-00391260.
99US-00447966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLYKKWKKKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 KLLKLWKKLLKKLK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wolff JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis DL;
                                                                                                                                                                                                                HAGSTROM J E.
                                                                                                                                                                                                                                                WOLFF J A.
MONAHAN S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-419484/39.
                                                                                                                                                                                                                                      (WOLF/) WOLFF J A.
(MONA/) MONAHAN S D.
(ROZE/) ROZEMA D B.
(BUDK/) BUDKER V G.
(SLAT/) SLATITUM P M.
(LEWI/) LEWIS D L.
                                                                                                                                                                                                                                                                                                       ROZEMA D B.
BUDKER V G.
                                                                                                                                                                                                                                                                                                                                                                  SLATTUM P M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004072785-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hagstrom JE,
                                                                                                                 07-SEP-1999;
23-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Slattum PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vasotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL72804;
                                                                                                                                                                                                                HAGS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL72804
$\frac{1}{2}$\frac{1}{2}$\frac
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Slattum PM;

Trubetskoy VS,

Budker VG,

(MONA/)

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The invention relates to the preparation of a compound for delivery to a active drug. The drug as a polymer in the presence of a biologically active drug. The drug is a polyion and the polymer (preferably containing a disulphide bond) is amodified in the presence of the polyion by (mixing with and) attaching a modecule. The molecule comprises a gene transfer enhancing signal selected from a nuclear localising signal, a ligand that binds a cell, and a releasing signal. The molecule changes the charge of the polymer and may be amphipathic, hydrophobic or hydrophilic. The mucleful for the delivery of nucleic acids, for condensing a nucleic acid, for forming nucleic acid binding polymers, for forming supramolecular complexes containing nucleic acid and polymer, and for
                                                                                                                                                                                                                                                                                                       polymer in presence of biologically active drug, useful e.g. for delivery and condensing nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             forming interpolyelectolyte complexes. The present sequence represents an amphipathic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heterophase system; supramolecular complex; interpolyelectrolyte;
gene therapy; protection; binding; phenylketonuría; tumour; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphipathic; polymer; drug; polymerisation; condensation; delivery;
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 14; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY49957 standard; peptide; 20 AA.
                                                                    97WO-US024089
                                                                                                               97US-00778657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00070299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.2%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLYKKWKKKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 KILKLWKKILKKIK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 71.4 nes 10; Conservative
                                                                                                                                                                                                      Hagstrom JE,
                                                                                                                                                                                                                                                                        WPI; 1998-446760/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphipathic peptide
                                                                                                                                                         (MIRU-) MIRUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 AA;
                                                                    30-DEC-1997;
                                                                                                                 3-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1999;
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                                                                                                                                                                                                                                Hanson LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                      Wolff JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY49957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a process for delivering polypeptides or companient for improving or enhancing blood flow in the tissue. The process comparies injecting or enhancing blood flow in the tissue. The process comparies injecting contaked polynucleotides encoding the polypeptide into a blood vessel lumen in vivo, increasing extravascular volume in the muscle tissue, and delivering the naked polynucleotides to extravascular cells, especially muscle cells outside of the blood vessel. The polypeptide consists of an angiogenic factor such as vascular endothelial growth factor (VEGF) or fibroblast growth factor (VEGF). The permeability of the vessel is increased by inserting papaverine into the vessel prior to or together with the polynucleotides. The delivery of the polynucleotides stimulates angiogenesis in the muscle tissue. The muscle tissue is heart muscle tissue, particularly human heart muscle tissue, cor human limb skeletal muscle tissue. In addition, the delivery of the polynucleotide improves abnormal cardiac function. The patient has cor human limb skeletal muscle tissue. In addition, the delivery of the polynucleotide may stimulate vascular cell migration or peripheral vascular disease, peripheral arterial occlusive disease, peripheral cor the method is useful for delivering therapeutic prolynucleotides to a tissue suffering from corpusion. The present sequence isolatemia, vascular disease or an occlusion. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                             Delivering a therapeutic polynucleotide or polypeptide to a tissue suffering from or potentially suffering from ischemia comprises injecting naked polynucleotides into blood vessel and increasing the extravascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amphipathic peptide; drug delivery; polyion; polymer; template drug; gene transfer enhancing signal; nuclear localising signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                     Budker VG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.2%; Score 46; DB 8; Length 18; 71.4%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                   Hagstrom JE, Rozema DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 15; SEQ ID NO 2; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW65895 standard; peptide; 20 AA.
28-JUL-2003; 2003US-00628734.
                                            99US-00447966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S KLLKLWKKLLKKLK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLYKKWKKKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       volume in muscle tissue
                                                                                                                                                                                                                                                   Monahan SD,
                                                                                     WOLFF J A.
MONAHAN S D.
HAGSTROM J E.
ROZEMA D B.
BUDKER V G.
                                                                                                                                                       (ROZE/) ROZEMA D B.
(BUDK/) BUDKER V G.
(SLAT/) SLATTUM P M.
                                                                                                                                                                                                                                                                                                                     WPI; 2004-315421/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amphipathic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
                                            23-NOV-1999;
                                                                                                                                                                                                                                              Wolff JA, M
Slattum PM;
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Gaps

ö

4; Indels

0; Mismatches

Budker VG;

Wolff JA, Hagstrom JE,

WO9829541-A1

Synthetic

AAW65895;

Query Match

Matches

ઠ 셤 (MIRU-) MIRUS CORP.

Score 46; DB 2; Length 20; Pred. No. 16;

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The present invention describes the preparation of a compound for delivery to a cell by modifying a molecule (I) in presence of a polyion (II). The method is used to deliver mucleic acids to cells or organisms for analytical purposes, for the preparation of new materials, for the purlication of nucleic acids and for other recombinant DNA techniques, e.g., the production of sequence-binding molecules or for protecting specific sequences against nuclease digestion), and especially for drug delivery and gene therapy (e.g. treating inherited metabolic defects such as phenylketonuria or using antisense sequences to treat tumours or infections). Polymerisation can be performed in the presence of nucleic acids without chemical modification or loss of function of the nucleic acid; The method eliminates the need for aggregation and precipitation of acid. The method eliminates the need for aggregation and precipitation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amphipathic peptide monomer; drug delivery; nucleic acid-binding monomer; nucleic acid delivery; nucleic acid condensation; nucleic acid binding polymer; supramolecular complex;
                                 Preparing compound for delivery to a cell by reacting a molecule in presence of polyion, particularly for delivering nucleic acids, e.g. for
                                                                                                                                                                                                                                                                                                                                                     the nucleic acid and can produce consistent supramolecular complexes (including new and better-defined complexes of a relatively small size, better suited for delivery to cells) and at very high nucleic acid concentrations (in contrast to the use of preformed polylysine at low concentrations). Also polymers can be formed that can not be associated with a nucleic acid when preformed. The present sequence represents an example of an amphipathic peptide given in the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 3; Length 20;
Pred. No. 16;
0; Mismatches 4; Indels
                                                                                                       Disclosure; Page 14; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE34633 standard; peptide; 20
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97US-00778657.
99US-00464871.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62.2%;
ilarity 71.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amphipathic peptide monomer.
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BUDKER V G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLATTUM P M.
HANSON L J.
WPI; 2000-023352/02
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les 10; Conserv
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03-JAN-1997;
16-DEC-1999;
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                                                                      gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE34633;
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(BUDK/)
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(HANS/)
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                Complexes formed by covalently forming a polymer in the presence of polyion, useful for e.g. delivery of nucleic acids, for condensing nucleic acids and for forming nucleic acid binding polymers.
 Slattum PM;
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Pred. No. 16;
0; Mismatches 4; Indels
 Budker VG, Trubetskoy VS,
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                                                                                                                                                  Disclosure, Page 5; 19pp; English
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(first entry)
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Best Local Similarity 71.4
Matches 10; Conservative
 Hagstrom JE,
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                                               WPI; 2003-874534/81.
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26-NOV-1991
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                  Hanson LJ;
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Wolff JA,
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helical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13929 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA field.)
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Sequence 20 AA;

Gaps .; 0 Query Match
60.8%; Score 45; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 2; Indels

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Search completed: May 16, 2005, 08:38:31 Job time : 60.2931 secs

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173, App 1, Appli 6, Appli 10, Appli 10, Appl 17, Appl 17, Appl 61337, A 45811, A

6732, Ap 173, App 173, App

Sequence

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database :

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PEATURE:
CTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial COTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-6
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100.0%; Score 65; DB 4; Length 13
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09525269A

Patent No. 6743769

GENERAL INFORMATION:
APPLICANT: Seam, Michael R.
TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION WINDER: US/09/525,269A
CURRENT TILING DATE: 1200-03-13
PRIOR PILING DATE: 1200-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 13
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Patent No. 6743769

GENERAL INFORMATION:
APPLICANT: Seman, Michael R.
TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION: Metapeptides
TITLE REFERENCE: 66742-025 (HRS614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
                         US-08-734-6078-20

US-08-734-6078-20

US-09-270-767-40423

US-09-134-000C-6732

US-09-114-00C-6732

US-09-112-283-173

US-09-812-283-173

US-09-812-283-173

US-09-812-281-16

US-08-313-681A-6

US-09-322-911-6

US-09-322-911-6

US-09-322-911-6

US-09-322-911-6

US-09-222-911-6

US-09-222-911-6

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US-09-222-911-6

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US-09-2270-767-61313
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ORGANISM: Artificial Sequence
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US-09-525-269A-7
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RESULT 2
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Sequence 1, Appli
Sequence 11, Appli
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Sequence 2, Appli
Sequence 3, Appli
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-525-269A-7
US-09-525-269A-4
US-09-525-269A-9
US-09-525-269A-9
US-09-525-269A-9
US-09-313-6BLA-11
US-09-322-911-11
US-09-322-911-11
US-09-322-911-17
US-09-322-911-7
US-09-323-203-7
US-08-760-903-3
US-09-5213-999C-5446
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US-08-338-882-22
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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65
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Match Length DB
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Maximum DB seq length: 74
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TYPE: PRT ORGANISM: Artificial Sequence
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US-09-525-269A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
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                                                                                                                                                                                                                                      Length 13;
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APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION: Metapeptides
FILE REFRENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Shem, Alexander N.
APPLICANT: Shem, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR APPLICATION NUMBER: US 09/025,319
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 13
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Pred. No. 0.002;
2; Mismatches
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Pred. No. 0.013;
2; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7 LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09525269A Patent No. 6743769 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09525269A Patent No. 6743769 GENERAL INFORMATION:
                                                                                                                                                                                                                                      90.8%;
                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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76.9%;
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                               Gaps
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FEATURE:
COTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial
COTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                               Score 50; DB 4; Length 14;
Pred. No. 0.062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09525269A

Patent No. 6743769

GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HRS644)
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 18
                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HS5614)
CURRENT APPLICATION NUMBER: US 09/09/525,269A
CURRENT FILING DATE: 2000-03-13
FRIOR APPLICATION NUMBER: US 09/025,319
FRIOR FILING DATE: 199-18
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 9: SEQ ID NOS: 39
LENGTH: 13
                                                                                                                                                                                                  1; Mismatches
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Patent No. 6743769
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                  76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARYRKFKNKILKS 13
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                                                                                                                                               Query Match 76.9
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.8
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                             3 YRKFKNKLLK 12
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APPLICANT: Hirata, Mishi
APPLICANT: Balint, Rober
TITLE OF INVENTION: Huma
TITLE OF INVENTION: Lipc
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RYRKFKNKI 10
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Best Local Similarity
                                                                                                                                                                                                                  COUNTRY: USA
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US-09-525-269A-10
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Wright, Susan C.
APPLICANT: Wright, Susan C.
APPLICANT: Hirate Mishimasa
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                     ö
                                                                                                                                                     Gaps
; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon to THER INFORMATION: microbiocidal domains from platelet microbial COTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-3
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                                                                                                         Score 47; DB 4; Length 18;
Pred. No. 0.24;
                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
                                                                                                                                                   2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
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Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heelin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 1532:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2420
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.9%;
                                                                                                       Query Match 72.3%;
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                          1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                  1 ALYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 16 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Francisco
E: California
FRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 7; Conserv
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US-08-313-681A-11
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Robert F.
Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
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Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
                                                                                                              LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                            ADDRESSEE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
REIOR APPLICATION DATA:
REIOR APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1966
FILING DATE: August 1, 1966
FILING DATE: AUGUST 1, 1996
FILING DATE: JULY 17, 1992
FRICR APPLICATION NUMBER: 07/916,765
FILING DATE: JULY 17, 1992
FRICR APPLICATION NUMBER: PCT/US93/06731
FILING DATE: JULY 15, 1993
FRICR APPLICATION NUMBER: PCT/US93/06731
FILING DATE: JULY 15, 1993
REIOR APPLICATION NUMBER: 08/313,681
FILING DATE: SEPLEMBER: 37, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REPERENCE/DOCKET NUMBER: 155;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 11:
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 amino acids
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STRANDEDNESS: single
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                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                    STREET: Two Embarcad
CITY: San Francisco
STATE: California
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56.9%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                     Query Match
Best Local Similarity 77.5-
7, Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
                                                                                                                                                                                             2 RYRKFKNKI 10
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5 RLRKFRNKI 13
    Region
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                                                               US-08-313-681A-7
                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-322-911-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                           OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial Information: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-10
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                                                                                                                                                                                                                                                                                                Score 37; DB 4; Length 18;
Pred. No. 10;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Townsend and Townsend Khourie and Crew F: One Market Plaza, Steuart Tower, Suite 2000 San Francisco : California ?X: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBTURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note: "Xaa is a Gln or Ile"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/313,681A FILING DATE:
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heelin, James M.
REFERENCE/DOCKET NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 1532:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-240
TELEFRA: 415-326-242
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANBONESS: single
                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              3 YKKWKNKLKRS 13
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                      3 YRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 23
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Region
LOCATION: 23
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STREET: Or
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GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Westy L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                    ö
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                                                                                                                                                    Gape
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                                                                                                     DB 4; Length 60; 66;
                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION TO 514
PRIOR APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US/07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian # 32,928
REFERENCE/DOCKET NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Bristol-Myers Squibb Company, Patent ADDRESSEE: Department
                                                                                                                                                    3; Mismatches
                                                                                                         Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08233203
Patent No. 5409898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206/728-4800
206/448-4775
                      ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALYKKLLKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3005 First
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                          4 RKFKNKILK 12
                                                                                                                                                                                                                       49 KQYKNKILK 57
                                                                                                                                                                                                                                                                                                                          US-08-233-203-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-233-203-7
  LENGTH: 60
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Batent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A

FRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
SEQ ID NO 23756
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                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon ; OTHER INFORMATION: microbiocidal domains from platelet microbial ; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-8
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                                                                                                                                                                                                                                                           Length 29;
                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yearn, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REPERENCE: 66742-025 (RR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 14
                                                                                                         /note= "Xaa is a Gln or Ile'
                                                                                                                                                                                          /note= "Xaa is a Gly or Gln'
                        /note= "Xaa is Asp or Lys"
                                                                                                                                                                                                                                                         Score 37; DB 3;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09525269A Patent No. 6743769 GENERAL INFORMATION:
                                                                                                                                                                                                                                                           56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.6
France 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|:| |:||
3 YKKWKKKLLK 12
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5 RLRKFRNKI 13
                                                                                                                                                                                                                                                                                                                                              2 RYRKFKNKI 10
                      OTHER INFORMATION:
                                                                                       LOCATION: 26
OTHER INFORMATION:
                                                                                                                                                                    LOCATION: 27
COTHER INFORMATION:
US-09-322-911-7
                                                                                                                                                  NAME/KEY: Region
LOCATION: 27
                                                                 NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-248-796A-23756
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-525-269A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Score 34; DB 4; Length 18;
Pred. No. 31;
2; Mismatches 4; Indels
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APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTIONS: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                          FILING DATE: 07-4UN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATORNEY/AGENT INFORMATION:
ROALSTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9610227 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: O
TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 397-8338
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.6
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ARYRKFKNKILKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-482-191-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKTANI, MOHAMMED S.
APPLICANT: FIRCK, JOSEPH R
APPLICANT: FORM.
APPLICANT: PUGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: POGH, CHARLES
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
              Sequence 2, Application US/08760903
Patent No. S998381
GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILLI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: The P.C. COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                      SSEE: MEDLEN & CARROLL, LLP
F: 220 MONTGOMERY STREET, SUITE 2200
SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: MEDLEN & CARROLL
220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                        STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08482191
Patent No. 6579696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALYKKLIKKLIKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-760-903-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAN FRANCISCO
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COMPUTER READABLE FORM:
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
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                                                                                Score 34; DB 2; Length 19;
Pred. No. 33;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 4; Length 19;
Pred. No. 33;
2; Mismatches 4; Indels
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: STEAT, JOSEPH R.
APPLICANT: STATZ, ROBERT W.
APPLICANT: STATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANAIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATORNEY AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSER: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08482191
Patent No. 6579696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative ;
                                                                                Query Match 52.3%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               1 ARYRKFKNKILKS 13
                                                                                                                                                                                                             1 ALYKKLLKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ARYRKFKNKILKS 13
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               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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STRANDEDNESS: 81:
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US-08-760-903-3
                                                                                                                                                                                                                                                                                                                            US-08-482-191-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Sequence 3, Application US/08760903
| Patent No. 5998381
| GENERAL INFORMATION:
| APPLICANT: SHEKANI, MOHAWMED S.
| APPLICANT: ANDERSON, BYRON
| TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
| NUMBER OF SEQUENCES: 9
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MEDLEN & CARROLL, LLP
| STREET: 220 MONTGOMERY STREET, SUITE 2200
| CONTY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                             PRIOR APPLICATION NUMBER: US 08/169,/U1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAWE: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: 0PHD-02557
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34;
Pred. No. 3
                                   08/169,701
PILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 06
FILING DATE: 17-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.3%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALYKGLIKKLIKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALI FORNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06
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US-08-760-903-3
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: PUGH, CHARLES
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES:
ADDRESSEE: MEDLESS:
ADDRESSEE: MEDLESS:
ADDRESSEE: MEDLESS:
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Pred. No. 33;
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                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                           E: MEDLEN & CARROLL
220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFTCATION:
PRIOR APPLICATION DATA:
PELING DATE:
FILING DATE:
PRIOR APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-UTW-1995
PRIOR APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATE: OB-DEC-1993
PRIOR APPLICATION DATE: OB-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 190-DEC-1992
ATTONNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOF 0938
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
US-09-583-110-5000
S. Sequence 5000, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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FOR DIAGNOS
APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REPERIOR: PATHOLO-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/081,553
PRIOR APPLICATION NUMBER: US 60/051,553
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 5000
LENGTH: 68
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Ratent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND ANTNO ACID
TITLE OF INVENTION: THERAPEUTICS
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 4; Length 68;
Pred. No. 1.1e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433
FILING DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: JULY 2, 1997
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM
COMPUTER: <Unknown-
OPERATING SYSTEM: <Unknown-
SOFTWARE: <Unknown-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-583-110-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2777:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781)893-827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 62.5
Enes 5; Conservative
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40 KFRKFKNR 47
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US-09-107-433-2777
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ORGANISM: Streptococcus pneumoniae

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Sequence 11, Application US/08233203 Patent No. 5409898
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24 SKYSLVKNKISKS 36
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YRKFKNKIL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YNKFKNMFL 9
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; NAME/KEY: PEPTIDE
; LOCATION: (1)...(18)
US-09-121-211-6
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; Sequence S464, Application US/09513999C
; Patent No. 6783961
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; PILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1090-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5446
                                                                                                                                                                                                                                                                                                                                       Sequence 58595, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PALIAND NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58595
LENGTH: 62
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Pred. No. 1.5e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 62;
                                                                                                                                   Query Match 52.3%; Score 34; DB 4; Length 70; Best Local Similarity 62.5%; Pred. No. 1.1e+02; Matches 5; Conservative 3; Mismatches 0; Indels
                                                                                                                                       Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 4; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-58595
                          , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...70
; SEQUENCE DESCRIPTION: SEQ ID NO: 2777:
US-09-107-433-2777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.8%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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52 FRKCKNKII 60
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US-09-513-999C-5446
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                                                                                                                                                                                                                                                       42 KPRKPKNR 49
                                                                                                                                                                                                                  2 RYRKFKNK 9
                                                                                                                                                                                                                                                                                                                                       US-09-270-767-58595
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                    FEATURE
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1 ARYRKFKNKILKS 13

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GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
RESULT 25
US-09-121-211-6
; Sequence 6, Application US/09121211
; Patent No. 6750052
; GENERAL INFORMATION:
; APPLICANT: Shinoh, Dhirendra P.
; APPLICANT: Shinoh, Dhirendra P.
; APPLICANT: Shinoh, Dhirendra P.
; TITLE OF INVENTION: Factor
; TITLE OF INVENTION: Factor
; TITLE OF INVENTION: Pactor
; FILE REFERENCE: B0801/7116
; CURRENT FILING DATE: 1998-07-23
; EARLIER PILING DATE: 1999-07-23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LEMCHT: IB
; WARDER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; LEMCHT: IB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 4; Length 18;
Pred. No. 66;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Bristol-Myers Squibb Company, Patent ADDRESSEE: Department STREET: 3005 First Avenue CITY: Seattle Stattle STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION UMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
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STHODS FOR TREATING
BY ORGANISM SENSITIVE TO BETA-LACTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Bristol-Myers Squibb Company, Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISTITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Ginsberg, Mark H.
APPLICANT: O'TOOle, Tim
TITLE OF INVENTION: METHODS FOR IDENTIFYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOR, BRIAN W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            Sequence 12, Application US/08233203
Patent No. 5409898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08214770 Patent No. 5523209
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54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B: Department
3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 amino acids
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                                   2 RYRKFKNKILKS 13
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YES
                                                                                             11 KFGKFKGAILKA 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:| |:||
8 YKKLLKKLLKS 18
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Best Local Similarity
Matches 6; Conserv
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CITY: Seattle
STATE: Washingt
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98121
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US-08-338-882-22
| Sequence 22, Application US/08338882
| Sequence 22, Application US/08338882
| Settle No. 5912231
| GENERAL INFORMATION:
| APPLICANT: Houghten, Richard A. APPLICANT: Cuervo, Julio H. TITLE OF INVENTION: Substitution Analogues of Magainin TITLE OF INVENTION: Peptides | NUMBER OF SEQUENCES: 58
| NUMBER OF SEQUENCES: 58
| CORRESPONDENCE ADDRESS: | ADDRESSE: Minamow, Ltd. | STREET: 180 No. 5912231th Stetson, Suite 4700 |
| STREET: Chicago | STREET: Illinois | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.2%; Score 32; DB 2; Length 22; 50.0%; Pred. No. 79; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.2%; Score 32; DB 1; Length 20; 54.5%; Pred. No. 72;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gamson, Edward P
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 186.1
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 616-5460
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/615,125
FILING DATE: 15-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                             ON0063A
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OPERATING SYSTEM: PC-DOS/MS-DOS
                             NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
                                                                                                                                                                           TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      20 amino acids
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: YES
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
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GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
CURRENT FILING DATE: 1999-03-17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 40423
                                              Gaps
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PCT-0895-02885-11
; Sequence 11, Application PC/TUS9502885
; GENERAL INFORMATION:
; APPLICANT: Ginebrg, Mark H.
APPLICANT: O'Toole, Timothy
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INHIBITORS
; TITLE OF INVENTION: OF INTEGRIN ACTIVATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
...... Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 5; Length 46;
Pred. No. 1.6e+02;
3; Mismatches 2; Indels
                                              Indels
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PRIDASIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/214,770
FILING DATE: March 14, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02885
                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
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; Sequence 40423, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11:
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54.5%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 54.5
Matches 6; Conservative
                                              6; Conservative
                                                                                       3 YRKFKNKILKS 13
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12 YRRFEKEKLKS 22
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12 YRRFEKEKLKS 22
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STRANDEDNESS:
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PCT-US95-02885-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                              Matches
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APPLICANT: Daw, Debbie A.

APPLICANT: Law, Debbie A.

APPLICANT: Alaimo, Lisa N.

TITLE OF INVENTION: Modulation of Integrin-mediated Signal Transduction
FILE REFERENCE: 44481-5008-01-US

CURRENT FILING DATE: 1996-10-18

PRIOR APPLICATION NUMBER: US 60/005,567

PRIOR PILING DATE: 1995-10-18

PRIOR FILING DATE: 1995-10-18

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.2%; Score 32; DB 1; Length 46; 54.5%; Pred. No. 1.6e+02;
NUMBER OF INVENTION: INHIBITORS OF INTEGRIN NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
STREET: Fish
                                                                                                                                                                                                                         ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18M PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,770
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06410/002001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1542-5070
TELEFRAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: GPIIIa Beta 2 subunit
US-08-734-607B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 20, Application US/08734607B ; Patent No. 6210913
                                                                                                                           ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 54.5
Best Local Similarity 54.5
Conservative
                                                                                                                                                                                       Massachusetts
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12 YRRFEKEKLKS 22
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LENGTH: 46
TYPE: PRT
ORGANISM: Homo gapiens
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Best Local Similarity
                                                                                                                                                                                                              U.S.A.
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US-08-734-607B-20
                                                                                                                                                                   CITY: BOE
STATE: Ma
COUNTRY:
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LENGTH: 58

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Query Match
Best Local Similarity 60.03
Matches 6; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Arabidopsis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 324
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                   RESULT 35
US-09-177-249-173
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| Patent No. 6617156
| Patent No. 6617156
| GENERAL INFORMATION:
| APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,000C | CURRENT PILING DATE: 1998-08-13 | PRIOR APPLICATION NUMBER: US 60/055,778 | PRIOR PILING DATE: 1997-08-15 | SPRIOR FILING DATE: 1997-08-15 | SPRIOR FILING DATE: 1997-08-15 | SEQ ID NOS: 6812 | SEQ ID NO 6732 | LENGTH: 67
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                                                                                                                                                                                                                                                                                                           Sequence 55639, Application US/09270767

| Sequence 55639, Application US/09270767
| Patent No. 6703491
| GENERAL INFORMATION:
| APPLICANT: Homburger et al.
| TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
| CURRENT APPLICATION NUMBER: US/09/270,767
| CURRENT FILING DATE: 1999-03-17
| NUMBER OF SEQ ID NOS: 62517
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 55639
| TYPE: PRT
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                                                                                                                  Score 32; DB 4; Length 58;
Pred. No. 2e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.2%; Score 32; DB 4; Length 58; 50.0%; Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 4; Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                         ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-40423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Drosophila melanogaster FEATURE:
TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                    49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                             6; Conservative
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                                                                                                                                                                                                     2 RYRKFKNKILKS 13
                                                                                                                                                                                                                             1 RYLNFPSSVLKS 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||| ::|||
33 KYRKSESKIL 42
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                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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US-09-134-000C-6732
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                                          FEATURE:
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18-Sequence 1.77 249-173
18-Sequence 1.77 249
18-
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GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hizata, Mishimasa
APPLICANT: Hizata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                       Score 31; DB 1; Length 37;
Pred. No. 1.9e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15325-000920
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: AMOUNT 1, 1996
PRIOR APPLICATION NUMBER: 07/916,761
FILING DATE: JULY 17, 1992
PRIOR APPLICATION DATA: 7/916,765
FILING DATE: JULY 17, 1992
PRIOR APPLICATION NUMBER: 07/916,765
FILING DATE: JULY 17, 1992
PRIOR APPLICATION NUMBER: 07/916,765
FILING DATE: JULY 15, 1993
PRIOR APPLICATION NUMBER: 08/313,681
FILING DATE: SEPTEMBER: 08/313,681
FILING DATE: SEPTEMBER: 27, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09322911
Patent No. 6103888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35,136
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REGISTRATION NUMBER: 35,136
REPERENCE JOCKET NUMBER: 1E
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-326-2400
                                                                                                                                                                           Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two concentrations of the contract of 
                                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-313-681A-6
       single
                                                                                                                                                                                                                                                                                                                        2 RYRKFKNKILK 12
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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APPLICANT: Stryker Corporation
APPLICANT: Stryker Corporation
APPLICANT: Stryker Corporation
APPLICANT: Stryker Corporation
TITLE OF INVENTION: Modified Morphogenic Proteins
FILE REFERENCE: STK-076
CURRENT APPLICATION NUMBER: US/09/374,958C
CURRENT APPLICATION OF STRY 1699-08-16
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08313681A
; Sequence 6, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wishimasan C.
APPLICANT: Hirata, Mishimasan C.
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/313,681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 4; 1
Pred. No. 1.8e+02;
4; Mismatches 1,
                                                                                                                                                                                                                                          Sequence 1, Application US/09374958C Patent No. 6677432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REPRENCE/DOCKET NUMBER: 1532:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.78;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                            6 YRKPKTNYTK 15
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; OTHER INFORMATION: 60-A
US-09-374-958C-1
   3 YRKFKNKILK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RKFKNKILKS 13
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22 KKYRNMIVKS 31
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                                                                                                                                                                                                                   US-09-374-958C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 35
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Gaps
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Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: LENTZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: BCK, Jurgen
APPLICANT: BCK, Jurgen
APPLICANT: Axel
APPLICANT: Axel
TITE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 6745022003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT APPLICATION NUMBER: PCT/RE96/02273
EARLIER FILING DATE: 1999-06-15
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
SOFTWARE: PATENT ON S: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                             SOFTWARE: Word Perfect 5.0.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,721
FILING DATE: 24-AUG-1998
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/942,330
FILING DATE: 5-SEPT-1997
ATTORNEY/AGENT INFORMATION:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08776059B Patent No. 6271368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Saponaria officinalis
                                                                                                                                                                                                                                                                                                                                                          NAME: Meyer, Scott J. REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: WU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 314-694-3117
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative
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34 ARFRYIQNLVIKN 46
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Best Local Similarity 53.8
Matches 7; Conservative
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21 AYYLKLENQSLKS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-09-138-721-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 42
US-08-776-059-17
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Patent No. 6022946

GENERAL INFORMATION:
APPLICANT:
GOldberg, Gregory I.
TITLE OF INVENTION: Method of Cell Surface Activation
TITLE OF INVENTION: and Inhibition
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer
STREET: 800 No. 6022948th Lindbergh Blvd.
CITY: St. Louis
STATE: No.
                   Score 31; DB 3; Length 37;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 46;
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Patent No. 6274703
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method of Cell Surface Activation
TITLE OF INVENTION: and Inhibition
NUMBER OF SEQUENCES: 19
CORRESPONDENCE: 19
CORRESPONDENCE: 800 No. 6274703th Lindbergh Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3e+02;
                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,330A
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%; Score 31;
53.8%; Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026,226
FILLING DATE: 17-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meyer, Scott J.
REGISTRATION UNDRER: 25,275
REPRENCE/DOCKET NUMBER: WU-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-694-3117
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                 47.7%;
Query Match
Best Local Similarity 63.6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ARYRKFKNKILKS 13
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21 AYYLKLENQSLKS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                            5 RFRKSKEKIGK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                       2 RYRKFKNKILK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                   US-08-924-330A-10
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US-09-138-721-10
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Gaps

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Score 31, DB 4, Length 60; Pred. No. 2.9e+02; 2; Mismatches 2; Indels

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Search completed: May 16, 2005, 08:40:40 Job time : 14.8966 secs
                                                                                                                               47.7%;
                                           TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                   Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                     4 RKFKNKILKS 13
                                                                                                                                                                                                                                              | || |::||
13 RNFKFKLIKS 22
                                                                                      US-09-248-796A-21333
SEQ ID NO 21333
LENGTH: 60
                                                                                                                                 Query Match
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APPLICANT: Keith Weinstock et al
APPLICANTON: UNCLEIC AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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Patent No. 6703491

GRNERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PALLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45811
LENGTH: 52
                                                                               APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: THE REFERENCE: TO 126-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SSG ID NO 61337
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 2.4e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-61337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21333, Application US/09248796A Patent No. 6747137
             Sequence 61337, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                    47.78;
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Best Local Similarity 66.7
Matches 6; Conservative
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39 YRKRENRIL 47
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42 YRKRENRIL 50
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Best Local Similarity
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US-09-248-796A-21333
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US-09-270-767-45811
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US-09-270-767-61337
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RESULT 2
US-10-131-433-1
; Sequence 1, Application US/10131433
; Publication No. US20030054422A1
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Sequence 283343,
Sequence 281095,
Sequence 284593,
Sequence 285440,
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                                                                                                                                                           May 16, 2005, 08:38:44; Search time 48.8621 Seconds (without alignments) 88.876 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications Asia.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-131-433-1
US-10-060-102-5
US-10-721-839-5
US-10-344-709C-15
US-10-424-599-263628
US-10-424-599-283343
US-10-424-599-281095
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US-10-424-599-284593
US-10-424-599-285440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1432185 segs, 334051727 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Applications AA:
                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                1 ARYRKFKNKILKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0 Maximum DB seq length: 74
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Match
                                                                                                                                                                                                                                                                            Title:
Perfect score:
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14 32 49.2 17 14 US-10-225-567A-2018 Sequence 2018, App 15 32 49.2 29 14 US-10-097-065-517 Sequence 517, App 21 17 14 US-10-097-065-517 Sequence 517, App 21 18 32 49.2 29 15 US-10-424-599-156622 Sequence 272450, 20 32 49.2 45 15 US-10-424-599-156622 Sequence 272450, 20 32 49.2 45 15 US-10-424-599-156622 Sequence 20, Appl 21 32 49.2 52 14 US-10-66-698-8400 Sequence 20, Appl 22 49.2 52 15 US-10-434-599-18932 Sequence 20, Appl 22 49.2 52 15 US-10-437-963-189993 Sequence 20, Appl 22 49.2 52 15 US-10-437-963-189993 Sequence 20, Appl 22 49.2 52 15 US-10-437-963-189993 Sequence 20, Appl 22 49.2 53 13 US-10-424-599-202804 Sequence 20, Appl 22 49.2 53 13 US-10-424-599-202804 Sequence 20, Appl 22 49.2 53 15 US-10-424-599-202804 Sequence 20, Appl 22 49.2 54 16 US-10-424-599-24733 Sequence 216, Appl 23 49.2 54 16 US-10-424-599-24733 Sequence 216, Appl 23 49.2 54 16 US-10-798-512-304 Sequence 216, Appl 23 49.2 56 15 US-10-424-599-24733 Sequence 216, Appl 24 49.2 56 15 US-10-424-599-2433 Sequence 217, Appl 23 49.2 60 16 US-10-424-599-24339 Sequence 217, Appl 24 49.2 60 16 US-10-424-599-24339 Sequence 217, Appl 24 49.2 60 15 US-10-424-599-26319 Sequence 217, Appl 24 49.2 60 15 US-10-424-599-26319 Sequence 217, Appl 24 49.2 77 19 15 US-10-424-599-26319 Sequence 217, Appl 24 49.2 77 19 15 US-10-424-599-26513 Sequence 217, Appl 24 49.2 17 17 19 15 US-10-424-599-26513 Sequence 217, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 217, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 217, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 216563, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 2173, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 216563, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 2173, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 2173, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 2173, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 2173, Appl 24 49.3 11 47.7 44 15 US-10-424-599-26513 Sequence 2173, Appl 24 49.3 11 47.7 44 15 US-10-424-5
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ALIGNMENTS

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RESULT 1.

RESULT 1.

Sequence 158393, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 2003-04-28

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 158393

CURRENT FILING

ACALLISM: COMEANIEM: G1/74; Score 44; DB 15; Length 73;

Best Local Similarity 72.74; Pred. No. 7;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Matches 3 YRKFKNKIKKS 13

CONSTRUCTS 13

STAKFKNKIKKS 63
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TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI? TITLE OF INVENTION: CATHELICIDINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a cathelicidin
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Publication No. US20040170642A1

RENERAL INFORMATION:

AERIREAL INFORMATION:

TITLE OF INVENTION: Vaccine which comprises at least one antigen and a catheli

TITLE OF INVENTION: Vaccine which comprises at least one antigen and a catheli

TITLE OF INVENTION: Vaccine which comprises at least one antigen and a catheli

TITLE OF INVENTION: Vaccine which comprises at least one antigen and a catheli

FILE REFERENCE: SONN:030US

CURRENT APPLICATION NUMBER: US/10/344,709C

CURRENT APPLICATION NUMBER: PCT/EP01/09529

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1

LENGTH: 37
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APPLICANT: RUDOLEH, CARSTEN MARTIN
APPLICANT: PLANK, CHRISTIAN
TITLE OF INVENTION: POLYPEPTIDES COMPRISING MULTIMERS OF NUCLEAR
TITLE OF INVENTION: LOCALIZATION SIGNALS OR OF PROTEIN TRANSDUCTION DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 15; Length 37;
Pred. No. 50;
1; Mismatches 1; Indels
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                                                           US-10-156-570A-8
; Sequence 8, Application US/10156570A
; Publication No. US20030125242A1
; GENERAL INFORMATION:
; APPLICANT: ROSENECKER, JOSEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 56.9
Best Local Similarity 77.8
Matches 7; Conservative
                            TITLE OF INVENTION: CATHEI FILE REFERENCE: IOWA:035US
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5 RLRKFRNKI 13
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ORGANISM: Ovis aries
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| RLRKFRNKI
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US-10-344-709C-15
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| Sequence 5, Application US/10060102
| Publication No. US20030022829A1
| GENERAL INFORMATION:
| APPLICANT: MAURY, WENDY
| APPLICANT: STAPLETON, JACK
| APPLICANT: STAPLETON, JACK
| APPLICANT: STAPLETON, DACK
| APPLICANT: STAPLETON, DATE OF STAPLETON NUMBER: US/10/060,102
| TITLE OF INVENTION: CATHELICIDINS
| TITLE OF INVENTION NUMBER: 60/309,368
| FILE REFERENCE: 2001-08-01
| PRIOR FILING DATE: 2001-01-30
| PRIOR FILING DATE: 2001-01-30
| PRIOR FILING DATE: 2001-01-30
| SOFTWARE: PALCHIN VEY: 2.1
| SEQ ID NO 5
| LENGTH: 37
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                       APPLICANT: UNILEVER, PLC
TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
FILE REFERENCE: Lipopolysaccharide Immunoassay
CURRENT APPLICATION NUMBER: US/10/131,433
CURRENT FILING DATE: 2002-04-23
PRIOR PILINGIDATE: 2002-04-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTION OF: 2.1
SEQ ID NO 1
LENGTH: 32
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Pred. No. 50;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.9%;
77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conservative
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5 RLRKFRNKI 13
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5 RLRKFRNKI 13
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                                                                                                                                                                                                                                                                                                        ORGANISM: Lapine
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5:223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 283343
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TTTLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TTLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TTLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EIENGTH: 74
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US-10-424-599-281095
                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_18560C.1.pep
US-10-424-599-195497
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US-10-424-599-283343
                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 15;
Pred. No. 1.7e+02;
2; Mismatches 2.
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Pred. No. 2.1e+02;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                     53.8%;
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        NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 195497
LENGTH: 58
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APPLICANT: LA ROSA THOMAS J
APPLICANT: Kovalic David K
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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ORGANISM: Glycine max
                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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US-10-424-599-281095
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Should Reserve to the state of the sta
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Publication No. US2004003107241
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROW Thomas J
APPLICANT: About Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: importin-alpha nuclear i OTHER INFORMATION: localization sequence from the IBB domain US-10-156-570A-8
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TITLE OF INVENTION: AND THEIR USE FOR TRANSFERRING NUCLEIC ACID MOLECULES TITLE OF INVENTION: INTO CELLS FILE REPERENCE: VOS.35
FILE REPERENCE: VOS.35
CURRENT APPLICATION NUMBER: US/10/156,570A
CURRENT FILING DATE: 2002-05-24
PRIOR PLLING DATE: 2002-05-24
PRIOR PLLING DATE: 2000-11-23
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 41
TYPE: PRI
TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.4%; Score 36; DB 14; Length 41; 87.5%; Pred. No. 81; tive 0; Mismatches 1; Indels
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US-10-424-599-263628
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Best Local Similarity 58.3
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Best Local Similarity 87.5
Matches 7; Conservative
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ORGANISM: Glycine max
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US-10-424-599-195497
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Sequence 2018, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Rurmer, Glenna C.
APPLICANT: RURMATION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
                                       Sequence 285440, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vinua
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EBNGTH: 67
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Pred. No. 1.5e+02;
0; Mismatches 2
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45.5%; Pred. No. 4.1e+02;
iive 4; Mismatches 2
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Publication No. US20030055236A1
GENERAL INFORMATION:
APPLICANT: Moore, Paul A. et al.
TITLE OF INVENTION: 110 Human Secreted Proteins
FILE REFERENCE: PZ021P1
CURRENT APPLICATION NUMBER: US/10/097,065
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 2018
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Best Local Similarity 77.6
From 7; Conservative
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; ORGANISM: Homo sapiens
US-10-225-567A-2018
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ORGANISM: Glycine max
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Matches 5; Conserv
    RESULT 13
US-10-424-599-285440
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US-10-424-599-201725
; Sequence 201725, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Rosa Thomas J
; APPLICANT: Cao Yongwei
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 30-216323) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201725
; LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 284593, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREENCE: 38-21(53233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EENGTH: 62
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                                                  Gaps
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Score 35; DB 15; Length 74;
Pred. No. 2.1e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_24183C.1.pep
US-10-424-599-201725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_99012C.1.pep
US-10-424-599-284593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
      53.8%;
Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Matches 7; Conservative
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42 RNFKFKIIKS 51
                                                                                                                       || | ||:|
39 YRSFINKUL 47
                                                                                           3 YRKFKNKIL 11
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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Best Local Similarity
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US-10-424-599-284593
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Sequence 15622, Application US/10424599

Sequence 15622, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
CAO YOUGHOUS
APPLICANT:
CAO YOUGHOUS
TITLE OF INVENTION:
FILE REPERENCE:
TILE REPERENCE:
TILE REPERENCE:
TILE REPERENCE:
TOWNER OF INVENTION NUMBER:
US/10/424,599
CURRENT APPLICATION NUMBER:
US/10/424,599
CURRENT FILING DATE:
CURRENT PILING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 272450, Application US/10424599

Bublication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: Acvalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/203-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 272450

LENGTH: 40
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   PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,169
PRIOR FILING DATE: 1997-12-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 517
LENGTH: 29
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Pred. No. 2.6e+02;
2; Mismatches 2; Indels
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US-10-424-599-272450
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Pred. No. 3.6e+02;
4; Mismatches 2.
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Best Local Similarity 45.5%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Glycine max
FEATURE:
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Best Local Similarity
Matches 6; Conserv
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Pred. No. 2.6e+02;
2; Mismatches 2; Indels
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Publication No. US20030204071A1
GENERAL INFORMATION:
APPLICANT: Moore, Paul A. et al.
TITLE OF INVENTION: 110 Human Secreted Proteins
FILE REFERENCE: P2021P1
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CURRENT PELLOATION NUMBER: US/10/372,876
CURRENT PELLING DATE: 2003-02-26
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-106-17
PRIOR PELLING DATE: 1998-12-17
PRIOR PELLING DATE: 1998-12-17
PRIOR PELLING DATE: 1997-12-18
PRIOR PELLOATION NUMBER: 60/068,007
PRIOR PELLOATION NUMBER: 60/068,007
PRIOR PELLOATION NUMBER: 60/068,007
PRIOR PELLOATION NUMBER: 60/068,006
PRIOR PELLING DATE: 1997-12-18
PRIOR PELLING DATE: 1997-12-18
PRIOR PELLING DATE: 1997-12-18
PRIOR PELLING DATE: 1997-12-18
PRIOR PELLING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,367
PRIOR PELLING DATE: 1997-12-19
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: PCT/US98/27059
PRIOR PLILING DATE: 1998-12-17
PRIOR PELICATION NUMBER: 60/068,007
PRIOR PILING DATE: 1997-12-18
PRIOR PLILNG DATE: 1997-12-19
PRIOR PLILNG DATE: 1997-12-18
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Best Local Similarity 60.0%;
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LENGTH: 29
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US-LU-100-050-0400. Application US/10106698
; Sequence 8400. Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides;
; TILE REPERBNE: PA005P1
; TILE REPERBNE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR PLILNG DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SEQ ID NO 8400
; SEQ ID NO 8400
; LENGTH: 51
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Sequence 188932, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Show Yihuua
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 188932
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE LOCATION: (8) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE LOCATION: (24)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-8400
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Pred. No. 4.6e+02;
0; Mismatches 4; Indels
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Best Local Similarity 63.6%;
Matches 7; Conservative (
                              3 YRKFKNKILKS 13
                                                                      12 YRRFEKEKLKS 22
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US-10-424-599-188932
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US-10-106-698-8400
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| Publication No. US20040031072A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Cao Yongue
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| CURRENT APPLICATION NUMBER: US/10/424,599
| CURRENT PLICATION NUMBER: US/10/424,599
| CURRENT FILING DATE: 2003-04-28
| SEQ ID NO 167177
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49.2%; Score 32; DB 10; Length 46;
Best Local Similarity 54.5%; Pred. No. 4.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 15; Length 45;
Pred. No. 4e+02;
4; Mismatches 3; Indels
                                                                      Score 32; DB 15; Length 45; Pred. No. 4e+02;
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112450C.1.pep
US-10-424-599-156622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_121977C.1.pep
US-10-424-599-167177
                                                                                                                4; Mismatches
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US-09-801-089-20
                                                                    Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 41.7%;
Matches 5; Conservative
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26 RFRMLKUNLLRA 37
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29 RWRKYGQKVVK 39
                                                                                                                                                          2 RYRKFKNKILK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                   US-10-424-599-167177
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US-09-801-089-20
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Gaps
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OTHER INFORMATION: MAP TO AC005562.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53

OTHER INFORMATION: SWISSPROT HIT: P13264, EVALUE 1.60e+00

OTHER INFORMATION: EST_HUMAN HIT: AW369688.1, EVALUE 1.00e-18

US-09-864-761-47051
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TITLE OF INVENTION: GENES REGULATING PROGRAMMED CELL DEATH
FILE REFERENCE: 4115-131
CURRENT APPLICATION NUMBER: US/10/016,768
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ 1D NOS: 12
SOFTWARE: Patentin version 3.1
SEQ 1D NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR PTLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
PRIOR FILING DATE: 2001-01-29
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47051
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Pred. No. 4.7e+02;
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COTHER INFORMATION: X can be any amino acid
US-10-016-768-4
                                                                                         APPLICATION NUMBER: PCT/USO1/00667

R FILING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R FILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/USO1/00669

R PILING DATE: 2001-01-30

R APPLICATION NUMBER: PCT/USO1/00665
                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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Publication No. US20020142443A1
GENERAL INFORMATION:
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Matches 6; Conservative
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NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-016-768-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Vongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Di, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 189893
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                                                                                                                                                                Score 32; DB 15; Length 52; Pred. No. 4.7e+02; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 16; Length 52;
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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CTHER INFORMATION: Clone ID: PAT_MRT4530_86358C.1.pep
US-10-437-963-189893
                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_14161C.1.pep
US-10-424-599-188932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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Publication No. US20040123343A1
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Patent No. US20020048763A1
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                            Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                       3 YRKFKNKILKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Oryza sativa
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-437-963-189893
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Squence 247535, Application US/10424599
Suguence 247535, Application US/10424599
Sublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 247535
LENGTH: 54
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49.2%; Score 32; DB 15; Length 54
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 5; Mismatches 0; Indels
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49.2%; Score 32; DB 16; Length 54
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_65553C.1.pep
US-10-424-599-247535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 304, Application US/10798512
Fublication No. US20040152164A1
GENERAL INPORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: PZ039P1
CURRENT APPLICATION NUMBER: US/10/798,512
CURRENT FILING DATE: 2004-03-12
FRIOR APPLICATION NUMBER: PCT/US00/08979
FRIOR FILING DATE: 2000-10.10
FRIOR FILING DATE: 2000-0.10
FRIOR FILING DATE: 1999-04-06
FRIOR FILING DATE: 1999-04-26
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29 QYQKFRSEIL 38
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US-10-798-512-304
|:||:|; |
14 YOKFRNOFL 22
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14 YQKFRNOFL 22
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ORGANISM: Glycine max
                                                                                                                                            US-10-424-599-247535
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                                                                                                                                                                                                                                                                                                                    Sequence 202804, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cav Yongwei
APPLICANT: Cav Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFREENCE: 38-21(5323.3)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 53
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Pred. No. 4.7e+02;
                          Score 32; DB 13; Length 53;
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_25157C.1.pep
US-10-424-599-202804
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Publication No. US20030050442A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 62 Human Secreted Proteins

FILE REFERENCE: PS039P1

CURRENT APPLICATION NUMBER: US/10/050,704

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: 09/684,524

PRIOR APPLICATION NUMBER: ECT/US00/08979

PRIOR PILING DATE: 2000-10-10

PRIOR FILING DATE: 1999-04-06

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-06

PRIOR PELING DATE: 1999-04-06

PRIOR PELING DATE: 1999-04-06

NUMBER OF SEQ ID NOS: 344

SECTIVARE: PATENTIN VET. 2.0
                                                                                   5; Mismatches
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                          49.2%;
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Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                5; Conservative
                                                                                                                                            2 RYRKFKNKILK 12
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9 RYRQYNSEILE 19
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US-10-050-704-304
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                       Query Match
Bést Local Similarity
Matches 5; Conserva
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LENGTH: 54
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US-10-437-963-198724

Sequence 198724, Application US/10437963

Sequence 198724, Application US/10437963

Publication No. US20040123343A1

GENERAL INPORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bucharuk, Brad

APPLICANT: APPLICANT: Size Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 198724
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                   PRIOR PELICATION NUMBER: 1997-12-19
PRIOR PELING DATE: 1997-12-19
PRIOR PELICATION NUMBER: 60/068,367
PRIOR PELICATION NUMBER: 60/068,368
PRIOR PILING DATE: 1997-12-19
PRIOR PELICATION NUMBER: 60/068,169
PRIOR PELING DATE: 1997-12-19
PRIOR PELING DATE: 1997-12-19
PRIOR PELING DATE: 1997-12-19
PRIOR PELING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-12-19
PRIOR FILING DATE: 1997-12-12-19
PRIOR FILING DATE: 1997-12-12-19
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
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US-10-437-963-198724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 16;
Pred. No. 5.4e+02;
2; Mismatches 2
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Sequence 55582, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
            APPLICATION NUMBER: 60/068,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.2%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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17 RYLKIKSKLL 26
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34 YMKQKNEVLK 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                         TITLE OF INVENTION: 110 Human Secreted Proteins TITLE OF INVENTION: 110 Human Secreted Proteins CURRENT APPLICATION: 110 Human Secreted Proteins CURRENT APPLICATION NUMBER: US/10/097,065 CURRENT FILING DATE: 2002-03-14 PRIOR APPLICATION NUMBER: ECT/US98/27059 PRIOR APPLICATION NUMBER: 60/070,923 PRIOR PELING DATE: 1997-12-18 PRIOR APPLICATION NUMBER: 60/068,007 PRIOR PILING DATE: 1997-12-18 PRIOR APPLICATION NUMBER: 60/068,057 PRIOR PILING DATE: 1997-12-18 PRIOR PILING DATE: 1997-12-19 PRIOR PILING DATE: 1997-12-19 PRIOR PILING DATE: 1997-12-19 PRIOR PILING DATE: 1997-12-19 PRIOR PELING DATE: 1997-12-19 PRIOR PILING DATE: 1997-12-19 PRIOR PELING DATE: 1997-12-19 PRIOR PELING DATE: 1997-12-19 PRIOR PILING DATE: 1997-12-18 PRIOR PILING DATE: 1997-12-19 PRIOR PILING PI
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Sequence 516, Application US/10372876

Sequence 516, Application US/10372876

BUBLICARION:
THENERAL INFORMATION:
TITLE OF INVENTION: 110 Human Secreted Proteins
FILE REFERENCE: PZ021P1

CURRENT APPLICATION NUMBER: US/10/372,876

CURRENT FILING DATE: 2003-02-26

PRIOR PILING DATE: 1999-06-17

PRIOR PILING DATE: 1999-06-17

PRIOR PILING DATE: 1998-12-17

PRIOR PILICATION NUMBER: 60/070,923

PRIOR PILING DATE: 1997-12-18

PRIOR PILING DATE: 1997-12-18

PRIOR PILING DATE: 1997-12-18

PRIOR PILING DATE: 1997-12-18
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Pred. No. 5e+02;
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Application US/10097065
o. US20030055236A1
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Best Local Similarity 60.0%;
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US-10-097-065-516
Sequence 516, Applica
Publication No. US200
GENERAL INFORMATION:
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CURRENT APPLICATION: LORDARIS US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 05/191,078

PRIOR PILING DATE: 2000-03-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-24

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-12-22

PRIOR PILING DATE: 2001-12-22

PRIOR PILING DATE: 2001-10-2-9

PRIOR PILING DATE: 2001-10-2-16

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                               Gaps
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Pred. No. 6.3e+02;
2; Mismatches 1; Indels
                                                                                                              Score 32; DB 15; Length 69
Pred. No. 6.2e+02;
4; Mismatches 2; Indels
      , OTHER INFORMATION: Clone ID: PAT_MRT3847_130894C.1.pep
US-10-424-599-177050
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54299, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 49.2%;
Similarity 62.5%;
5; Conservative
                                                                                                                    49.2%;
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Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                    Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                      2 RYRKFKNKILK 12
                                                                                                                                                                                                                                                                                              42 RWRKYGOKVVK 52
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Best Local Similarity
Matches 5; Conserv
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US-10-282-122A-54299
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FEATURE:
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Sequence 243309, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Roba Thomas J
APPLICANT: Con Valic David K
APPLICANT: Can Valua
APPLICANT: Can Vangwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 12023)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 243309
LENGTH: 67
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APPLICANT: LA ROBE Thomas J
APPLICANT: LA ROBE Thomas J
APPLICANT: CAN STAIN APPLICANT: CAN STAIN APPLICANT: CAN STAIN APPLICANT: CAN STAIN APPLICANT: CAN STAIN APPLICANT: CAN STAIN APPLICANT: CAN STAIN APPLICANTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(3323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REPERENCE: 38-21(53535)B
CURRENT APPLICATION WHERE: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
LENGTH: 60
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Pred. No. 6e+02;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
49.2%; Score 32; DB 16; Length 60;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels
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US-10-424-599-243309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: 30164225.pep
US-10-767-701-55582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||: |||:|
59 RYQFFKNEI 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |||:|:
42 YNKFKHKV 49
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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US-10-424-599-177050
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US-10-424-599-243309
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LENGTH: 69
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APPLICANT: Goldberg, Robert B.
APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
FILE REFERENCE: 023070-086110US
CURRENT APPLICATION NUMBER: US/10/213,512
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: US/09/177,206
PRIOR PILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-10-22
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOUTHARE: Patentin Ver. 2.0
SEQ ID NO 173
LENGTH: 17
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TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
FILE REFERENCE: 63040-010210
CURRENT APPLICATION NUMBER: US/10/430,685
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/US01/44000
PRIOR PILING DATE: 2001-11-06
PRIOR PLILNG DATE: 2000-11-06
PRIOR FILING DATE: 2000-11-06
                                                                                                                                    Gaps
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                                                                                     Score 31; DB 9; Length 17;
Pred. No. 2.2e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 14;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                         Sequence 173, Application US/10213512
Publication No. US20030110536A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 107, Application US/10430685 Publication No. US20040039543A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fischer, Robert L. APPLICANT: Ohad, Nir APPLICANT: Kiyosue, Tomohiro APPLICANT: Yadegari, Ramin APPLICANT: Margossian, Linda APPLICANT: Harada, John
                                                                                       47.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.2
SEQ ID NO 107
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.7%;
                                                                                  Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-173
                , MOLECULE TYPE: peptide US-09-071-838-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 240
                                                                                                                                                                                 3 YRKFKNKILK 12
                                                                                                                                                                                                                            6 YRKFKTNYTK 15
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  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                      US-10-213-512-173
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; ORGANISM: HOm
US-10-430-685-107
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Sequence 260117, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE SEPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 260117
LENGTH: 74
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Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Vadegari, Ramohiro
APPLICANT: Vadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Pruit Development in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,838
FILING DATE: 01-MAY-1998
CIASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: BASTIAN NUMBER: 34,774
REPERRINCE/DOCKET NUMBER: 023070-086100US
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
INFORMATION OR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
TEMPORE CHARACTERISTICS:
TEMPORE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              ; ' OTHER INFORMATION: Clone ID: PAT_MRT3847_7690C.1.pep
US-10-424-599-260117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 173, Application US/09071838 Patent No. US20020152501A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KFKNKILK 12
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
FILE REPERENCE: PA065P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR PAPLICATION NUMBER: PCT/US00/26524
PRIOR PAPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR PILING DATE: 1999-10-3
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver: 3.0
SEQ ID NO 7310
                                       Sequence 276563, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Show Yihua
APPLICANT: Can Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/303-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 276563
LENGTH: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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US-10-424-599-276563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.7%; Score 31; DB 15; I
100.0%; Pred. No. 5.8e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 14;
Pred. No. 6e+02;
0; Mismatches 2;
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US-10-424-599-143885
; Sequence 143885, Application US/10424599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7310, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
47.7%;
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.78;
77.88;
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Best Local Similarity 77.8
Matches 7; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE LOCATION: (8)
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ORGANISM: Glycine max
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                           US-10-424-599-276563
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                                                                                                                                                                                                                               Sequence 147853, Application US/10424599
Sequence 147853, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Acoustic David K
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENTE: 38-21(52233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 147853
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 196568, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.7%; Score 31; DB 15; Length 28; 36.4%; Pred. No. 3.7e+02; tive 5; Mismatches 2; Indels
    Score 31; DB 15; Length 19;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_104533C.1.pep
US-10-424-599-147853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_19527C.1.pep
US-10-424-599-196568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                4; Mismatches
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50.08;
  47.7%;
50.0%;
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Best Local Similarity 36.4
Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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15 KFQKLKNSLIK 25
                                                                                                                     : |::| |:||
6 KKYRNMIVKS 15
                                                                                            4 RKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                   RESULT 41
US-10-424-599-147853
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                                                                                                                                     셤
```

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### Publication No. US20040031072A1
### GENERAL INFORMATION:
### APPLICANT: La Rosa Thomas J
### APPLICANT: La Rosa Thomas J
### APPLICANT: About Vihua
### APPLICANT: Cao Yongwei
### APPLICANT: Cao Yongwei
### APPLICANT: Cao Yongwei
### TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
### TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
### FILE REFERENCE: 38-21(53223)B
### CURRENT PILING DATE: 2003-40-28
### NUMBER OF SEQ ID NOS: 285684
### SEQ ID NO 143885
### ILENGTH: 46
### TYPE: PRT
### ORGANISM: Glycine max
### PEATURE:
### ORGANISM: Glycine max
### PEATURE:
### ORGANISM: Clone ID: PAT_MRT3847_100941C.1.pep
### OTHER INFORMATION: Clone ID: PAT_MRT3847_100941C.1.pep
### US-10-424-599-143885
### OTHER INFORMATION: Clone ID: PAT_MRT3847_100941C.1.pep
### US-10-424-599-143885
### OTHER INFORMATION: Clone ID: Mismatches 2: Indels 0; Gaps 0;
### ON SECTION OF S
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Search completed: May 16, 2005, 09:23:41 Job time : 50.8621 secs

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us-09-648-816b-5.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein May 16, 2005, 08:21:21; Search time 14.9655 Seconds (without alignments) 69.833 Million cell updates/sec Run on:

1 KLYRKFKNKLLKLK 14 US-09-648-816B-5 70 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched:

301394 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued Patents AA:*

(/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(/cgn2_6/ptodata/1/iaa/backfiles1.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Appli	Appli	Appli	Appl	Appli	Appli	App	Appli	Appl	12, App]	25854, 7	22015, 7	Appl	Appl	App	Appl	1, Ap		81, 7	7, Ap	Appl	Appl	App	Appl	App]	Appl	Appl
	ជ	5,	ω,	è,	6	3,	7,	10,	4	11,	12,	258	220	27,	29,	27,	29,	7521,	5000,	25381	2777,	95,	95,	95,	95,	95,	95,	89,
	Description	uce	nce	oce	nce	nce	nce	nce	Sce	nce	ce	gce	nce	oce.	ace.	ge				Ce	ce	ace.	nce	ge	nce	nce	nce	nce
	cri	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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ű		69A	69A	69A	69A	69A	69A	69A	69A	9-	9-	96A	96A	31-	31-	047	047	990	10-	96A	33-	11A	83-	05-	73A	62-	- 44	03-
SUMMAKIES		-525-269A-5	US-09-525-269A-8	-525-269A-6	US-09-525-269A-9	25-2	25-2	US-09-525-269A-10	US-09-525-269A-4	US-08-233-203-11	US-08-233-203-12	US-09-248-796A-25854	US-09-248-796A-22015	US-07-725-331-27	US-07-725-331-29	PCT-US91-05047-2	PCT-US91-05047-29	13-9	US-09-583-110-5000	US-09-248-796A-25381	US-09-107-433-277	US-08-311-611A-9	US-08-372-783-95	-08-372-105-95	US-08-306-473A-95	US-08-209-762-95	US-08-473-344-95	US-08-621-803-89
		-09-5	9-5	9-5	9-5	9-5	9-5	9-5	9-5	8-2	8-2	9-2	9-2	7-7	7-7	·US9	·US9	9-5	9-5	9-2	9-1	8-3	8-3	8-3	8-3	8-2	18-4	9-8
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Sequence Seq
US-08-485-445A-95 US-08-621-259A-33 US-09-119-263-95 US-08-657-162-95 US-09-203-539-95 US-09-217-332-89 US-09-217-332-89 US-09-677-664B-33 US-09-677-664B-33 US-09-677-664B-33 US-09-677-664B-33 US-09-677-664B-33 US-09-677-664B-33 US-09-677-664B-33 US-09-677-664B-33 US-09-677-684B-33 US-09-677-684B-33 US-09-322-931-7 US-09-322-931-54 US-07-725-331-54
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ALIGNMENTS

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PEATURE:
OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
                                                                                                           APPLICANT: Shen, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antindrobbial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 1990-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.
                        Sequence 5, Application US/09525269A Patent No. 6743769 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
JS-09-525-269A-5
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Gaps ö 100.0%; Score 70; DB 4; Length 14; 100.0%; Pred. No. 0.00029; ative 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 14; Conservative

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RESULT 2 US-09-525-269A-8

Sequence 8. Application US/09525269A;
Patent No. 6743769;
GENERAL INFORMATION:
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Mecapeptides
TITLE OF INVENTION: Mecapeptides
FILE REFERENCE: 66742-025 (HR6614);
CURRENT APPLICATION NUMBER: US/09/525,269A;
CURRENT APPLICATION NUMBER: US 09/025,319;
PRIOR APPLICATION NUMBER: US 09/025,319;
PRIOR APPLICATION NUMBER: US 09/025,319;
NUMBER OF SEQ ID NOS: 39

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RESULT 6
US-09-525-269A-7
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                                                                                                                                  OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial CTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-8
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80.0%; Score 56; DB 4; Length 14;
Best Local Similarity 78.6%; Pred. No. 0.034;
Matches 11; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yearn, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT PEPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT PILING DATE: 2000-03-13
PRIOR PILING DATE: 1998-02-18
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 13
TYPE: PRT
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8 LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09525269A; Patent No. 6743769; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09525269A; Patent No. 6743769
                                                                                        ORGANISM: Artificial Sequence
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tes 9; Conserv
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US-09-525-269A-6
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US-09-525-269A-9
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                                                                      IYPE: PRT
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                                                                   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
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Patent No. 6743769

GENERAL INPORMATION:
APPLICANT: Shem, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HRS614)
CURRENT APPLICATION NUMBER: US/09/525,269A

CURRENT APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 2000-03-13

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                        DB 4; Length 13
                                                                                                                                                                                                                                      0; Indels
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Sequence 3.7.7.

Patent No. 6743769

GENERAL INFORMATION:

APPLICANT: Shen, Alexander J.

TITLE OF INVENTION: Antimicarchial Peptides and Derived

TITLE OF INVENTION: Metapeptides

FILE REFERENCE: 66742-025(RR5614)

CURRENT APPLICATION NUMBER: US/09/525,269A

CURRENT PILING DATE: 2000-03-13

PRIOR PAPLICATION NUMBER: US 09/025,319

PRIOR FILING DATE: 1998-02-18
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Pred. No. 0.49;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 18
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                        68.6%;
81.8%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Annea J.
APPLICANT: Darveau, Sames J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 1; Length 20;
Pred. No. 15;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Bristol-Myers Squibb Company, Patent ADDRESSEE: Department STREET: 3005 First Avenue CITY: Seattle STATE: Mashington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                               1; Mismatches
                                                  Score 43; I
Pred. No. 2.
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FILING DATE:
CLASSIPICATION: 514

RIOR APPLICATION DATE:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
APPLICATION NUMBER: US 07/484,020
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 32,928
TELECOMMUNICATION INFORMATION:
TELEPHONE: 26/728-4800
                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/08233203
Patent No. 5409898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 12, Application US/08233203
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                                                  61.4%;
80.0%;
                                               Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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TOPOLOGY: linear
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     US-09-525-269A-4
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; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon ; OTHER INFORMATION: microbiocidal domains from platelet microbial ; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
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Pred. No. 2.6;
2; Mismatches 0; Indels
                                                                                                                        4; Length 13;
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Patent No. 6743769

GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A

CURRENT APPLICATION NUMBER: US 09/025,319

PRIOR PILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yearnam, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antinicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT PEPLICATION NUMBER: US/09/525,269A
CURRENT PELING DATE: 200-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
INVENTIOR PRIOR PRIOR MINDOWS NUMBER OF SEQ ID NO 10
SEQ ID NO 10
INVENTIOR PRIOR PRIOR MINDOWS NUMBER OF SEQ ID NO 10
SEQ ID NO 10
                                                                                                                        Score 44; DB
Pred. No. 1.9;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09525269A Patent No. 6743769 GENERAL INFORMATION:
                                                                                                                        62.9%;
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80.0%;
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                                                                                                                   Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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KLYKKWKNKL 10
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YRKFRNKILR 12
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US-09-525-269A-10
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GENERAL INFORMATION:
APPLICANT: Keith Weinstcock et al
APPLICATION UNDER: US (90/248,796A
CURRENT PAPLICATION NUMBER: US (90/074,725
PRIOR APPLICATION NUMBER: US (00/074,725
PRIOR PRIOR APPLICATION NUMBER: US (00/074,725
PRIOR PLIING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
SRIOR PLIING DATE: 1998-08-13
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| Patent No. 5294605
| GENERAL INPORMATION:
| APPLICANT: Houghten, Richard
| APPLICANT: Houghten, Richard
| TITLE OF INVENTION: Ampliphilic Peptide Compositions and
Inventions and Invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 66;
88;
                                                                                                                                                       DB 4; Length 61;
58;
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                                                                                                                                                                                                                          3; Mismatches
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Pred. No. 8
                                                                                                                                                           Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22015, Application US/09248796A Patent No. 6747137
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patenti-
                                                                                                                                                           54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.9%;
                                                                                                                                                                                                                                                                                                                             1 KLYRKFKNKLLKLK 14
                                 TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLYRKFKNKLLKL 13
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10 RIYHSFKTKLVEL 22
                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 46.2
Matches 6; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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US-09-248-796A-22015
                                                                                            US-09-248-796A-25854
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US-07-725-331-27
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LENGTH:
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Sequence 25854, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
FALL MEDILAMTION:
FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:
FILE PEPERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

FRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

SEQ ID NO 25854
                                                    APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
APPLICANT: Cosand, Wesley L.
APPLICANT: WINTER COSAND AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
ANTIMER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brietol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: ON0063A
TELECOMUNICATION INFORMATION:
TELEPHONE: 206/728+800
TELEFAX: 206/448-4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98121
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 66.77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLYRKFKNKLLK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
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US-09-248-796A-25854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-233-203-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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PCT-US91-05047-27
Sequence 27, Application PC/TUS9105047
Sequence 27, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Sylvie
ITILE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Ampliphilic Peptide Compositions and TITLE Peptide Comp
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                                                                            OTHER INFORMATION: May be a C-terminal amide, and/or may OTHER INFORMATION: be acetylated at N-terminus. US-07-725-331-29
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                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                    4; Indels
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                                                                                                                                                                                                                                                          Score 36; DB 1
Pred. No. 39;
1; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION S14
PRIOR APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 29,381
REFRENCE/DOCKET NUMBER: 4212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEPHONE: 3126165460
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                      Query Match 51.4%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLYRKFKNKLLKL 13
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KLLKKLKKKLKKL 14
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        MOLECULE TYPE: peptide
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STRANDEDNESS:
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Matches 8; Conserva
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Patent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE COMPOSITION Amphiphilic Peptide Composition Amphiphilic Peptide Composition Amphiphilic Peptide Composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: May be a C-terminal amide, and/or may OTHER INFORMATION: be acetylated at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.4%; Score 36; DB 1; Length 18; 61.5%; Pred. No. 39;
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                    NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEPHONE: 3126165408
INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLYRKFKNKLLKL 13
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-07-725-331-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-725-331-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Sequence 25381, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                          Sequence 5000, Application US/09583110 Patent No. 6699703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans
                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                            1 KLYRKFKNKL 10
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16 RLWRKYSNKL 25
                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 KKFRKFKNR 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lynn Doi
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US-09-248-796A-25381
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                                                                                        US-09-513-999C-7521
                                                                                                                                                                                                                                                                                                                             US-09-583-110-5000
          SEQ ID NO 7521
LENGTH: 62
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| Sequence 7521, Application US/09513999C
| Patent No. 6783961
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Dumas Milne Edwards, J.Y.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| PATENT APPLICATION NUMBER: US/09/513,999C
| CURRENT APPLICATION NUMBER: US 60/122,487
| PRIOR APPLICATION NUMBER: US 60/122,487
| PRIOR FILING DATE: 1999-02-26
| WINMER OF SEQ ID NOS: 36681
| SOFTWARE: Patent.pm
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PCT-US91-05047-29
; Sequence 29, Application PC/TUS9105047
; GENERAL INFORMATION:
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
; TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May be a C-terminal amide, a be acetylated at N-terminus.
                                                                                                                                                                                     ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow STREET: 180 North Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 5;
Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILLING DATE: 19910717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REPERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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; OTHER INFORMATION:
PCT-US91-05047-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPOLOGY: linear
                                                                                                                                                                                                                                             Chicago
                                                                                                                                                                                                                                                                                      USA
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US-09-513-999C-7521
                                                                                                                                                                                                                                                                                                       60601
                                                                                                                                                                                                                                                                                      COUNTRY:
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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANK
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR RILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 25381
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Nucleic Acid and Therapeutics
FILE REFERENCE: PATHON-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT APPLICATION NUMBER: US 09/107,433
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1999-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 5000
LENGTH: 68
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   Length 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
51.4%; Score 36; DB 4; I
60.0%; Pred. No. 1.2e+02;
:ive 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 4; I
Pred. No. 1.8e+02;
2; Mismatches 1;
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APPLICANT: Lambert, Jr., Lewis H.
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
TITLE OF INVENTION: Infection by Administration of
TITLE OF INVENTION: Bactericidal/Permeability-Increasing
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 95, Application US/08372783
Patent No. 5578572
GENERAL INFORMATION:
APPLICANT: Horwitz, Arnold H.
APPLICANT: Lambert, Lewis H.
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.3%; Score 34.5; DB 1; Length 28; 56.2%; Pred. No. 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PRETENTING Release #1.0, Version #1.25

SOFTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/311,611A

FILING DATE: 11-701-1994

FILING DATE: 11-701-1994

PRIOR APPLICATION NUMBER: 08/125,651

FILING DATE: 22-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sharp, Jeffrey S.

REGISTRATION NUMBER: 31,979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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N. "BPI.101"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLYRKFKNK---LLKL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
Kung, Ada H.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.2<sup>3</sup>
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , NAME/KEY: misc feat; OTHER INFORMATION: US-08-311-611A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Se
CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-372-783-95
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                                                                                                                                                                                                                                                                                                       FOR DIAGNO
                                                                                                                                                                             Sequence 2777, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.0%; Score 35; DB 4; I Best Local Similarity 66.7%; Pred. No. 1.8e+02; Matches 6; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
SOFTWARE: cUnknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/085131
FILING DATE: July 2, 1997
ATTORNEY/ACENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 60/089
REFERENCE/DOCKET NUMBER: 67-011
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...70
SEQUENCE DESCRIPTION: SEQ ID NO: 2777:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-311-611A-95; Sequence 95, Application US/08311611A Fatent No. 552328; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2777:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cohen, Jonathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYPE: amino acid
                                                |:||| | | |:
16 KVYRKVKKKONLR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :||||||
41 KKFRKFKNR 49
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                                                                                                                                                              US-09-107-433-2777
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                                                                                                                                        RESULT 20
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DB 1; Length 28;
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TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Biologically Active Peptides from
TITLE OF INVENTION: Functional Domains of Bactericidal/.
TITLE OF INVENTION: Permeability-Increasing Protein and
TITLE OF INVENTION: Uses Thereof
NOWBER OF SEQUENCES: 226
NOWBER OF SEQUENCES: 226
NORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: Suite 3000, 10 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,473A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
49.3%; Score 34.5; Di
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                    NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 95, Application US/08306473A Patent No. 5652332
           FILING DATE: 11-002-PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/209,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
FILING AGENT INFORMATION:
                                                                                      FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
08/273,540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: "XMP.101"
US-08-372-105-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             TELERAX: 312/4/2 CTELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 95
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLYRKFKNK---LLKL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-306-473A-95
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US-08-372-105-95
i Sequence 95, Application US/08372105
j Patent No. 5627123
i GENERAL INFORMATION:
APPLICANT: Little, Roger G.
APPLICANT: Limbert, Lewis H.
APPLICANT: Cambor, Patrick J.
ITTLE OF INVENTION: Anti-Fungal Materials and Methods
ITTLE OF SEQUENCES: 227
i CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 28;
                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,783
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.3%; Score 34.5; 56.2%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERNCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                             PRIOR PETITION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.101"
US-08-372-783-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KLYRKFKNK---LLKL 13
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KLFFKFKSKVKWLIKL 24
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Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide FEATURE:
                         COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
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When the state of 
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Patent No. 5851802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of TITLE OF INVENTION: Pusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWAREN PACELLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,344
FILING DATE: T-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,473
FILING DATE: 15-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,762
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: "BPI.101"
US-08-473-344-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
9 KLFFKFKSKVKWLIKL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLYRKFKNK---LLKL 13
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 56.2<sup>3</sup>
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Biologically Active Peptides from TITLE OF INVENTION: Functional Domains of Bactericidal/Permeability-Increasing NUMBER OF SEQUENCES: 98 CORRESPONDENCE ADDRESS: ADDRESSE: Allegrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.3%; Score 34.5; DB 1; Length 28; 56.2%; Pred. No. 96; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/209,762
FILING DATE: U1-JAN-1994
CLASSIFICATION: 514
ATTONREY/AGRAT INPORMATION:

REGISTRATION NUMBER: 35,303
REFERENCE/POCKET NUMBER: 35,303
REFERENCE/POCKET NUMBER: 93,1133
TELEFRAX: 312-715-1000
TELEFRAX: 312-715-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 11linois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         49.3%; Score 34.5; 56.2%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 95, Application US/08209762
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OTHER INFORMATION: "BPI.101"
                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
OTHER INFORMATION: "BPI.101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5733872
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologics
TITLE OF INVENTION: Functions
TITLE OF INVENTION: Proctein a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLYRKFKNK---LLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|||:|
9 KLPPKPKSKVKWLIKL 24
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                    TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 56.27
Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 28 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                       US-08-306-473A-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
US-08-209-762-95
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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DB 2; Length 28;
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          APPLICATION NUMBER: 08/209,762
PILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/ASET INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 11018USO8/100-224.P4.C1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-9889
TELEPAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TOPOLOGY: linear
WOLECUE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 21-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-621-259A-33
; Sequence 33, Application US/08621259A
; Patent No. 5858974
; GENERAL INFORMATION:
APPLICANT: Little II, Roger G
APPLICANT: Little III, Roder G
APPLICANT: Fadem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
; VUMBER OF SEQUENCES: 252
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCANDIEWS, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.2%; Pred. No. 96
Matches 9; Conservative 3; Mismatche
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CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,841
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 1102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9889
TELEFRAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
OTHER INFORMATION: "BPI.101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KLYRKFKNK---LLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 KLFFKFKSKVKWLIKL 24
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LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
  APPLICATION NUMBER:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-485-445A-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
LOCATION: C-Terminus
CTHER INFORMATION: /label= Amidation
CTHER INFORMATION: /note= "The C-Terminus is Amidated."
US-08-621-803-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.3%; Score 34.5; DB 2; Length 28; 56.2%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biologically Active Peptides from
Functional Domains of Bactericidal/
Permeability-Increasing Protein and
Uses Thereof
                                                                                           CZIP: 60606-6402
CCMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGESTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELEPAX: 312/474-6300
TELEPAX: 312/474-6448
TELEPAX: 25-3856
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LYPE: amino acid
TYPE: amino acid
TYPE: amino acid
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,445A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: Suite 3400, 500 West Madison Street
CITY: Chicago
STATE: Illinois
ZIPE: USA
ZIP: 60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 28
US-08-485-445A-95
Sequence 95, Application US/08485445A
Sequence 95, Application US/08485445A
RENERAL INFORMATION:
APPLICANT: Little. Roger G.
TITLE OF INVENTION: Biologically Act
TITLE OF INVENTION: Permeability-Inc
TITLE OF INVENTION: Uses Thereof
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
OTHER INFORMATION: "XMP.101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLYRKFKNK---LLKL 13
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||KLFFKFKSKVKWLIKL 24
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
                                                 Illinois
                       Chicago
                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps
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APPLICANT: Cohen, Jonathan

APPLICANT: Kung, Ada H.C.

APPLICANT: Lambert, Jr., Lewis H.

TITLE OF INVENTION: Infection by Administration of

TITLE OF INVENTION: Bactericidal/Permeability-Increasing

TITLE OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 49.3%; Score 34.5; DB 3; Length 28; Best Local Similarity 56.2%; Pred. No. 96; Matches 9; Conservative 3; Mismatches 1; Indels
                                                                                                            49.3%; Score 34.5; DB 3; Length 28; 56.2%; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,162
FILING DATE: 03-UW-1996
CLASSIFICATION: 514
APPLICATION DATA:
APPLICATION NUMBER: 08/311,611
FILING DATE:
                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION UTMBER: 08/273,401
FILING DATE: 11-JUL-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,651
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REJESTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 3251
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application US/08657162 Patent No. 6140306
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.101"
(US-09-119-263-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
COTHER INFORMATION: "BPI.101"
US-08-657-162-95
                                                                                                                                                                                                    1 KLYRKFKNK---LLKL 13
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INPORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: line...
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TELEFAX: 312/474-0448
                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 SCITY: Chicago STATE: Illinoid COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                        US-08-657-162-95
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Patent No. 6054431

GENERAL INFORMATION:
APPLICANT: Horwitz, Arnold H.
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Materials
NUMBER OF SEQUENCES: 237
CORRESPONDENCE ADDRESS:
                                       NAMEKEY: misc feature

OTHER INFORMATION: "XMP.101"

FEATURE:
NAMEKEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /label= Amidation

US-08-621-259A-33
                                                                                                                                                                                                                                                   DB 2; Length 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60606-6402
COMPUTER REABALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,263
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/119,263
APPLICATION NUMBER: US/08/758,116
                                                                                                                                                                                                                                              Query Match 49.3%; Score 34.5; D
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: 08/372,783
FILING DATE:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          1 KLYRKFKNK---LLKL 13
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9 KLFFKFKSKVKWLIKL 24
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LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEB: Marsha
STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
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US-09-119-263-95
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DB 3; Length 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,539
                                                             E: Banner & Allegretti, Ltd.
10 South Wacker Drive, Suite 3000
  Protein and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.5;
Pred. No. 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,762
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REPERENCE/DOCKET 1000
TELECOMMUNICATION INFORMATION:
TELEFHONE: 312-715-1000
TELEFHONE: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sears Tower, 250 CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk PC. compartible
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,473
                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/473,344
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.101"
US-09-093-539-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TITLE OF INVENTION: Pr.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                              STREET: 10 South
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                               ADDRESSEE:
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Biologically Active Peptides from
Functional Domains of Bactericidal/Permeability-Increasing
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                                                                                                                                                                                                                                      Biologically Active Peptides from Functional Domains of Bactericidal/Permeability-Increasing Protein and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTONENYAGENT INFORMATION:
NAME: MONICHOIAS, Janet M.
REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 11018US08/100-224.P4.C1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,480
                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: Suite 3400, 500 West Madison Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.3%; Score 34.5; 56.2%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           Sequence 95, Application US/09224480 Patent No. 6153730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 95, Application US/09093539 Patent No. 6228834 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
COTHER INFORMATION: "BPI.101"
US-09-224-480-95
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologice
TITLE OF INVENTION: Functions
TITLE OF INVENTION: Permeabil
TITLE OF INVENTION: Uses Then
                                              ||:|||:|
9 KLFFKFKSKVKWLIKL 24
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Best Local Similarity 56.27
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-707-9155
TELEFAX: 312-707-9155
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Little,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                         RESULT 32
US-09-224-480-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-093-539-95
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: IBM PC compatible
OPERATING SYSTEM: P-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 257
CORRESPONDENCE ADDRESSS:
ADDRESSE: MCANDTEWN, Held & Malloy, Ltd.
STREET: 500 West Madison Street
                                                                                                                                                                                                                                                                                                                                              Similarity 56.2%; Pred: No. 96; 9; Conservative 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/677,664B
FILING DATE: 07-Mar-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/227,659
FILING DATE: 08-Jan-1999
ATTORNEY AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11021US06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Little II, Roger G
Lim, Edward
Padem, Mitchell B.
TITLE OF INVENTION: Anti-Fungal Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States of America
ZIP: 60661
                                                                                                                                                                                                           NAME/KEY: misc feature

CTHER INFORMATION: "BPI.101"

SEQUENCE DESCRIPTION: SEQ ID NO: 95:

US-09-790-230-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/09677664B Patent No. 6664231 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 312/775-8000
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                         TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-Terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/775-8100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 33 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLYRKFKNK---LLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc fea
OTHER INFORMATION:
                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserva
                      TELEPHONE: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-677-664B-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
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Patent No. 6495516
GENERAL INFORMATION:
APPLICANT: Little, Roger G
TITLE OF INVENTION: Biologically Active Peptides from
Functional Domains of Bactericidal/Permeability-Increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.3%; Score 34.5; DB 3; Length 28; 56.2%; Pred. No. 96; 1; Indels tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: /label= Amidation

CTHER INFORMATION: /note= "The C-Terminus is Amidated."

US-09-217-352-89
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/790,230
FILING DATE: 21-Feb-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 SOUTH Wacker Drive, Suite 3000
                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/473,344
                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27,129/33
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
OTHER INFORMATION: "XMP.101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLYRKFKNK---LLKL 13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp:
                                                                                                                                                                                                                                                                           TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
LOCATION: C-Terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.29
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                      FILING DATE
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US-09-790-230-95
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RESULT 39
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                                                                                                             Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 224
CARRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 96, Application US/09689097
Patent No. 6686332
GENERAL INFORMATION:
APPLICANT: Van Leeuwan, Paul A.M.
APPLICANT: Woan Leeuwan, Paul A.M.
TITLE OF INVENTION: Method of Treating Depressed
TITLE OF INVENTION: Reticuloendothelial System Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: 11linois
COUTRY: United States of America
COUTRY: United States of America
COUTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEM: Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/689,097
                                                                                                             49.3%; Score 34.5; DB 4; 56.2%; Pred. No. 96; tive 3; Mismatches 1;
  OTHER INFORMATION: /label= Amidation
/note= "The C-Terminus is Amidated.";

SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-677-6648-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 49.3%; Score 34.5; I
Best Local Similarity 56.2%; Pred. No. 96;
Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27129/32294
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APPLICATION NUMBER: 09/466,412
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
COTHER INFORMATION: "BPI.101"
US-09-689-097-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 271
TELECOMMUNICATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELBEAK: 312/
TELEFAK: 312/
TELEK: 25-3856
INFORMATION FOR SEG
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|||:|
KLFFKFKSKVKWLIKL 24
                                                                                                                                                                                                   1 KLYRKFKNK---LLKL 13
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KLFFKFKSKVKWLIKL 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTORNEY/AGENT INFORMATION:
                                                                                                                                 Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                              RESULT 37
US-09-689-097-96
                                                                                                                 Query Match
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RESULT 38 PCT-US94-02465-95

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Biologically Active Peptides from Functional Domains of Bactericidal/Permeability-Increasing Protein and Uses Thereof
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TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
TITLE OF INVENTION: Materials
NUMBER OF SEQUENCES: 237
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                              ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US94/02465
FILING DATE: 11-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00498
FILING DATE:
                                                                                                                                                                                   ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.3%; Score 34.5; 56.2%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Sears Tower, 233 South CITY: Chicago STATE: 111inois COUNTRY: United States of America COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATED: OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CT-1395-00498-95
Sequence 95, Application PC/TUS9500498
GENERAL INFORMATION:
Sequence 95, Application PC/TUS9402465 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93,1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGIETRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc feature
; OTHER INFORMATION: "BPI.101"
PCT-US94-02465-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 KLFFKFKSKVKWLIKL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLYRKFKNK---LLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                           STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
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Gaps

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<u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09262
                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION: Anti-Fungal Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Searce CITY: Chicago
STATE: 111inois
COUNTY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 27129/10040
PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 41
PCT-US95-09262-33
; Sequence 33, Application PC/TUS9509262
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,105
PILING DATE: 13-JAN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/306,473
PILING DATE: 11-JUL-94
PRIOR APPLICATION NUMBER: 08/203,540
FILING DATE: 11-JUL-94
PRIOR APPLICATION NUMBER: 08/203,762
FILING DATE: 11-MAR-94
PRIOR APPLICATION NUMBER: 08/183,222
PRIOR APPLICATION NUMBER: 08/183,222
PRIOR APPLICATION NUMBER: 08/093,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-WAR-93
ATTORNEY/AGENT INFORMATION:
NAME: BOYUM, Michael F.
REGISTRATION NUMBER: 25.447
REFERENCE/COMMENT
                                                                                                                           TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc feature

CTHER INFORMATION: "XMP.101"
                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLYRKFKNK---LLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 KLFFKFKSKVKWLIKL 24
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TELEFAX: 312/474-0448
                                                                                                         28 amino acida
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 56.2
Matches 9; Conservative
                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acide
            312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
            TELEFAX:
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Anti-Fungal Materials and Methods NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00656
                                               FILING DATE: 11-UUL-1994
PRIOR APPLICATION DATA:
FILING DATE: 11-UUL-1994
PRIOR APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
FILING DATE: 14-UAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: RIN-Laures, Li-Heien
RGGISTRATION NUMBER: 33,547
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENCE, 02,7474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.3%; Score 34.5;
illarity 56.2%; Pred. No. 96
Conservative 3; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REPERENCE/DOCKET NUMBER: 27129/32415
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COMPUTER READABLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 95, Application PC/TUS9500656 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/183,222
FILING DATE: 14-JAN-1994
ATTORNEY AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/273,540
FILING DATE: 11-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
; OTHER INFORMATION: "XMP.101"
PCT-US95-00498-95
                                                                                                                                                                                                                                                                                                                                                                                                                            95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLYRKFKNK---LLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||: |||:|
|KLFFKFKSKVKWLIKL 24
                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTER.STICS:
LENGTH: 28 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-00656-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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Gaps

1,

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Query Match 49.3%; Score 34.5; DB 1; Length 29; Best Local Similarity 60.0%; Pred. No. 99; Matches 9; Conservative 2; Mismatches 3; Indels
  OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
                                                            LOCATION: 27; OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 3411.3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15325-000920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US93/06731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION NUMBER: 07/916,765
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 92,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 15325-000
TELEPROMUNICATION INPORMATION:
                                                                                                                                                                                                                             1 KLYRKFKNKLL-KLK 14
                                                                                                                                                                                                                                                                      4 KRLRKFRNKIKEKLK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
          FEATURE:
NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                       JS-09-322-911-7
                                                                                                                                                                                                                                                                                                                                  RESULT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             49.3%; Score 34.5; DB 5; Length 28;
56.2%; Pred. No. 96;
tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                           LOCATION: C-Terminus
COTHER INFORMATION: /label= Amidation
COTHER INFORMATION: /note= "The C-Terminus is Amidated"
PCT-US95-09262-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           NAME/KEY: misc feature
OTHER INFORMATION: "XMP.101"
                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLYRKFKNK---LLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                         ||: |||:|
|KLFFKFKSKVKWLIKL 24
                                                                                                                                                                                                         NAME/KEY: Modified-site
                                      LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 56.2
Matches 9; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rEATURE:
NAME/KEY: Region
LOCATION: 26
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US-08-313-681A-7
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Gapa

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Indels

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Pred. No. 73; 1; Mismatches

57.1%;

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1 KLYRKFKNKLLKLK 14
     Best Local Similarity 57.1
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                         DB 3; Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 54, Application US/07725331

Ratent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Ampliphilic Peptide Compositions and
TITLE OF INVENTION: Ampliphilic Peptide Compositions and
TITLE OF INVENTION: Ampliphilic Peptide Compositions and
TITLE OF INVENTION: Address: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6 Milnamow
                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-terminal amide, acetylated at N-terminus.
                                                                                                                                     /note= "Xaa is a Gln or Ile"
                                                                                                                                                                                                                 /note= "Xaa is a Gly or Gln'
                                                             /note= "Xaa is Asp or Lys"
                                                                                                                                                                                                                                                                     11arity 60.0%; Score 34.5; 1 Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421250-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 180 No. 5294605th Stetson
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                           | |||:||: |||
4 KRLRKFRNKIKEKLK 18
                                                                                                                                                                                                                                                                                                                                                     1 KLYRKFKNKLL-KLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
PEATURE:
NAME/KEX:
Region
LOCATION: 23
OTHER INFORMATION:
PEATURE
LOCATION: 26
LOCATION: 26
OTHER INFORMATION: /
                                                                                                                                                                                             LOCATION: 27
COTHER INFORMATION:
US-09-322-911-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION:
; OTHER INFORMATION:
US-07-725-331-54
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                           NAME/KEY: Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 44
US-07-725-331-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                         셤
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48.6%; Score 34; DB 1; Length 17;

Query Match

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Gaps
                                                             RESULT 45

PCT-US91-05047-54

; Sequence 54, Application PC/TUS9105047
; GENERAL INFORMATION:
APPLICANT: Houghten, Richard
; APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: & Milnamow
; STREET: 180 North Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 48.6%; Score 34; DB 5; Length 17; Best Local Similarity 57.1%; Pred. No. 73; Matches 8; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: C-terminal amide, acetylated ; OTHER INFORMATION: at N-terminus. PCT-US91-05047-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: GAMBON, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 16, 2005, 08:40:39
Job time : 15.9655 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
2 KLLKKLLKKLKKKK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLYRKFKNKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KILKKILKKIKKIK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3126165418
3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15
CLASSIFICATION:
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May 16, 2005, 08:38:44 ; Search time 52.6207 Seconds (without alignments) 88.876 Million cell updates/sec
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ptodata/1/pubpaa/USO7_PUB PUB.pep:
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ptodata/1/pubpaa/USO8_PUBGOMB.pep:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ptodata/1/pubpaa/US07_PUBCOMB.pep:
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*
| /cgn2 6 ptodata/1/pubpaa/PCT
| /cgn2 6/ptodata/1/pubpaa/PCT
| /cgn2 6/ptodata/1/pubpaa/US06
                                                                                                                                                                                                                                                                                                   1432185 seqs, 334051727 residues
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                            1 KLYRKFKNKLLKLK 14
                                                                                                                                                                    US-09-648-816B-5
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6
                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 74
                                                                                                                                                                                                                                                 Scoring table:
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Perfect score:
                                                                  OM protein
                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	uo	Sequence 158393,	Sequence 208605,	e 281095,	e 49, Appl	e 55, Appl	e 56, Appl	e 49, Appl	e 55, Appl	e 56, Appl	Sequence 48627, A	Sequence 113, App	e 113, App	44674 A
	Description	Sequenc	Seguence	Sequence	Sednenc	Sequenc	Seguenc	Sequenc	Sequenc	Seguenc	Sequence	Seguenc	Sequenc	Segmenter
	11	US-10-424-599-158393	US-10-424-599-208605	US-10-424-599-281095	US-09-820-053A-49	US-09-820-053A-55	US-09-820-053A-56	US-10-109-171-49	US-10-109-171-55	US-10-109-171-56	US-09-864-761-48627	US-09-798-889-113	US-10-633-680-113	11S-09-864-761-44624
		15	15	15	10	10	10	14	14	14	6	10	15	σ
	Query Match Length DB	73	55	74	23	23	23	23	23	23	24	49	49	73
مدن	Query	60.09	55.7	54.3	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52 9
	Score	42	39	38	37	37	37	37	37	37	37	37	37	17
	Regult No.		7	m	4	ß	9	7	80	0,	10	11	12	13

Sequence 250149, Sequence 147853, Sequence 263628, Sequence 37456, A Sequence 33, Appl Sequence 39, Appl Sequence 95, Appl Sequence 95, Appl Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 15, Appli Sequence 125, Appli	Sequence 124, App Sequence 124, App Sequence 45380, A Sequence 262608, Sequence 16702, Sequence 167072, Sequence 304, App Sequence 20615, Sequence 22615, Sequence 260111, Sequence 260117, Sequence 260117, Sequence 26017, Sequence 218617, Sequence 218617, Sequence 218617, Sequence 225047,
15 US-10-424-599-250149 15 US-10-424-599-147853 15 US-10-424-599-147853 15 US-10-424-599-151016 9 US-09-864-761-37456 9 US-09-765-527-89 9 US-09-765-527-89 15 US-10-768-95 15 US-10-131-431-1 14 US-10-131-431-1 14 US-10-00-102-5 15 US-10-721-839-5 16 US-10-344-709C-15 17 US-10-344-709C-15 18 US-10-344-709C-15 19 US-10-109-171-125	
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115 116 117 118 118 118 118 118 118 118 118 118	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(51223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 158393
LENGTH: 73
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                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114047C.1.pep
US-10-424-599-158393
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US-10-424-599-208605
Sequence 208605, Application US/10424599
Publication No. US20040031072A1
US-10-424-599-158393

Sequence 158393, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Glycine max
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51 RIYKKFKNKI
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                                                                                                                                                                                                      Length 23;
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                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                    Score 37; DB 10;
Pred. No. 68;
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Pred. No. 68;
2; Mismatches 3
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US-09-820-053A-55
Sequence 55, Application US/09820053A
Publication No. US20000083243A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TILLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
TILLE REFERENCE: HELXO27
CURRENT PEPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 55
LENGTH: 23
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                         TYPE: PRT
ORGANIEM: ARTIFICIAL SEQUENCE
PEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD_RES
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OTHER INFORMATION: SYNTHETIC SEQUENCE
US-09-820-053A-55
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                                                                                                                                                                                                      Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                              ; OTHER INFORMATION: AMIDATION US-09-820-053A-49
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Best Local Similarity 58.3.
Best Local 7; Conservative
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10 KLFKKFAKKLAK 21
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Rosa Thomas J
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Diants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; LENGTH: 74
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Kovalic David K

APPLICANT: Cao Yongwei

TITLE CAO YONGWEI

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERBNCE: 38-21(53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 208605:

LENGTH: 55
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US-10-424-599-208605
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Pred. No. 79;
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TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SCFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
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; Sequence 49, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
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69.2%;
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Best Local Similarity 69.2
Matches 9; Conservative
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US-10-424-599-281095
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                           Sequence 49, Application US/10109171
Publication No. US20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
FILE REFERENCE: HELXO28
CURRENT APPLICATION UNDERR: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 55, Application US/10109171
Publication No. US20030109452A1
Publication No. US20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
TILE REPERENCE: HELKO28
CURRENT APPLICATION NUMBER: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE PATENTING DATE: 2002-03-28
SOFTWARE PATENTING DATE: 2002-03-28
SOFTWARE PATENTING DATE: 2002-03-28
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 55
LENGTH: 23
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Publication No. US20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE FILE REPERENCE: HELX028
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Pred. No. 68;
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OTHER INPORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD RES
LOCATION: (23)
OTHER INFORMATION: AMIDATION
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ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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10 KLPKKFAKKLAK 21
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3 KLFKKFAKKLAK 14
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10 KLFKKFAKKLAK 21
                                                                                     RESULT 7
US-10-109-171-49
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US-10-109-171-55
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LENGTH: 23
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Sequence 46627, Application US/09864761
Sequence 46627, Application US/09864761
Fatent No. US20020048763A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION HUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 68;
2; Mismatches 3; Indels
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PRIOR PELLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELLING DATE: 2001-01-30
CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SSOFTWARE: PatentIn Ver. 2.1
SSO ID NO 56
LENGTH: 23
                                                                                                                                                                                                                                                                                          PEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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US-10-633-680-113
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/393,022

PRIOR PILING DATE: EARLIER FILING DATE: 1999-09-09

PRIOR PILING DATE: EARLIER FILING DATE: 1998-03-12

PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 185

SOTTWARE: PARENTIN FILING DATE: 1998-03-12

SEQ ID NOS: 185

SEQ ID NO 113
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Pred. No. 1.4e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                            Length 24;
                                                                                                  FEATURE:
OTHER INFORMATION: MAP TO AC018814.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
US-09-864-761-48627
                                                                                                                                                                                                                                                                         3; Indels
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TITLE OF INVENTION: 31 Human secreted proteins
FILE REFERENCE: POJOGEPICA
FURRENT APPLICATION NUMBER: US/10/633,680
CURRENT FILING DATE: 2003-08-05
PRIOR APPLICATION NUMBER: 09/787,889
PRIOR APPLICATION NUMBER: 09/393,022
PRIOR APPLICATION NUMBER: 09/393,022
PRIOR PILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: PCT/US99/05721
                                                                                                                                                                                                                         52.9%; Score 37; DB 9; 58.3%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 113, Application US/09798889
Publication No. US20030004324A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 31 Human secreted proteins
FILE REPRENCE: P2026A1
CURRENT APPLICATION NUMBER: US/09/798,889
CURRENT FILING DATE: 2001-03-06
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APPLICATION NUMBER: 09/393,022
FILING DATE: 1999-09-09
APPLICATION NUMBER: PCT/US99/05721
FILING DATE: 1999-03-11
APPLICATION NUMBER: 60/077,714
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; Sequence 113, Application US/10633680
; Publication No. US20040030115A1
; GENERAL INFORMATION:
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                  TYPE: PRT
ORGANISM: Homo sapiens
SEQ ID NO 48627
LENGTH: 24
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acondica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.4e+02;
1; Mismatches 2
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-0-04
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-07
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00661
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 1,550 C. PRIOR APPLICATION NUMBER: 60/077,687 PRIOR FILING DATE: 1998-03-12 PRIOR APPLICATION NUMBER: 60/077,696 PRIOR FILING DATE: 1998-03-12 NUMBER OF SEQ ID NOS: 185 SOFTWARE PATENTIN VET. 2.0 SEQ ID NO 113 LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44624, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                    52.9%;
70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovallc David K
APPLICANT: An Ear Son You a
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 1910/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 263628
LENGTH: 52
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; Sequence 151016, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53223)
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                                                                                                                                                                                               Length 28;
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                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_104533C.1.pep
US-10-424-599-147853
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US-10-424-599-151016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_80076C.1.pep
US-10-424-599-263628
                                                                                                                                                                                               Score 35; DB 15;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 15;
Pred. No. 3.1e+02;
3; Mismatches 1
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 57
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Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
60.0%;
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Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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16 FQKLKNSLIKYK 27
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43 KYKNQILKTK 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                        TYPE: PRT
ORGANISM: Glycine max
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         SEQ ID NO 147853
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                                                                                                       FEATURE:
                                    LENGTH:
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AROU Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 250149
LENGTH: 70
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                               OTHER INFORMATION: MAP TO AC005597.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
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58.3%; Pred. No. 2.9e+02;
tive 2; Mismatches 3; Indels
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 44624
'LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                             52.9%;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.0
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4 LFGKLKKKMLKVK 16
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51 YPKFKTORIKLK 62
                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-10-424-599-147853
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US-10-424-599-250149
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Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUNTY: Chicago
STATE: 11inois
COUNTY: United States of America
COUNTY: United States of America
COUNTY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
APPLICATION NUMBER: US/09/765,527
FILING DATA:
APPLICATION NUMBER: 08/621,803
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMPUTERICATION INFORMATION:
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97 US-09-864-761-37456
                                                                                                                                                         Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                         Score 35; DB 9;
Pred. No. 3.7e+02;
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OTHER INFORMATION: (Jabel= Amidation
Onte= "The C-Terminus is Amidated."
SEQUENCE DESCRIPTION: SEQ ID NO: 89:
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TELEFAX: 312/474-0448
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OTHER INFORMATION: "XM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 28 amino acids
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INFORMATION FOR SEQ ID NO: 89:
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Best Local Similarity 56.2%;
Matches 9; Conservative 3
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                                                                                                                                                         50.0%;
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 KLFFKFKSKVKWLIKL
                                                                                                                                                         Query Match 50.0
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          : | | : | | | 46 KKMKMKMLKLK 56
                                                                                                                                                                                                                                                                       4 RKFKNKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
US-09-765-527-89
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                                                                                                                                                                                                                                                                                              Sequence 37456, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                 Gaps
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EXPRESSED IN HEART, SIGNAL = 1.4
EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
EXPRESSED IN BT474, SIGNAL = 1.5
EXPRESSED IN BRAIN, SIGNAL = 1.9
EXPRESSED IN BONE MARROW, SIGNAL = 1.3
EXPRESSED IN LING, SIGNAL = 1.3
                                                 Indels
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SEQ ID NO 37456
LENGTH: 63
                       Pred. No. 3.4e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE REPRENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-09-03
PRIOR PELING DATE: 2000-09-03
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
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                    Best Local Similarity 72.7%;
Matches 8; Conservative
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                                                                                                        1 KLYRKFKNKLL 11
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42 KLSNLFKNKLL 52
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                          RESULT 18
US-09-864-761-37456
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APPLICANT: Little, Roger G
TITLE OF INVENTION: Biologically Active Peptides from
Functional Domains of Bactericidal/Permeability-Increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.3%; Score 34.5; DB 15; Length 28; 56.2%; Pred. No. 2e+02;
                                                                                                                                                                                                                               Sequence 95, Application US/10446628
Publication No. US20040023884A1
GENERAL INFORMATION:
APPLICANT: Little, Roger G.
TITLE OF INVENTION: Biologically Active Peptides from TITLE OF INVENTION: Biologically Active Peptides from TITLE OF INVENTION: Bronchional Domains of Bactericidal/TITLE OF INVENTION: Permeability-Increasing Protein and TITLE OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

EDWITTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: DEPOPY disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: DECOMPATION COMPUTER: DECOMPATE: DECOMPUTER: DECO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: Suite 3400, 500 West Madison Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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US-10-319-786-95
; Sequence 95, Application US/10319786
; Publication No. US20040024179A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
OTHER INFORMATION: "BPI.101"
1 KLYRKFKNK---LLKL 13
                                       ||:|||:||||
9 KLFFKFKSKVKWLIKL 24
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TELEPAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                               RESULT 21
US-10-446-628-95
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49.3%; Score 34.5; DB 9; Length 28;
Best Local Similarity 56.2%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                               APPLICANT: Little II, Roger G.
Lim, Edward
Lim, Edward
Mitchell B.
TITLE OF INVENTION: Atti-Fungal Peptides
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th FloorDrive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/881,490
FILING DATE: 14-Jun-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MONICOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 100-238/11021US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPRAX: 312/707-9155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: «Unknown»
APPLICATION NUMBER: 08/372,105
FILING DATE: 13-JAN-95
APPLICATION NUMBER: 08/306,473
FILING DATE: 15-SEP-94
APPLICATION NUMBER: 08/273,540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-JUL-94
APPLICATION NUMBER: 08/209,762
FILING DATE: 11-MAR-94
APPLICATION NUMBER: 08/183,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/119,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-JAN-94
APPLICATION NUMBER: 08/093,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-JUL-93
APPLICATION NUMBER: 08/030,644
FILING DATE: 12-MAR-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc feature
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                                                                                                                                   Sequence 33, Application US/09881490 Patent No. US20020077298A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                               RESULT 20
US-09-881-490-33
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us-09-648-816b-5.rapb

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US-10-060-102-5

US-10-060-102-5

Sequence 5. Application US/10060102

Publication No. US2033022829A1

GENERAL INFORMATION:

APPLICANT: WARK; WENCH, WARK

APPLICANT: STAPLETON, JACK

APPLICANT: TACK, BRIAN

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIF

TITLE OF INVENTION: CATHELICIDINS

FILE REPERENCE: IOWA:035US

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/309,368

PRIOR PILING DATE: 2001-08-01

PRIOR PILING DATE: 2001-08-01

PRIOR PILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE PATENTIN VOR: 2.1

SEQ ID NO 5

LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-721-839-5

Sequence 5, Application US/10721839

Sequence 5, Application US/10721839

Publication No. US20040086535A1

GENERAL INFORMATION:
APPLICANT: MARK

APPLICANT: STAPLETON, JACK
APPLICANT: TACK, BRIAN

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: UOYEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEPENSINS AND MAMMALLI

TITLE OF INVENTION: CATHELICIDINS

TITLE OF INVENTION: CAL-11-25

CURRENT PELING DATE: 2003-11-25

PRIOR PELING DATE: 2001-08-01

PRIOR PELING DATE: 2001-08-01

PRIOR PELING DATE: 2001-08-01

PRIOR PELING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PATENTING DATE: 201-08-01

SOFTWARE: PATENTING DATE: 201-08-01

TYPE: PRI

TYPE: PRT
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  Length 32;
                                                  Indels
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Score 34.5; DB 14;
Pred. No. 2.3e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.5; DB 14;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.3%;
       49.3%;
                                                                                                1 KLYRKFKNKLL-KLK 14
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4 KRLRKFRNKIKEKLK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KRLRKFRNKIKEKLK 18
    Query Match
Best Local Similarity 60.09
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
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Sequence 1, Application US/10131433

Publication No. US20030054422A1

GENERAL INFORMATION:

APPLICATV: UNITEVER.

TITLE OF INVENTION: Lipopolysaccharide Immunoassay

CURRENT APPLICATION NUMBER: US/10/131,433

CURRENT FILING DATE: 2002-04-23

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

NUMBER: OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

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9; Conservative 3; Mismatches 1; Indels
                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
CONTRY: USA
ZIP: 66666
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
  Protein and Uses Thereof NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/319,786
FILING DATE: 13-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/473,344
FILING DATE: 7-UN-1995
APPLICATION NUMBER: US 08/306,473
FILING DATE: 11-SEP-1995
APPLICATION NUMBER: US 08/209,762
FILING DATE: 11-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: "BPI.101"
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: McDonnell, John J.
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KLYRKFKNK---LLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserva
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; ORGANISM: Lapine
US-10-131-433-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-319-786-95
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US-10-131-433-1
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Sequence 125, Application US/10109171
Publication No. US20030109452A1
SEMERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 124, Application US/10109171
Publication No. US20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
CURRENT APPLICATION UNMBER: US/10/109,171
CURRENT PILING DATE: 2002-03-28
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Pred. No. 1.5e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 14;
Pred. No. 1.4e+02;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 124, Application US/09820053A; Publication No. US20030083243A1; Fublication No. US20030083243A1; GENERAL INFORMATION:
APPLICANT: Owen, Donald R.; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES; TILL REPERRENCE: HELMO27; CURRENT APPLICATION NUMBER: US/09/820,053A; CURRENT FILING DATE: 2001-03-28; NUMBER OF SEQ ID NOS: 165; SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 124
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 125
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION; SYNTHETIC SEQUENCE US-10-109-171-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: SYNTHETIC SEQUENCE NAME/KEY: MOD_RES
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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1 KLWKKWAKKWLKL 13
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                                     RESULT 28
US-10-109-171-125
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                                                                                                                                                                                                                                                                                                          APPLICANT: JORG FRITZ ET AL.
APPLICANT: JORG FRITZ ET AL.
TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof FILE REFERENCE: SONN: 030US
CURRENT APPLICATION NUMBER: US/10/344,709C
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: PCT/EP01/09529
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 37
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                                                                                               Gaps
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                                                       Score 34.5; DB 15; Length 37;
Pred. No. 2.6e+02;
2; Mismatches 3; Indels 1
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Pred. No. 1.4e+02;
3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                             Sequence 15, Application US/10344709C Publication No. US20040170642A1 GENERAL INFORMATION:
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                                                       Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
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4 KRLRKFRNKIKEKLK 18
                                                                                                                                 1 KLYRKFKNKLL-KLK 14
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; ORGANISM: Ovis aries US-10-721-839-5
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US-10-344-709C-15
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Other Molecules Associated With
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Sequence 48512, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: NUCLeic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT APPLICATION NUMBER: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 48512
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APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
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                                                                                                  OTHER INFORMATION: MAP TO AC006054.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BULLT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BURAIN, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: SWISSPROT HIT: P29747, EVALUE 6.50e+00
US-09-864-761-45380
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Pred. No. 2.9e+02;
0; Mismatches 5; Indels
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US-10-424-599-262608
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 45380
LENGTH: 34
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Pred. No. 3.3e+02;
1; Mismatches 5
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; Sequence 262608, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity 57.1%;
Matches 8; Conservative
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SEQ ID NO 262608
LENGTH: 39
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                                                                   ORGANISM: Homo sapiens FEATURE:
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ORGANISM: Glycine max
FEATURE:
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                                                       TYPE: PRT
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Pred. No. 1.5e+02;
3; Mismatches 3; Indels
                                                                                                                     OTHER INFORMATION: SYNTHETIC SEQUENCE NAME/KEY: MOD RES LOCATION: (17)
                                                                  TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                             1 KLYRKFKNKLLKL 13
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 124
LENGTH: 17
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Pred. No. 4.5e+02;
                                         Length 53;
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Sequence 304, Application US/10798512

Sequence 304, Application US/10798512

PUBLication No. USCO040152164A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 62 Human Secreted Proteins

FILE REFERENCE: PZ039P1

CURRENT FILING DATE: 2006-03-12

PRIOR APPLICATION NUMBER: US/10/798,512

CURRENT FILING DATE: 2000-10-10

PRIOR PILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/128,693

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-06

PRIOR FILING DATE: 1999-04-06

PRIOR FILING DATE: 1999-04-06

PRIOR FILING DATE: 1999-04-06

SEQ ID NOS: 344

SEQ ID NOS: 344

LENGTH: 54
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Sequence 304, Application US/10050704-
Fublication No. US20030050442A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 62 Human Secreted Proteins
FILE REFERENCE: P2039P1
CURRENT APPLICATION NUMBER: US/10/050,704
CURRENT FILING DATE: 2002-01-18
FRIOR APPLICATION NUMBER: PCT/US00/08979
FRIOR FILING DATE: 2000-10-10
FRIOR APPLICATION NUMBER: FCT/US00/08979
FRIOR APPLICATION NUMBER: 60/128,693
FRIOR APPLICATION NUMBER: 60/128,693
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-05
FRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 344
SOFTWARE: FALCHTON UN OFF. 2.0
SEQ ID NO 304
LENGTH: 54
                                         Score 34; DB 15;
Pred. No. 4.4e+02;
                                                                                     1; Mismatches
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Best Local Similarity 50.0%;
Matches 5; Conservative
                                       Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                 2 LYRKFKNKLLKLK 14
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12 LLTKFHDKLLKSK 24
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13 MYQKFRNOFL 22
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; ORGANISM: Homo sapiens
US-10-050-704-304
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CORGANISM: Homo sapiens
US-10-798-512-304
US-10-424-599-167072
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US-10-050-704-304
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TITLE OF INVENTION: Plants and Wolecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERSENCE: 38-21(53221)B
CURRENT APPLICATION WIMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 116406
LENGTH: 52
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Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Cao Vongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53223) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 167072

LENGTH: 53
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                                                                                                                                                   Query Match 48.6%; Score 34; DB 16; Length 44; Best Local Similarity 50.0%; Pred. No. 3.7e+02; Matches 6; Conservative 3; Mismatches 3; Indels
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                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-039-P1-K1-D11.pep
US-10-767-701-48512
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OTHER INFORMATION: Clone ID: PAT_MRT3847_121880C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_19910C.1.pep
US-10-437-963-116406
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 116406, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                    TYPE: PRT ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                             1 KLYRKFKNKLLK 12
                                                                                                                                                                                                                                                                     2 LYRKFKNKLLK 12
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ORGANISM: Oryza sativa
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  LENGTH: 44
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US-10-44-599-260117

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APPLICANT: TANG, Y. Tom; NGUYEN, Danniel B.;
APPLICANT: TANG, Y. Tom; NGUYEN, Danniel B.;
APPLICANT: TANG, Y. Tom; NGUYEN, Danniel B.;
APPLICANT: TELBOULEY. Catherine M.; SANDAWALA, Madhusudan M.;
APPLICANT: TELBOULEY. Catherine M.; APPLICANT: TELBOULEY. Stephanie K.; Lal. Preeti G.;
APPLICANT: THORNTON, Michael B.; GANDHI, Amenna R.;
APPLICANT: THORNTON, Michael B.; GANDHI, Amenna R.;
APPLICANT: THORNTON, Michael B.; DING, Li;
APPLICANT: GIETZEN, Kimberly J.; DING, Li;
APPLICANT: GIETZEN, Kimberly J.; DING, Li;
APPLICANT: DUGGAN, Bridget A.; GURURAJAN, Rajagopal;
APPLICANT: DUGGAN, Brendan M.; HONCHELL, Cynthia D.;
APPLICANT: WARREN, Bridget A.; GURURAJAN, Rajagopal;
APPLICANT: WARREN, Bridget A.; GURURAJAN, Rajagopal;
APPLICANT: WARREN, Bridget A.; GURURAJAN, Rajagopal;
APPLICANT: HAFALIA APILI J.A.
TITLE OF INVENTION: SECRETED PROTEINS
FILE REPERENCE: PI-0240 USN
TITLE OF INVENTION: SECRETED PROTEINS
FILE REPERENCE: PI-0240 USN
TITLE REPERENCE: PI-0240 USN
FRIOR APPLICATION NUMBER: US 60/242,218
PRIOR APPLICATION NUMBER: US 60/242,218
PRIOR APPLICATION NUMBER: US 60/242,218
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-11
PRIOR PILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-11
PRIOR PILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-11
PRIOR PILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-12
PRIOR PILING DATE: 2000-10-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.5%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50, Application US/10398037 Publication No. US20040138414A1 GENERAL INFORMATION:
        10 YRTFQIKLLILK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Road Thomas J
APPLICANT: APPLICANT: Cavalic David K
APPLICANT: Cava Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 194171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Acoustic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT FILE OF THOMABER: US/10/424,599
CURRENT FILE OF DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 220615
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48.6%; Score 34; DB 15; Length 66;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 8; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 48.6%; Score 34; DB 15; Length 62; Best Local Similarity 45.5%; Pred. No. 5.2e+02; Matches 5; Conservative 5; Mismatches 1; Indels
    Pred. No. 4.5e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41246C.1.pep
US-10-424-599-220615
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US-10-424-599-194171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(62)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 220615, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
        50.08;
Best Local Similarity 50.0
Matches 5; Conservative
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46 KLYRDWQNRII 56
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13 MYOKFRNOFL 22
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                      US-10-424-599-220615
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US-10-424-599-194171
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Sequence 225047, Application US/10424599
Publication No. US2004003107241
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Royal Thua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 225047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4036, Application US/10472928
; Sequence 4036, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; TITLE OF INVENTION: US/10/472,928
; CURRENT FILING DATE: 2003-99-26
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4036
; LENGTH: 37
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                                                    Score 33; DB 15; Length 30;
Pred. No. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT_MRT3847_45248C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.1%; Score 33; DB 15; 54.5%; Pred. No. 4.1e+02;
                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                    47.18;
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Best Local Similarity 53.0%
The Conservative
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9 LYLKFTDKLPLLK 21
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                                                    Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                               RESULT 44
US-10-424-599-225047
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     US-10-424-599-218617
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US-10-472-928-4036
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| Publication No. US20030072794A1
| Publication No. US20030072794A1
| GENERAL INFORMATION:
| APPLICANT: BOULIKAS, TENI
| TITLE OF INVENTION: ENCABEULATION OF PLASMID DNA (LIPOGENES TW) AND THERAPEUTIC
| TITLE OF INVENTION: CONUCGATES INTO TARGETED LIPOSOME COMPLEXES
| TITLE OF INVENTION: CONUCGATES INTO TARGETED LIPOSOME COMPLEXES
| TITLE OF INVENTION: CONUCGATES INTO TARGETED LIPOSOME COMPLEXES
| TITLE OF INVENTION: CONUCGATES INTO TARGETED LIPOSOME COMPLEXES
| TITLE OF INVENTION: CONUCGATES INTO TARGETED LIPOSOME COMPLEXES
| TITLE OF INVENTION: CONUCGATES INTO TARGETED LIPOSOME COMPLEXES
| TITLE OF INVENTION: CONUCGATES INTO TARGETED LIPOSOME COMPLEXES
| TITLE OF INVENTION NUMBER: US 60/210,925
| PRIOR FILING DATE: 2000-06-09
| SOFTWARE: PALENTIN Ver. 2.1
| SEQ 1D NO 392
| LENGTH: 12
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APPLICANT: Rovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 218617
LENGTH: 30
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US-09-876-904A-392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT3847_3943C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 10;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 4102938CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Sequence 218617, Application US/10424599
, Publication No. US20040031072A1
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative 5
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                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Glycine max
SOFTWARE: PERL Program
SEQ ID NO 50
LENGTH: 74
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67 RLYKKYKN 74
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US-10-424-599-218617
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US-09-876-904A-392
                                                                                                                                                                                                         US-10-398-037-50
                                                                              TYPE: PRT
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Search completed: May 16, 2005, 09:23:39 Job time : 53.6207 Becs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 12.069 Seconds (without alignments) 111.611 Million cell updates/sec Run on:

US-09-648-816B-5 70 Title: Perfect score:

1 KLYRKFKNKLLKLK 14 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

22893 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

.BS	Description				1	hypothetical prote	_					hypothetical prote	-1	type I restriction	hypothetical prote	hypothetical 4.4K	probable ribosomal	prophage pil prote	interleukin-3 rece	ribosomal protein	protein V6, trunca		hypothetical prote			hypothetical prote		ᇋ	m	coat protein B pre
SUMMARIES	Ω	E70239	G69058	AB0406	A41669	B85569	AC2335	E70043	E95226	G81343	C72262	D97734	A25188	D82933	C49753	JU0329	377866	D86681	I57554	S72293	E64108	820039	S20040	VCBPZ2	H81263	JT0460	D69384	H81379	VCBPF1	VCBPFD
	DB	2	N	~	N	~	~	~	N	~	~	~	7	~	7	~	~	~	~	~	~	~	~	Н	~	7	7	~	-	Н
	Query Match Length	34	67	68	41	44	72	65	37	61	69	61	67	69	20	37	59	68	74	74	35	43	43	20	20	61	62	70	73	73
æ	Query Match	57.1	51.4	51.4	50.0	50.0	50.0	48.6	47.1	47.1	47.1	45.7	45.7	45.7	44.3	44.3	44.3	44.3	44.3	43.6	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9
	Score	40	36	36	35		35	34	33	33	33	32	32	32	31	31	31	31	31	30.5	30	30	30	30	30	30	30	30	30	30
	Result No.		7	m	4	2	9	7	89	o	10	11	12	13	14	15	16	17	18	19	20		, 22	23	24	25	56		28	53

hypothetical protein MTH1440 - Methanobacterium thermoautotrophicum (strain Delta H)
C'Species: Methanobacterium thermoautotrophicum
C'Spacesion: GS058
R'Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
'Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.,
K,; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct)
A;Accession: G8058
A;Accession: G8058
A;Acteus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-67 with.ac.al/
A;Genetics:
A;Genetics:

coat protein B pre	regulatory protein	conserved hypothet	very hypothetical	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	preprotein translo	hypothetical prote	ribosomal protein	hypothetical prote	homeotic protein e	30S ribosomal prot	30S ribosomal prot	AcMNPV orf122 - Bo
VCBPM3	838900	C81738	C81372	F72429	\$20042	G81360	G90010	B70149	AE0934	S48688	140760	S18301	H90020	F86885	T41859
н	~	~	~	N	N	~	~	~	~	7	7	~	~	~	7
73	74	74	46	31	32	48	21	26	57	9	09.	9	61	61	61
42.9	42.9	42.9	42.1	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4	41.4
30	30	30	29.5	29	29	29	29	29	29	29	29	29	29	29	29
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 B70239
	hypothetical protein BBH39 - Lyme disease spirochete plasmid H/lp28-3 C;Species: Borrelia burgdorferi (Lyme disease spirochete) C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Ju1-2004
	C;Accession: E70239 R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, ann. D.: Pererson, J.: Kerlayage, A.R.; Onackenbush, J.; Salzberg, S.; Hanson, M.: Vuct.
,	; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horet, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
	A;Authors: Smith, H.O.; Venter, J.C. A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A;Reference numbor: A70100; MUID:98065943; PMID:9403685
	A;Accession: E70239 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
	A;Residues: 1-34 <kle> A;Resserveferences: UNIPROT:O50694; GB:AE000784; NID:g2690041; PIDN:AAC66012.1; PID:g2696 A;Experimental source: strain B31</kle>
	Cjemerica: A;Genome: plasmid
	Query Match Best Local Similarity 58.3%; Pred. No. 6.7; Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
	Oy 3 YRKFKNKLIKLK 14 : :

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A; Molecule type: DNA
A; Residues: 1-72 < KUR>
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                                                                                                                                                                             C.Genetics:
A.Gene: Z0840
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                                                                                                                                                                                                                                                                 C; Species: Yerbinia pestis
C;Decies: Yerbinia pestis
C;Date: 02-NOV-2001 #sequence_revision 02-NOV-2001 #text_change 09-Jul-2004
C;Accession: AB0406
E;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MuID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C'Species: Bscherichia coli
C'Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85569
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8ZBR3; GB:ALS90842; PIDN:CAC92574.1; PID:g15981271; GSPDB:C
C;Genetics:
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B85569
hypothetical protein 20840 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
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A41669

S18 protein - chicken (fragments)

C;Species: Gallus gallus (chicken)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-May-1996

C;Accession: A41669

G;Accession: A41669

A;Title: A novel 53-kDa polypeptide from chicken embryo.

A;Atitle: A novel 53-kDa polypeptide from chicken embryo.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                               AB0406
hypothetical protein YPO3344 [imported] - Yersinia pestis (strain CO92)
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                           Length 67;
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                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2;
Pred. No. 56;
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                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 51;
0; Mismatches
                         Score 36;
Pred. No.
                         51.4%;
62.5%;
                                                                                                             1 KLYRKFKNK--LLKLK 14
                                                                                                                                                    12 KOFLKFKNKNVLLTLK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.4%;
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Query Match
Best Local Similarity 62.3.
Best Local 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 41.7
Matches 5; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YRKFKNKLLKLK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-41 ...... C;Superfamily: calreticulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-41 < BAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA A; Residues: 1-68 < KUR>
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85569
A;Atatus: preliminary
A;Molecule type: DNA
A;Residues: 1-44 <STO>
A;Cross-references: UNIPROT:08X421; GB:AE005174; NID:g12513596; PIDN:AAGS5014.1; GSPDB:Gr
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein asl4234.[imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. etrain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC2335
R;Kaneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; WuID::21595285; PMID::11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cipacesion: E70043

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Broughi, C.V.; Caldwell, B.; Captano, V.; Carter, N.M.; Choi A.; Ehrlich, S.; Brunschi, C.V.; Caldwell, B.; Captano, V.; Carter, N.M.; Choi A.; Ehrlich, S.; Brunschi, C.V.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Lardinois, K.; Lapidus, A.; Lazerevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R; Reiger, M.; Rivolta, C.; Roche, B.; Rosch, M.; Sadaie, Y.; Sako, T.; Sachlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Guister, M.; Tamakoshi, A.; Tanaka, T.; Tarpstra, P.; Tosano, V.; Uchiyama, T.; Minters, P.; Wipter, A.; Yamamoto, H.; Yamanoto, K.; Yasta, K.; Yoshida, K.; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A.Experimental source: strain PCC 7120
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C;Species: Bacillus subtilis
C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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Pred. No. 54;
5; Mismatches 2; Indels
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pred. No. 86;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.0%;
Best Local Similarity 41.7%;
Matches 5; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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33 IWRRFNNKLITI 44
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52 LFRKLLNKLMAL
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Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequa; Ricesasion: A;Accession: C72262
A;Accession: C72262
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-69. <ARN>
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A,Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Rickettsia conorii
Cipate: 30-5ep-2011 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
Cipate: 30-5ep-2011 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
Riogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rot
Science 293, 2093-22094, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                                                                                                                                                                                                                                   C,Accession: C72262
R,Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Breen, G.A.M.; Miller, D.L.; Holmans, P.L.; Welch, G.
J. Biol. Chem. 261, 11680-11685, 1986
A;Title: Mitochondrial DNA of two independent oligomycin-resistant Chinese hamster ovary
A;Reference number: A25188; MUID:86304297; PMID:3017940
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                                                                                                                                                                                                                                             C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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Pred. No. 2.2e+02;
4; Mismatches 4; Indels
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                                                                                                                                                                                                   hypothetical protein - Thermotoga maritima (strain MSB8)
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Pred. No. 1.7e+02;
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nilarity 42.9%;
Conservative
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27 KFDKKFSSKLMTLR 40
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    30 KFKNKVQKI 38
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54 YERFKNELEK
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Best Local Similarity
Matches 6; Conserva
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-61 < KUR>
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C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95226
C;Accession: E95226
On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q97NS6; GB:AE005672; PIDN:AAK76006.1; PID:g14973443; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81343
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C:W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
                                                                          A;Cross-references: UNIPROT:034719; GB:299121; GB:299122; GB:AL009126; NID:g2636029; PIC A;Experimental source: strain 168 C;Genetics: C;Genetics: A;Gene: yvlc
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A,Reference number: A81250, MUID:20150912; PMID:10688204
A,Accession: G81343
A,Status: Perliminary
A,Molecule type: DNA
A,Residues: 1-61 <PAR>
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A,Experimental source: serotype O2, strain NCTC 11168
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G81343
hypothetical protein Cj0724 [imported] - Campylobacter jejuni (strain NCTC 11168)
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                                                                                                                                                                                                                                                                              Query Match 48.6%; Score 34; DB 2; Length 65; Best Local Similarity 77.8%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 2; Indels
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Pred. No. 96;
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53.8%;
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Best Local Similarity 53.0.
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Best Local Similarity 66.74
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A; Molecule type: DNA
A; Residues: 1-65 < KUN>
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Molecule type: DNA
Residues: 1-37 <KUR>
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45.7%;

Query Match
Best Local Similarity 58.3
Matches 7; Conservative

2 LYRKFKNKLLKL 13 |::| || ||| 33 LHKKPSNKYLKL 44

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C;Species: Streptococcus pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Date: 13-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
R;Diaz, E.; Garcia, J.L.
Gene 90, 157-162, 1990
A;Title: Characterization of the transcription unit encoding the major pneumococcal autol
A;Reference number: JU0329; MUID:90337339; PMID:1974230
                                                                                                                                                                                                       A;Accession: JU0329
A;Molecule type: DNA
A;Residues: 1-37 <DIA3
A;Cross-references: UNIPROT:Q54890; GB:M13812; GB:M55414; GB:M55415; NID:g153693; PIDN:AJ
A;Experimental source: strain M31
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A,Residues: 1-59 <BOR>
A,Cross-references: UNIPROT:Q49052; EMBL:Z33246; NID:g541716; PIDN:CAA83801.1; PID:g95007
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A./Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg A; Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:09CIB2; GB:AE005176; PID:g12723330; PIDN:AAK04550.1; GSPDB:GPA;Experimental source: strain IL1403
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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N;Alternate names: protein MC334
C;Species: Mycoplasma capricolum
C;Date: 09-Oct.1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 2;
Pred. No. 2e+02;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                               44.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 KLVANPAKKNEALKLK 46
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Best Local Similarity 58.3
Matches 7; Conservative
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3 RTYRDCKNILLK 14
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A; Residues: 1-68 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Genetic code: SGC3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type I restriction enzyme S protein, truncated homolog UU097 [imported] - Ureaplasma ure Species: Ureaplasma ureallyticum C;Species: Ureaplasma ureallyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: D82933 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. Brichaft to Genblank, Pebruary 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
A;Residues: 1-67 <BRE>
A;Cross-references: UNIPROT:P14414; GB:M14311; NID:g336719; PIDN:AAA68615.1; PID:g336720
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Serratia marcescens
C; Date: O'-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C; Accession: C49753; S11643
R; Omori, K.; Suzuki, S.I.; Imai, Y.; Komatsubara, S.
Gen. Microbiol. 137, 509-17, 1991
A; Title: Analysis of the Serratia marcescens proBA operon and feedback control of prolin A; Reference number: A49753; MUID:91237315; PMID:1851803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-69 GGLA-
A,Cross-references: GB-AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30503.1; GSPDB:GN001
A,Experimental source: serovar 3; biovar 1
                                                                                    Genome: mitochondrion
.Genetic code: SGCI
phyperfamily: H+-transporting ATP synthase protein 8
.Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxi
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C49753
hypothetical protein (proB 5' region) - Serratia marcescens (fragment)
C.Species: Serratia marcescens
C.Date: 07-Apr-1994 #economical
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JU0329
hypothetical 4.4K protein (lytA 5'region) - Streptococcus pneumoniae
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                                                                                                                                                                                                                                      Score 32; DB 2; Length 67;
Pred. No. 2.4e+02;
2; Mismatches 3; Indels
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
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6; Conservative

Best Local Similarity Matches 6; Conserv

Query Match

Gene: hads-2; UU097 A, Genetic code: SGC3

Status: preliminary

Accession: D82933

ઠે 셤 44.3%;

Query Match Best Local Similarity 75.0°

A; Molecule type: DNA A; Residues: 1-20 < OMO>

6 FKNKLLKL 13 || ||:|| 11 FKEKLIKL 18

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Gaps

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hypothetical protein 1 - Haemophilus influenzae insertion sequence IS1016(V-1) (fragment)
C;Species: Haemophilus influenzae
C;Date: 07-May_1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q48234; GB:U32782; GB:L42023; NID:g1574041; PID:g1574052; TIC
A,Experimental source: strain Rd KW20
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J. D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: E64108
A;Accession: E64108
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-35 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kroll, J.S.; Loynds, B.M.; Moxon, E.R.
Mol. Microbiol. 5, 1549-1560, 1991
A;Title: The Haemophilus influenzae capsulation gene cluster: a compound transposon.
A;Reference number: S16288; MUID:92157882; PMID:1664907
A;Accession: S20039
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Mol. Microbiol. 5, 1549-1560, 1991
A;Title: The Haemophilus influenzae capsulation gene cluster: a compound transposon.
A;Reference number: S16288; MUID:92157882; PMID:1664907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 35;
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Pred. No. 2.8e+02;
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A;Mobile element: insertion sequence IS1016 (V-2)
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A,Status: preliminary; translation not shown
A,Molecule type: DNA
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7 KLKKSIONKLLE 18
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Best Local Similarity
Matches 6; Conserva
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Best Local Similarity
Matches 6; Conserv
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Cidacesion: S72293
Riwilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyt
J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa
A;Reference number: S72277; MUID:96346169; PMID:8757284
A;Accession: S72293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: UNIPROT:Q64130; GB:S78451; NID:g998544; PIDN:AAB34209.1; PID:g998545; Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
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                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: 157554
R;Hannemann, J.; Hara, T.; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
Roll Cell. Biol. 15, 2402-2412, 1995
A;Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-smediated by a truncated beta C subunit.
A;Reference number: 157554; MUID:95257920; PMID:7739524
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E64108

protein V6, truncated - Haemophilus influenzae insertion sequence IS1016

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C;Accession: E64108

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
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A;Note: this apparently degenerate plastid is referred to as the apicoplast
C;Keywords: plastid; protein blosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                    interleukin-3 receptor beta subunit - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 29-May_1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 44.3%; Score 31; DB 2; Length 74; Similarity 50.0%; Pred. No. 3.9e+02; 5; Conservative 3; Mismatches 2; Indels
                                       Indels
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C,Species: plastid Plasmodium falciparum
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Pred. No. 4.6e+02;
         Pred. No. 3.6e+02; 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
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Local Similarity 43.8%;
nes 7; Conservative 4
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58 KYYKKSKYCNNKVIKI 73
      53.8%;
                                                                                                                                          |||| |::|:|
43 LYRKI--KIIKIK 53
                                                                                                     2 LYRKFKNKLLKLK 14
   Best Local Similarity 53.8
Matches 7; Conservative
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65 RTYRKWKEKI 74
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Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-74 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA; Residues: 1-74 <WIL>
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hypothetical protein AF1076 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change O9-Jul-2004
C;Accession: D69384
C;Accession: D69384
C;Accession: D69384
C;Accession: A; Alou, B.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson, F.F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69280; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "30S ribosomal protein S21 Cj0370 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Bar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81379
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C;W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: H81379
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-70 <PAR>
A,Cross-references: UNIPROT:Q9PID2; GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB74206
A,Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: 029187; GB: AE001028; GB: AE000782; NID: 92689351; PIDN: AAB9016:
                                                                     A;Status: translation not shown
A;Modecule type: DNA
A;Residues: 1-61 <700N>
A;Cross-references: UNIPROT:Q9YPJ6; GB:D00295; NID:g221380; PIDN:BAA00202.1; PID:g221393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62 <KLE>
                                                                                                                                                                                                                       Query Match
42.9%; Score 30; DB 2; Length 61;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 2; Mismatches 5; Indels
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66.7%; Pred. No. 4.7e+02;
tive 1; Mismatches 2; Indels
A;Reference number: JT0442; MUID:88229622; PMID:2836548
A;Accession: JT0460
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C;Superfamily: Escherichia coli ribosomal protein S21
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                                                                                                                                                                                                                                                                                                                                                               1 KLYRKFKNKLLKLK 14
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Matches 6; Conservative
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C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
S;Accession: H81263
R;Parkhill, J: Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein, 7.5K - fowlpox virus (isolate HP-438[Munich])
N;Alternate names: hypothetical protein f
C;Species fowlpox virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JT0460
C;Accession: JT0460
S;Tomley, F.; Binns, M.; Campbell, J.; Boursnell, M.
J;Gom. Virol. 69, 1025-1040; 1988
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHi fragment of fowlpox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:Q9PM10, GB:AL1139079; GB:AL111168; NID:g6968971; PIDN:CAB7365
A,Experimental source: serotype O2, strain NCTC 11168
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                                                                                                                                                                                                                          coat protein B - phage ZJ-2
C;Species: phage ZJ-2
C;Species: phage ZJ-2
C;Accession: H04226; A04226
R;Snell, D.T.; Offord, R.E.
Biochem. J. 127, 167-178, 1972
A;Title: The amino acid sequence of the B-protein of bacteriophage ZJ-2.
A;Reference number: A90260; MUID:73009813; PMID:5073740
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A;Residues: 1-50 <SNB>
A;Cross-references: UNIPROT:P03618
C;Comment: Coat protein B is the major coat protein of the virion.
C;Genetics:
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Pred. No. 3.9e+02;
1; Mismatches 3; Indels
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42.9%; Score 30; DB 1; L
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 1;
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57.1%;
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Matches 8; Conservative
                                              7 KLKKSIQNKLLE 18
         KLYRKFKNKLLK 12
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40 KLFKKFTSK 48
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A;Molecule type: DNA
A;Residues: 1-50 <PAR>
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H81263
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C;Accession: D04226; A04226
R;van Wezenbeek, P.M.G.F.; Hulsebos, T.J.M.; Schoenmakers, J.G.G.
Gene 11, 129-148, 1980
A;Fitle: Nucleotide sequence of the filamentous bacteriophage M13 DNA genome: comparison
A;Reference number: A91470; MUID:81067903; PMID:6254849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A,Residues: 1-73 «VAN»
A,Crosel-references: UND:914959; PIDN:CA
G,Comment: Coat protein B is the major coat protein of the virion. There are about 2,700
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C;Species: Mycoplasma sp.
C;Species: Mycoplasma sp.
C;Species: Mycoplasma sp.
C;Accession: S38900
R;Siksnys, V.; Zareckaja, N.; Valsvila, R.; Timinskas, A.; Stakenas, P.; Butkus, V.; Janusubitted to the RMBL Data Library, November 1993
A;Description: CAATTG-specific restriction-modification MunI genes from Mycoplasma: homola, Reference number: S38899
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A,Molecule type: DNA
A,Residues: 1-74 <SIX-
A,Cross-references: UNIPROT:P43640; EMBL:X76192; NID:g431927; PIDN:CAA53787.1; PID:g43195
A,Title: Reinvestigation of a region of the fd bacteriophage coat protein sequence.
A,Reference number: A92951; MUID:75097503; PMID:4449122
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C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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                                                                                                                     A,Molecule type: DNA
A,Residues: 24-73 <NAK>
C,Comment: Coat protein B is the major coat protein of the virion.
C,Genetics:
A,Gene: VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%; Score 30; DB 1; Length 73; 55.6%; Pred. No. 5.5e+02; tive 3; Mismatches 1; Indels
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Pred. No. 5.5e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                 C;Superfamily: Lixement C;Superfamily: Lixement C;Keywords: coat protein C;Keywords: coat protein B #status predicted <CFB>F;24-73/Product: Coat protein B #status predicted <CFB>F;24-73/Product <CFB>F;
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C.Keywords: coat protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-73/Product: coat protein B #status predicted <CPB>
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Best Local Similarity 55.6%;
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Matches 5; Conservative
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63 KLFKKFTSK 71
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                                                                                      A; Accession: C04226
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A; Gene: munIC
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S38900
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A;Experimental source: strain 478, Heidelberg
R;Asbeck, F.; Beyreuther, K.; Kohler, H.; von Wettstein, G.; Braunitzer, G.
Hoppe-Seyler's Z. Physiol. Chem. 350, 1047-1066, 1969
A;Title: Die Konstitution des Huellproteins des Phagen fd.
A;Reference number: A91643; MUID:70028989; PMID:5349375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-73 <BEC>
A; Residues: 1-73 <BEC>
A; Residues: 1-73 <BEC>
A; Cross-references: UNIPROT: P03617; GB: V00606; GB: J02449; GB: M10881; NID: g14974; PIDN: CA
R; Hill, D. F.; Petersen, G. B.
J. Virol. 34, 40-50, 1980
A; Title: Mucleotide sequences in bacteriophage fl DNA: nucleotide sequence of genes V, V
A; Reference number: A92980; MUID: 80185134; PMID: 7373712
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                                                                                                                                                                                                       C;Species: phage f1
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: E04226; F04226; G04226; A04226
R;Beck, E.; Zink, B.
Gene 16, 35-58, 1981
A;Title: Nucleotide sequence and genome organisation of filamentous bacteriophages f1 A;Reference number: A91490; MUID:82211801; PMID:6282703
A;Accession: E04226
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C.Jace: 18-Dec-1981 #sequence revision 18-Dec-1981 #text_change 09-Jul-2004
C.Jacession: A04226; B04226; C04226
R.Jeck, E.; Sommer, R.; Auerswald, E.A.; Kurz, C.; Zink, B.; Osterburg, G.; Schaller,
Nucleic Acids Res. 5, 4495-4503, 1978
A.Jtile: Nucleotide sequence of bacteriophage fd DNA.
A.Reference number: A93690; MUID:79136480; PMID:745987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-73 «HIL»
A; Cross-references: GB: J02450; NID: g166212; PIDN: AAA32220.1; PID: g166214
A; Cross-references: GB: J02450; Hill, D.F.; Petersen, G.B.
B; Bailey, G.S.; Gillett, D.; Hill, D.F.; Petersen, G.B.
J. Biol. Chem. 252, 2318-22255, 1977
A; Title: Automated sequencing of insoluble peptides using detergent. Bacteriophage fl
A; Reference number: A92201; MUID: 77140968; PMID: 321454
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A;Residues: 24-73 <BAI>
C;Comment: Coat protein B is the major coat protein of the virion.
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Pred. No. 5.5e+02;
3; Mismatches 1; Indels
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A;Reaidues: 24-49,'X',51-73 <ASB>
A;Experimental Bource: strain 478, Heidelberg
A:Bxbashima, Y.; Konigaberg, W.
J. Mol. Biol. 88, 598-600, 1974
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                                                                                                                                                                     precursor - phage fl
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Best Local Similarity 55...
5; Conservative
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63 KLPKKPTSK 71
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A; Residues: 1-73 < BEC>
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A;Cross-references: UNIPROT:Q9WXL9; GB:AE001689; GB:AE000512; NID:g4980483; PIDN:AAD35098
A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein 1 - Haemophilus influenzae insertion sequence IS1016 (V-5) (fragment) C; Species: Haemophilus influenzae (C; Species: Haemophilus influenzae (C; Species: Haemophilus influenzae (C; Species: Haemophilus influenzae revision 17-Jul-1998 #text_change 09-Jul-2004 (C; Accession: S20042 B.M.; Moxon, E.R. Mol. Microbiol. 5, 1549-1560, 1991 Mol. Microbiol. 5, 1549-1560, 1991 A; Title: The Haemophilus influenzae capsulation gene cluster: a compound transposon. A; Reference number: S16288; MUID:92157882; PMID:1664907 A; Accession: S20042 A; Status: preliminary; translation not shown A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-35 < MRO>
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C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Dates: 31-Nar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C;W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel.
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
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  Hickey,
                                                                              Nature 399, 323-329, 1999
A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Accession: F72429
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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Pred. No. 3.6e+02;
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Pred. No. 4e+02;
2; Mismatches
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A;Experimental source: serotype 02,
C;Genetics:
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66.78;
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55.6%;
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Similarity 54.5%;
6; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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7 KLKKSIQNKLL 17
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-31 <ARN>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-48 < PAR>
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81372
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-669, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A/Cross-references: UNIPROT:Q9FNW4; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB7323
A/Experimental source: serotype O2, strain NCTC 11168
C/Genetics:
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R.C; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, K.F.; Aread, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9PLH0; GB:AE002280; GB:AE002160; NID:g7190162; PIDN:AAF3901
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                         conserved hypothetical protein TC0134 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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F72429
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Uun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72429
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Score 30; DB 2; Length 74;
Pred. No. 5.6e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 2; Length 74;
Pred. No. 5.6e+02;
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54.5%;
  42.9%;
60.0%;
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16 LVKKLKNKQSLKIK 29
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                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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61 LFRKVAERLLK 71
                                                                                                                                                5 KFKNKLLKLK 14
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Best Local Similarity
Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 8; Conserv
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Residues: 1-46 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <TET>
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K;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Reference number: ABD502; MUD:21534947; PMID:11677608
A;Reference number: ABD502; MUD:21534947; PMID:11677608
A;Reference number: ABD502; MUD:21534947; PMID:1167608
A;Residues: 1-57 cPAR
A;Residues: 1-57 cPAR
A;Residues: 1-57 cPAR
A;Conse-references: GB:AL513382; PIDN:CAD09495.1; PID:g16504612; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Bacillus stearothermophilus
C;Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Dates: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48688; S59054
C;Herfürth, E.; Briesemeister, U.; Wittmann-Liebold, B.
FRBS Lett. 351, 114-118, 1994
A;Title: Complete amino acid sequence of ribosomal protein S14 from Bacillus stearothermc
A;Reference number: S48688; MUID:94357263; PMID:8076678
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C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 140760; S47318
R;Hani, B.K.; Chan, V.L.
J. Bani, B.K.; Chan, V.L.
A;Hale: Expression and characterization of Campylobacter jejuni benzoylglycine amidohydi
A;Reference number: 140758; MUID:95247673; PMID:7730270
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A, Residues: 1-60 (HER)
R;Urlaub, H.; Kruft, V.; Bischof, O.; Mueller, B.C.; Wittmann-Liebold, B.
BMBO J. 14, 4578-4588, 1995
A;Title: Protein-rRNA binding features and their structural and functional implications
A;Reference number: S59051; MUID:96003638; PMID:7556101
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S.Superfamily: Escherichia coli ribosomal protein S14
C;Keywords: protein biosynthesis; ribosome
F;1-60/Product: ribosomal protein S14 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 2; Leuster
Pred. No. 6.38+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 2; Length 60;
Pred. No. 6.7e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribosomal protein S14 - Bacillus stearothermophilus
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A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
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Similarity 83.3%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YRKFKNKLLKLK 14
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Best Local Similarity
Matches 4; Conserva
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A;Residues: 9-21 <URL>
C;Genetics:
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Best Local Similarity
Matches 5; Conserv
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32 VYRKFK 37
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C; Accession: AE0934
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                                                                                                                                                                                                                                                                                                C;Species: Staphylococcus aureus.
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G90010
C;Accession: G90010
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preprotein translocase secE homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: B70149
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Pujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
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A;Experimental source: strain B31
C;Superfamily: protein-export protein secE
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A,Experimental source: strain N315
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A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUD:98065943; PMID:9403685
A;Accession: B70149
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2; Indels
Mismatches
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MPRPIKOSILELK 13
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es 5; Conservative
6; Conservative
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                                                         FKNKLLKLK 14
                                                                                                                  32 PKNFYLKIK 40
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FHNKILKI 13
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: G90010
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-51 < KUR>
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Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 41.7
Matches 5; Conservative
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33 VYRKFK 38
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A; Residues: 1-61 <STO>
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                                                                                    Accession: F86885
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C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession + 1900c0
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeofic protein engrailed - Terebratulina retusa (fragment)
C;Species: Terebratulina retusa
C;Species: Terebratulina retusa
C;Species: Terebratulina retusa
C;Date: 19-Feb-1994 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
C;Accession: S18301; S22114
R;Holland, P.W.H.; Williams, N.A.; Lanfear, J.
R;Holland, P.W.H.; Williams, N.A.; Lanfear, J.
A;Holland, P.W.H.; Williams, N.A.; Lanfear, J.
A;Holland, P.W.H.; Williams, N.A.; Panfear, J.
A;Holland, P.W.H.; Williams, N.A.; Panfear, J.
A;Holland, P.W.H.; Williams, Williams, Williams, P.W.H.; Panfear, P.W.H.; Panfear, J.W.H.; Panfear, J.W.H
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A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q27054; EMBL:X62688; NID:g11045; PIDN:CAA44565.1; PID:g11046
(S.Superfamily: homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-49/Domain: homeobox homology (fragment) <HOX>
A,Residues: 1-60 <RES>
A,Cross-references: UNIPROT:Q46117; EMBL:236940; NID:g535805; PIDN:CAA85393.1; PID:g5356
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F86885
30S ribosomal protein S14 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
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Pred. No. 6.8e+02;
1; Mismatches 0; Indels
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                                                                                                            Score 29; DB 2; Length 60;
Pred. No. 6.7e+02;
3; Mismatches 5; Indels
                                                                                                                    Length 60;
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C;Superfamily: Escherichia coli ribosomal protein S14
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                                                                                                            Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                         46 KSNKKIYKKIIKLK 59
                                                                                                                                                                                                                                                                            1 KLYRKFKNKLLKLK 14
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Matches 5, Conservative
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40 FQNKRAKLK 48
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nes 6; Conserv
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A; Residues: 1-60 <HOL>
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A;Molecule type: DNA
A;Residues: 1-61 <KUR>
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R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg
A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:09CDX5; GB:AE005176; PID:g12725139; PIDN:AAK06184.1; GSPDB:GNA;Experimental source: strain IL1403
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J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: Z22020; MUID:99281911; PMID:10355780
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004;Accession: T41859
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C.Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A;Variety: isolate T3
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A,Experimental source: isolate T3
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41.7%; Pred. No. 6.8e+02;
ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 61;
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C;Superfamily: Escherichia coli ribosomal protein S14
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A;Molecule type: DNA
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Job time : 14.069 secs
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parachlamyd campylobact chilo iride

09bqk0 Q8c139

Q6mcs8

human immun plasmodium norwalk-lik bacillus ce

thermotoga

Q9ppi3 Q91g54 Q9x1a6 Q72084 Q7rnw0

norwalk-lik norwalk-lik bacillus ce bacteriopha

Scoring table:

Searched:

Database

Perfect score: Sequence:

Run on:

Q6qeg0 Q81c59 Q74p64 Q77mv7 Q8j8i9 Q8j8i9

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[1]

SEQUENCE FROM N.A.

STRAIN=ATC 35210 / B31;

MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;

MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;

Fraser C.M., Carajens S., Huang W.M., Sutton G.G., Clayton R.A.,

Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,

Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,

Richardson D.L., Peterson J.D., Karlavage A.R., Quackenbush J.,

Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,

Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid 1p28-3.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
BURGER G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.W.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF288090; AAG17734.1; -..
GO; GO:0005739; C:mitochondrion; IEA.
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Pred. No. 34;
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NCBI_TaxID=52970;
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REQUENCE 72 AA; 8959 MW; 221456EB5D4B7179 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Last sequence updat
01-JUN-2003 (TrEMBLrel. 24, Last annotation upo
Hypothetical protein BBH39.
Borrelia burgdorferi (Lyme disease spirochete)
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                                              Q9PPI3
Q91G54
Q9X1A6
Q72084
Q7RNW0
Q6QEG0
Q81C59
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Q8JSJ0
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59 EIIKKFRNKFLKL 71
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Matches 7; Conservative
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Mitochondrion.
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Query Match
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Q8zbr3 yersinia pe
Q716f7 bacteriopha
Q9az38 bacteriopha
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bacteriopha
gallus gall
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escherichia
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Q7cn57 streptococc
Q9ahx3 carsonella
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                                                                                                                 May 16, 2005, 08:21:21; Search time 59.0172 Seconds (without alignments) 121.475 Million cell updates/sec
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Q98ts9
Q8x421
Q8pyp9
Q7rmk5
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Q8f2m7
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027489
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                           1612378 segs, 512079187 residues
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Q9A016
Q9ACN57
Q9ACN53
Q6CA55
Q8ZBR3
Q9ZBR3
Q9BT39
Q9BTS9
Q9BTS9
Q9BTS9
Q9PYP9
Q7RMK5
Q65117
VG5117
Q67172
Q67117
Q67123
Q971869
Q34719
Q14L23
Q97311
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Listing first 45 summaries
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Q8F2Z2
Q65WT3
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Q8JSJ9
Q8JSK0
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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                                                                                                                                                                                 US-09-648-816B-5
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Streptococcus pyogenes
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46 ELYOKIKNKL
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SEQUENCE FROM N.A.
   [1]
SEQUENCE FROM N.A.
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STRAIN=5601 / Sercoyar lai;
MEDLINE=2598143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Oian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K., Roberts K.M., Hatch B., Smith H.O., Venter J.C.; "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Nagnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
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Pred. No. 23;
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Pred. No. 55;
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Complete proteome; Hypothetical protein; Plasmid.
SEQUENCE 34 AA; 4081 MW; FD687CA065B19056 CRC64;
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Last annotation update)
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Last annotation update)
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interrogans revealed by whole-genome sequencing.";
Nature 422:888-893(2003).
EMBL; AE011429; AAN49818.1;
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                                                                                                                         Nature 390:580-586(1997).
EMBL; AE000784; AAC66012.1;
PIR; E70239; E70239.
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Leptospira interrogans.
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                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 58...
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE 55 AA:
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Q8F2Z2;
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PERCENTION N.A.

REDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;

RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;

RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic C., Lyon K., RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., RA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.; Song L., White J., RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."; RL EMBL; AS006544; AAX33881.1; ...

KW Complete protecome; Hypothetical protein.

KW Complete protecome; Hypothetical protein.
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Chao Y.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
Chao Y.-T., Chang C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Lu Y.-F.,
Ii Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Wu H.-P., Shaw J.-F.;
"Oryza sativa PAC Po615512 genomic sequence.";
"Oryza sativa PAC Po615512 genomic sequence.";
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AC137004; AAU44280.1;
SEQUENCE 65 AA, 7579 MW; 2EFAB593226711FB CRC64;
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Pred. No. 87;
2; Mismatches 1; Indels
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Pred. No. 65;
4; Mismatches 1; Indels
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05-07L-2004 (TrEMBLrel. 27, Last sequence update)
05-07L-2004 (TrEMBLrel. 27, Last annotation update)
05-07L-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical phage protein.
05-07L-2004 (TrEMBLrel 27, Last annotation update)
Streptcoccus spyogenes (serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptcoccaee;
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Best Local Similarity 58...
7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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50 RLWRKFRVKILK 61
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Gaps

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Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Gafer H., Petrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Completer genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
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GO; GO:0005612; C:small nucleolar ribonucleoprotein complex; IEA.
GO; GO:0008248; P:pre-mRNA splicing factor activity; IEA.
InterPro; IFR010920; Sm like riboprot.
InterPro; IFR010163; snRNP_Sm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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Pred. No. 2.18+02;
1; Mismatches 3; Indels
                                                                                                                                                                                  Score 36; DB 2; Length 63; Pred. No. 2e+02;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX908798; CAF23641.1; -.
Complete proteons; Hypothetical protein.
SEQUENCE 63 AA; 7660 MM; C17E99528180C856 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Hypothetical protein.
SEQUENCE 67 AA; 7780 MW; OCDC7D6B9F09703A CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
ORFNames=YPTB0788;
Yersinia pseudotuberculosis IP 32953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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MEDLINE=98037514; PubMed=9371463;
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01-JAN-1998 (TrEMBLrel. 05, La
01-MAR-2004 (TrEMBLrel. 26, La
Hypothetical protein MTH1440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000905; AAB85915.1; -.
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Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                                                              h 51.4%;
Similarity 50.0%;
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  52 KMFFKMKNRLIK 63
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Best Local Similarity
Matches 6; Conserv
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STRAIN=MGAS8232;
MEDLINE=21927533; PubMed=11917108; DOI=10.1073/pnas.062526099;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Salva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Bares S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
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OrderedLoculanames=pc0917,
Parachlamydia Sp. (strain UWE25) (subsp. Acanthamoeba sp.).
Bacteria, Chlamydiae, Chlamydiales, Parachlamydiaceae; Parachlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-21125546; PubMed=11222582;

DDI-10.1126/JB.163.6.1853-1861.2001;

Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;

"Degenerative minimalism in the genome of a psyllid endosymbiont.";

J. Bacteriol. 183:1853-1852.12001).

EMBL; AF291051; AAK17108.1; -.
                                                                                                                                                                                                                                                         group A Streptococcus strains associated with acute rheumatic fever
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 2; Length 59;
Pred. No. 87;
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SEQUENCE 61 AA; 7897 MW; 433C44E0BB76C528 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    25B521C3EAC45A0C CRC64;
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Q6MCQ8
Q6MCQ8;
Q6MCQ8;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Ac.-HL-2004 (TrEMBLrel. 27, Last annotation update)
Ac.-HL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein.
                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002)
EMBL; AE010050; AAL97880.1; -.
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.3%;
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50:0%;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 59 AA;
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                                                                                                                                                                                                                                                                                          outbreaks.";
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09AHX3;
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EMBL; AJ414156; CAC92574.1;
EMBL; AE013687; AAM84431.1;
EMBL; AE017128; AAS60616.1;
PIR; AB0406; AB0406.
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50 FKKIKNKFIEMK 61
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                                                                                                                                                                                                                                                                                                                                             Gene 18 protein.
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STRANT=91001 / Biovar Mediaevalis;
SONG Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D., Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21470413; Pubmed=11586360; DOI=10.1038/35097083; MEDLINE=21470413; Pubmed=11586360; DOI=10.1038/35097083; MEDLINE=21470413; Pubmed=11586360; DOI=10.1038/35097083; Mern B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
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MEDLINE=22137863; PubMed=12142430;
DOI=10.1128/JB.184.16.4601-4611.2002;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
                                                                                     Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O., Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V., Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C., Simonet M., Chenler Francieque V., Souza B., Dacheux D., Elliott J.M., Derbise A., Hauser L.J., Garcia E., F. Suza B., Dacheux D., Elliott J.M., Insights into the genome evolution of Yersinia pestis through whole genome comparison with Yersinia pseudotuberculosis."; Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                   Score 36; DB 2; Length 68;
Pred. No. 2.1e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                           l protein.
68 AA; 8065 MW; D0B95D21BFB7E22A CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein YPO3344.
OrderedLocusNames=YPO343, YPO3344, y0846;
                                                                                                                                                                                                                                                                                                                                                                                                                                    68 AA
                                                                                                                                                                                                          BX936398; CAH20028.1; -.
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                                                                                                                                                                                                                                                                     51.4%;
 Enterobacteriaceae; Yersinia
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50 FKKIKNKFIEMK 61
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               NCBI_TaxID=273123;
                                                          STRAIN=IP 32953;
PubMed=15358858;
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                                                                                                                                                                                                                                                                                   Gaps
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NCBI_TaxID=155148;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
P22-like viruses.
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                                                                                                                                                                           Length 68;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Pred. No. 2.1e+02;
5; Mismatches 2;
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Complete proteome; Hypothetical SEQUENCE 68 AA; 8065 MW; D08
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Best Local Similarity 41.7%;
Matches 5; Conservative
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SEQUENCE 66 AA; 7678 MW;
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Best Local Similarity 69.2
Best Local 9; Conservative
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49 LYRDHCEFKONKLL 61
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Score 35; DB
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01-JUN-2003 (TrEMBLrel. 24, Last anno
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                            54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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28 KIMRKFQNSIL 38
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Best Local Similarity
Matches 5; Conserv
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                         SEQUENCE FROM N.A. MEDLINES=21410065; PubMed=11518522; DOI=10.1006/jmbi.2001.4868; MEDLINES=21410058; PubMed=11518522; DOI=1000 T.S.; Clark A.J., Inwood W., Cloutier T., Dhillon T.S.; "Nucleotide sequence of coliphage HK620 and the evolution of lambdoid
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Pred. No. 2.5e+02;
1; Mismatches 0; Indel8
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Pred. No. 92;
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Zhao Q., Collodi P.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR342953; AAK07664.1; -.
NON TER 1 1 1
SEQÜENCE 42 AA; 4706 MW; 149239B02EA68314 CRC64;
                                                                                                                                                             J. Mol. Biol. 311:657-679(2001).
EMBL, AR335538; AAK28851.1; -.
Hypochetical protein.
SEQUENCE 66 AA; 7678 MW; S87B519EF433DC5B CRC64;
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Last annotation update)
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Bassuk J.A., Berg R.A.;
An novel 53-KDa polypeptide from chicken embryo.";
J. Biol. Chem. 266:23732-23738(1991).
NON_TER
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01-JUN-2002 (TrEMBLrel. 21, Last annot
PDI-11ke 53 kDa polypeptide (Fragment)
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Best Local Similarity 69.2.,
Local 9; Conservative
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7 LVRLFKNALLK 17
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SEQUENCE
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OPPS6
AC 09PS6
AC 09PS6
DT 01-MA
DT 01
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10981789
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MEDLINE=22120827; PubMed=12125824;
Deppenmeier U., Johann A., Hattsch T., Merkl R., Schmitz R.A.,
Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,
Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,
Brutacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.
Fritz H.-J., Gotsenalk G.;
"The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea.";
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MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouais K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
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Pred. No. 2e+02;
5; Mismatches 2; Indele
Length 42;
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Last annotation update)
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                                                               3; Mismatches
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SEQUENCE FROM N.A.
STRAIN=ATCC 14580;
Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.
Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.
Rasmussen M.D., Andersen J.T., Jozgensen P.L., Larsen T.S.,
Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
                                            Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G., "The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential.", J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
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31 KFKNRFLKI 39
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                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 67 AA; 76
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          SEQUENCE FROM N.A.
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                                   PubMed=15383718;
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YJ72 PASMU
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Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Peterson J.D., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                              Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                    Score 35; DB 2; Length 59;
Pred. No. 2.7e+02;
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                                                                                                            2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
EMBL, AABLO100596; EAA21604.1; -.
Hypothetical protein.
SEQUENCE 59 AA; 6819 MW; 39D0FD94A7C11E30 CRC64;
                                                             75AD8AF9EC6CDBF4 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Microbiol. Biotechnol. 4:453-461(2002)
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Pred. No. 2.7e+02
2; Mismatches
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J. Mol. Microbiol. Biotechno
EMBL; AE013306; AAM30507.1;
InterPro; IPR007168; PSpC.
                                                                                    50.0%;
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                                                             59 AA; 6538 MW;
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                                                                       Ouery Match
Best Local Similarity 54.5
Best Local Similarity 64.5
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                           Pfam; PF04024; PspC; 1.
Complete proteome.
SEQUENCE 59 AA: 6428
                                                                                                                                      1 KLYRKFKNKLL 11
                                                                                                                                                    3 KLYRSKRNKII 13
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Q7RMKS;
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Q7RMKS
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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"Complete genome sequence of the industrial bacterium Bacillus
licheniformis and comparisons with closely related Bacillus species.";
Genome Biol. 5:R77-R77(2004).
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Pasteurellaceae; Pasteurella.
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                                                                                                                                                                                                                                             Score 35; DB 2; Length 67;
Pred. No. 3.1e+02;
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37C1C429168E8D55 CRC64;
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Complete proteome; Hypothetical protein; Signal.
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical protein PM1972 precursor.
OrderedLocusNames=PM1972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 AA
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                                                                                            EMBL; AE017333; AAU41297.1; -.
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Best Local Similarity 70.0%;
Matches 7; Conservative
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Schuitemaker H.;
"Analysis of the temporal relationship between human immunodeficiency virus type I quasispecies in sequential blood samples and various organs obtained at autopsy.";
J. Virol. 72:488-496(1998).";
J. Virol. 72:488-496(1998).";
GO, GO:0019028; AACO410.1;
GO, GO:0019028; C:viral capsid; IEA.
GO; GO:00191; C:viral envelope; IEA.
GO; GO:0019198; F:structural molecule activity; IEA.
InterPro; IPR008985; CorA like lec_gl.
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Stulke J., Karamata D., Saier M.H. Jr., Hillen W.;
"A novel protein kinase that controls carbon catabolite repression in
bacteria.";
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MEDLINE=98080439; PubMed=9420250;
van't Wout A.B., Ran L.J., Kuiken C.L., Kootstra N.A., Pals S.T.,
            Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 63;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 AA; 7178 MW; BB803E449B574C68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Last annotation update)
48.6%; Score 34; DB 2; Le 60.0%; Pred. No. 3.2e+02; ive 2; Mismatches 2;
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Pred. No. 4.3e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                    63 AA.
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01-37A-1998 (TrEMBLrel. 05, Created)
01-37A-1998 (TrEMBLrel. 05, Last sequent 25-OCT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Microbiol. 27:1157-1169(1998).
[2]
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MEDLINE=98230327; PubMed=9570401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Envelope glycoprotein (Fragment).
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Best Local Similarity 54.5%;
Matches 6; Conservative
    Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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52 KLREQFKNKII 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00516; GP120; 1
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                                                                                                                                                             1 KLYRKFKNKL 10
                                                                                                                                                                                                                                      6 KVYSKFLNKI 15
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1034719
10 034711
AC 034711
DT 01-JAN
DT 25-OC
DE YVIC.
GN Name::
COX NCEL!
COX NCEL!
RA REL!
RA REL
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SEQUENCE FROM N.A.

SEROISTOE FROM N.A.

STRAIN=56601 Serogroup Icterohaemorrhagiae / Serovar lai;

MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;

Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

Zhang Y.-X., Xiong H., Iu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21555285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Ishiqwa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Tabata S.; Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; EMBL: AP003595; BAB75933.1; -.
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Pred. No. 3.3e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A814234 protein.
OrderedocusNames=a814234;
Anabaena dictrain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                               72 AA.
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                                                                                                                                                                                                                                                                                                                                                                                            Created)
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EMBL; AE011440; AAN49942.1; -.
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58.3%;
                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=LA2743;
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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37 KMKNKKLKMK 46
                                    5 KPKNKLLKLK 14
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SEQUENCE 72 AA;
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108 PZM7
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08 YPG
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SEQUENCE FROM N.A.
STRAIN=ATCC BAA.334 / TIGR4;
STRAIN=ATCC BAA.334 / TIGR4;
STRAIN=ATCC BAA.334 / TIGR4;
MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E.K., Khouri H.W., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Peldblyum T.V., Angiuoli S.V., Dickinson T.,
Hickey B.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                Pridmore R.D., Barger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R., Mollet B., Macreniter A., Klaenhammer T., Arigoni F., Schell M.A.; Mischaenhammer T., Arigoni F., Schell M.A.; Lactobacillus Johnsonii NCC 533."; Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

EMBL; AB017201; AAS08392.1; - 101:2512-2517(2004).

SEQUENCE 72 AA; 8640 MW; 7A76FB52437ED8CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2; Length 37;
Pred. No. 3.7e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                  Score 34; DB 2; Length 72;
Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome; Hypothetical protein.
SEQUENCE 37 AA; 4416 MW; 0F5D75C4CBC3CC17 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=TDE2755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SP1938.
OrderedLocusNames=SP1938;
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                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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                                                                                                                                                                                                                                                                                     48.6%;
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EMBL; AE007484; AAK76006.1;
PIR; E95226; E95226.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            16 EMYQKFINKL 25
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                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                       NEDLINE-98044033; PubbWed=9384377; DOI=10.1038/36786;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

A Azevedo V., Berrero M.G., Bessieres P., Bolotinh A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Borriss R., Boursier L., Brans A., Braun M., Erignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Britz C., Fujita M., Pujita Y., Fuma S., Galizzi A., Galleron N.,

Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

Auiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,

Nones L., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,

Kumano M., Kurita K., Lapidus A., Liu H., Maswal S.,

Kumano M., Kurita K., Levine A., Liu H., Maswal S.,

Medigue C., Medina N., Mellado R.P., Mizuno M., Mosetl D., Porwollik S.,

Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,

Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,

Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche E.,

Scoffone F., Sato T., Sanlan E., Schleich S., Schroeter R.,

Scoffone F., Sakiguchi A., Tacconi E., Takapi T., Takahashi H.,

Ansmaru K., Takeuchi M., Tamakoshi A., Tanaka T., Tarpstra P.,

Scoffone F., Sato T., Sato T., Sanlan E., Wedler H.,

Nassacotti A., Viari A., Wanhutt R., Wedler E., Wedler H.,

Wassarotti A., Wata K., Yashida K., Yoshikawa H.F., Zumstein E.,

Nochikawa H. Danchin A. Taraka H., Parka H., Parka H., Parka H., Parka K., Washach H., Washach H., Parka H., Washach H., Washach H., Parka H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus
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SEQUENCE FROM N.A.
Lazarevic V., Soldo B., Rivolta C., Reynolds S., Mauel C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 2; Length 65;
Pred. No. 4.4e+02;
0; Mismatches 2; Indels
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                              Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6CAD1493369D5F70 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:249-256(1997).
EMBL; AF017113; AAC67275.1;
EMBL; 299121; CAB15516.1; --
PIK; E70043; E70043.
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Pfam; PF04024; PspC; 1.
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Matches 7; Conservative
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                                                                                                                                    SEQUENCE FROM N.A.
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RESULT 25 Q74L23

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Length 54; Indels

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MEDLINE-22084066; PubMed=12089655; Pankhauser R.L., Monroe S.S., Noel J.S., Humphrey C.D., Bresee J.S., Pankhauser R.L., Monroe S.S., Noel J.S., Humphrey C.D., Bresee J.S., Parashar U.D., And T., Glass R.I.; Epidemiologic and molecular trends of 'Norwalk-like viruses' associated with outbreaks of gastroenteritis in the United States."; J. Infect. Dis. 186:1-7(2002).

EMBL; AR493178; AAM45963.1; --
GO: 001003968; F.NA-directed RNA polymerase activity; IEA.
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Viruses; ssRNA positive-etrand viruses, no DNA stage; Caliciviridae;
Norovirus; Norovirus isolates.
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Norovirus; Norovirus isolates.
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Fankhauser R.L., Monroe S.S., Noel J.S., Humphrey C.D., Bresee J.S.,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 2; Length 57;
Pred. No. 5.7e+02;
4; Mismatches 3; Indels
                                                                                                 Laird G.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL117333; CAC36072.1; -. S4 54 54
                                                                                                                                                                                                   ACAEB71BAFBDFB3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 AA; 6559 MW; 070EFF9CAA9C0993 CRC64;
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24, Last annotation update)
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Putative RNA-dependent RNA polymerase (Fragment)
                                                                                                                                                                                                                                                 Score 33; DB 2;
Pred. No. 5.4e+02;
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                                                                                                                                                                                                                                                                                                     5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norwalk-like virus Hu/NLV/GI/684/US
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                                                                                                                                                                                                54 AA; 6745 MW;
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08/359;
01-OCT-2002 (TrEMBLrel. 22,
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Best Local Similarity 41.70,

Best Local Similarity 41.70,
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9 KVWREEKERLLKM 21
                                                                                                                                                                                                                                                                                                  6; Conservative
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30 KFYRKIANRVIO 41
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=194603;
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SEQUENCE FROM N.A.
                                                                             SEQUENCE FROM N.A.
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01-JUN-2003
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SEQUENCE
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                                                             STAIN-ATCC 3540S / DSM 14222;

X Pubmed-15064399; DOI=101073/pnas.0307639101;
X Bubmed-15064399; DOI=101073/pnas.0307639101;
X Submed-15064399; DOI=101073/pnas.0307639101;
X Submed-15064399; DOI=101073/pnas.0307639101;
X Seshadri R., Mavidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,
A Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
A Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
A Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
A Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
Vashisth P., Morbill T.Z., Xiang Q., Sodergren E., Baca E.,
Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
T. "Comparison of the genome of the oral pathogen Treponema denticola With other spirochete genomes.";
T. "Comparison of the Sanomes.";
T. Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
REMBL; AE017255; AAS13272.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94174282; PubMed=8128227; Jansson A., Gillin F.D., Kagardt U., Hagblom P.; Coding of hemolysins within the ribosomal RNA repeat on a plasmid in Entamoeba histolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
     Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema
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Pred. No. 3.8e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ631M13.5.1 (Novel protein (Isoform 1)) (Fragment)
Name=dJ631M13.5;
Homo sapiens (Human).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .7e+02;
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Pred. No. 3.7e+02
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Entamoeba histolytica.
Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759;
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EMBL; Z29969; CAA82857.1; -.
SEQUENCE 38 AA; 4824 MW;
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87.58;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity 87.5
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Best Local Similarity 41.7
Matches 5; Conservative
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Q24854;
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Best Local Similarity 70.v.
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Best Local Similarity
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09PPI3
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Parashar U.D., Ando T., Glass R.I.;
"Epidemiologic and molecular trends of 'Norwalk-like viruses'
associated with outbreaks of gastroenteritis in the United States.";
J. Infect. Dis. 1861-7(2002).
GBMBL; AF493177; AAM45962.1; -.
GO; GO:0003968; P:RNA-directed RNA polymerase activity; IEA.
RNA-directed RNA polymerase.
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Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Enterobacteriaceae, Yersinia.
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Pred. No. 5.7e+02;
4; Mismatches 3; Indels
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Pred. No. 6e+02;
5; Mismatches 2; Indels
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STRAIN=KIMS / Biovar Mediaevalis;
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Genew; HGNC:16126; C200xf133.
SEQUENCE 60 AA; 7299 MW;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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9 KVWREEKERLLKM 21
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Matches 6; Conservative
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OrderedLocusNames=y2284;
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0980K0
AC 0980K
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DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DT 01-MA DE 01-MA PETHOR RA PETHOR RA PETHOR MA                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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STRAIN=NCTC (1168)
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Ralyandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parachiamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
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Pred. No. 6e+02;
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Pred. No. 6e+02;
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J. Bacteriol. 184:4601-4611(2002).
EMBL. AE01381; AAM85843.1; -
Hypothetical protein.
SEQUENCE 60 AA; 6673 MW; EC4EFA771A1F761E CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Cj0724.
OrderedLocusNames=Cj0724;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=pc0897;
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MEDIATE-929206; PubMed=8021587;
Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
Koonin E.V., Darai G.;
"Insect inidescent virus type 6 encodes a polypeptide related to the
largest subunit of eukaryotic RNA polymerase II.";
J. Gen. Virol. 75:1557-1567(1994).
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MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
MIT Tidona C.A., Darai G.;
"The DNA sequence of Chilo iridescent virus between the genome coordinates of .101 and 0.391; similarities in coding strategy between insect and vertebrate iridoviruses.";
Virus Genes 15:235-245(1997).
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BEDLINE-29125233 PubMed=9926400; DOI=10.1023/A:1008017820941;
Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome
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                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CIV) (Insect iridescent virus type 6). no RNA stage, Iridoviridae, Iridovirus
                                                                                                  Score 33; DB 2; Length 61;
Pred. No. 6.1e+02;
2; Mismatches 1; Indels
                                                          4D4970AD1C1B0EF2 CRC64;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                       65 AA.
                                         protein.
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MEDLINE=93118242; Pubmed=1475907;
               PIR; G81343; G81343.
Complete proteome; Hypothetical
SEQUENCE 61 AA; 7176 MW; 4D4
EMBL; AL139076; CAB72998.1; -.
                                                                                                    47.18;
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Virus Genes 17:243-258(1998)
                                                                                                                                         6; Conservative
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                                                                                                Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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01-DEC-2001
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SEQUENCE FROM N.A.
MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
Jakob N.J., Muller K., Bahr U., Darai G.;
Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the first complete DNA sequence of an invertebrate iridovirus: coding strategy of the genome of Chilo iridescent virus."; Virology 286:182-196(2001).
EMBL; AF303741; AAK81978.1; -.
SEQUENCE 65 AA; 8129 MW; 20C3027198B98279 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89073752; PubMed=3201750;
Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and physical mapping of the genome of insect
iridescent virus type 6: further evidence for circular permutation of
                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDINE-86174607; PubMed=3959991;
Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
Insect iridescent virus type 6 induced toxic degenerative hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and mapping of origins of DNA replication within the DNA sequences of the genome of insect iridescent virus type 6."; Virus Genes 6:19-32(1992).
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Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
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Delius H., Darai G., Fluegel R.M.; "DNA analysis of insect iridescent virus 6: evidence for circular permutation and terminal redundancy.";
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MEDLINE=93260401; PubMed=8492091;
Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
"Identification of the gene encoding the major capsid protein oinsect iridescent virus type 6 by polymerase chain reaction.";
J. Gen. Virol. 74:873-879(1993).
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MEDLINE=87321126; PubMed=2820141;
Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
Delius H., Darai G.;
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MEDLINE=94167241; PubMed=8121799;
Schnitzler P., Hug M., Handermann M., Janssen W., Koonin B.V.,
Delius H., Darai C.;
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Pred. No. 6.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Med. Microbiol. Immunol. 175:43-53(1986).
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Similarity 70.0%;
7; Conservative
                                                                                                               J. Virol. 49:609-614(1984)
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7627 MW; 1ACE2DIB84F2173A CRC64;
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SEQUENCE FROM N.A.
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STRAIN=MSBB / DSM 3109 / ATCC 43589;

STRAIN=MSBB / DSM 3109 / ATCC 43589;

MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,

Heidelberg J.F., Sutton G.G., Fleischmann R.D., Bisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from
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MEDLINE=95264471; PubMed=7745725;
Briant L., Wade C.M., Puel J., Brown A.J., Guyader M.;
Briant Ls, Wade C.M., Puel J., Brown A.J., Guyader M.;
"Analysis of envelope sequence variants suggests multiple mechanisms of mother-to-child transmission of human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U24765; AAB07191.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:001502B; C:integral to membrane; IEA. GO; GO:001902B; C:irial capsid; IEA. GO; GO:0019031; C:irial envelope; IEA. GO; GO:00519B; F:structural molecule activity; IEA. Interpro; IPR000777; GP120. Feam; PF00516; GP120; ADS. ADS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermotoga maritima.
Thermotogae, Thermotogales, Thermotogaceae, Thermotoga
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Pred. No. 6.9e+02;
2; Mismatches 2; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
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J. Virol. 69:3778-3788(1995).
EMBL; U24765; AAB07191.1; -.
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OrderedLocusNames=TM1386;
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Matches 6; Conservative
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LYRKFKNKLL 11
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LYQKIKNCLL 12
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54 YERFKNELEK 63
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AC 09X1A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence and comparative analysis of the model rodent malaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium yoelii yoelii.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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Pred. No. 4.2e+02;
3; Mismatches 4; Indels
                                                           Indels
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Last annotation update)
Score 33; DB 2; Le.s.
Pred, No. 6.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12368865; DOI=10.1038/nature01099;
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50.0%;
             47.1%;
50.0%;
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48 KLGEQFKNKTIVFK 61
                                                                                                               1 KLYRKFKNKLLKLK 14
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8 KIKKKKKNKNKKIK 21
       Query Match
Best Local Similarity 50.0
Matches 7; Conservative
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Matches 7; Conservative
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related to Bacillus anthracis pXO1.";

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Gaps

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Length 46; 4; Indels

Score 32; DB 2; 1 Pred. No. 6.7e+02; 3; Mismatches

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Complete proteome.
SEQUENCE 46 AA; 5543 MW; EBCLCD78DA206BB3 CRC64;
adaptations and a large plasmid rela!
Nucleic Acids Res. 32:977-988(2004).
                                                                               45.7%;
                        EMBL; AE017195; AAS44880.1;
                                                                                                                            1 KLYRKFKNKLLKL 13
                                                                                                      6; Conservative
                                                                               Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                    TIGR; BCEA0030;
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Matches
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PubMed=14960714; DOI=10.1093/nar/gkh258;

Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;

"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman B., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbbeck R., Kyrpides N.C.; Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
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Fretz R., Beuret C., Svoboda P., Tanner M., Baumgartner A.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS45060; AAS57793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 2; Length 43;
Pred. No. 6.2e+02;
3; Mismatches 2; Indels
                                                                                          Length 37;
                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                    Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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NCBI_TaxID=222523;
                                                                   3200E6A5D616E7A3 CRC64;
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Last annotation update)
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Pred. No. 5.4e+02;
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                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                                              Created)
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Bacillus cereus (strain ATCC 10987)
Plasmid pBc10987.
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37 37
37 AA; 4152 MW;
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EMBL; AE017007; AAP09871.1;
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                                                                                                                 5; Conservative
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Best Local Similarity
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                                  Polyprotein.
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SEQUENCE 37
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Q74P64;
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STRAIN=IMN-C3;
MEDLINE=97254461; PubMed=9099871; DOI=10.1016/S0378-1119(96)00798-6;
Lillehaug D., Nes I.F., Birkeland N.K.;
"A highly efficient and stable system for site-specific integration of genes and plasmids into the phage phiLC3 attachment site (attB) of the Lactococcus lactis chromosome.";
Gene 188:129-136(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lillehaug D., Lindqvist B., Birkeland N.K.; "Characterization of phiLC3, a Lactococcus lactis subsp. cremoris temperature bacteriophage with cohesive single-stranded DNA ends."; Appl. Environ. Microbiol. 57:3206-3211(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses, dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=IMN-C3;
MEDLINE=21263014; PubMed=11370866; DOI=10.1007/80043800000407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birkeland N.K., Lonneborg A.M.;
"The cos region of lactococcal bacteriophage phi LC3.";
DNA Seq. 4:211-214(1993).
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MEDLINE=95007252; PubMed=7922887;
Birkeland N.K.;
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34 KKYKEYKGKLFVL 46
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Gaps

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3; Indels

4; Mismatches

Score 32; DB 2; Length 57; Pred. No. 8.3e+02;

45.7%;

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Parashar U.D., Ando T., Glass R.I.;
"Epidemiologic and molecular trends of 'Norwalk-like viruses'
associated with outbreaks of gastroenteritis in the United States.";
J. Infect. Dis. 186:1-7(2002).
EMBL; AF493188; AAM45973.1; --
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
                                                                                                                                                                                                  57 57
57 AA; 6420 MW; 959008CGBF260180 CRC64;
                                                                                                                                             RNA-directed RNA polymerase.

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NON TER 57 57

SEQUENCE 57 AA; 6420 MW;
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Best Local Similarity 41.7
Matches 5; Conservative
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                                                                                                                                                                      Pubmed=1497255; DOI=10.1016/j.virol.2003.09.019; Blatny J.M., Godager L., Lunde M., Nes I.F.; "Complete genome sequence of the Lactococcus lactis temperate phage phiLC3: comparative analysis of phiLC3 and its relatives in lactococci and streptococci.";
       expression of the genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses, seRNA positive-strand viruses, no DNA stage, Caliciviridae, Norovirus, Norovirus isolates.
                                                                                                                                                                                                                                                                                                                                                                                                                   Blatny J.M., Ventura M., Rosenhaven E.M., Risoen P.A., Lunde M., Brussow H., Nes I.F.;
Brussow H., Nes I.F.;
"Transcriptional analysis of the genetic elements involved in the lysogeny/lysis switch in the temperate lactococcal bacteriophage philc3, and identification of the Cro-like protein ORF76.";
Mol. Genet. Genomics 269:487-498(2003).
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=IMN-C3;
MEDLINE=22766050; PubMed=12759744; DOI=10.1007/s00438-003-0854-y;
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Pred. No. 7.6e+02;
3; Mismatches 2; Indels
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AF242738; AS66806.1;
Hypothetical protein.
SEQUENCE 52 AA; 6221 MW; C6431A74000C14DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=IMN-C3;
Blatny J.M., Lillehaug D., Nes I.F.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blatny J.M., Lillehaug D., Nes I.F.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update
01-UUN-2003 (TrEMBLrel. 24, Last annotation upda
Putative RNA-dependent RNA polymerase (Fragment)
  "Cloning, molecular characterization, con-
encoding the lytic functions of lactococcal
dual lysis system of modular design.";
Can. J. Microbiol. 40:658-665(1994).
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54.5%;
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8 RLYRKIIHKLI 18
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Q8JSI9
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J. Infect. Dis. 186:1-7(2002).
GO: GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
Norovirus; Norovirus isolates.
NCBI_TaxID=194612;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AA; 6420 MW; 959008C6BF260180 CRC64;
                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative RNA-dependent RNA polymerase (Fragment).
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                                                                                                                                                                                        PRT;
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41.7%;
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May 16, 2005, 08:21:21; Search time 54.1293 Seconds (without alignments) 92.887 Million cell updates/sec Run on:

US-09-648-816B-6 65 Title: Perfect score:

1 ARYRKFKNKILKS 13 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

1066881 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 16Dec04:* 1: geneseqp1980s:* 2: geneserm1000. geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		df			SOMMERIES		
×	Score	Query Match	Query Match Length	DB	ID	Description	ų,
i	65	100.0	13	5	AAY57468	Aay57468 A	Antimicro
	65	100.0	13	ഹ	ABG69892	_	Rabbit pl
	29	90.8	13	~	AAY57469		Antimicro
	29	90.8	-	Ŋ	ABG69893	_	Rabbit pl
	54	83.1	13	~	AAY57466		Antimicro
	54	83.1	-	Ŋ	ABG69890	_	Rabbit pl
	54	83.1	18	~	AAY57503		Antimicro
	54	83.1	18	ß	ABG69927	_	Rabbit pl
	25	80.0	7	7	AAY57505		Antimicro
	52	80.0	1	Ŋ	ABG69929	_	Rabbit pl
	20	76.9	14	~	AAY57467		Antimicro
	20	76.9	14	'n	ABG69891	_	Rabbit pl
	48	73.8	7	~	AAY57471		Antimicro
	48	73.8	1	Ŋ	ABG69895		Rabbit pl
	47	72.3	7	7	AAY57465		Antimicro
	47	72.3	18	2	ABG69889		Rabbit pl
	47	72.3	-	7	AAY57501		Antimicro
	47	72.3	-	~	AAY57499	-	Antimicro
	47	72.3	-	ß	ABG69923	_	Rabbit pl
	47	72.3	-	Ś	ABG69925	_	Rabbit pl
	47	72.3	7	7	AAY57502	•	Antimicro
	47	72.3	7	ß	ABG69926	_	Rabbit pl
	47	72.3	•	7	AAY57496		Antimicro
	47	72.3	6	Ŋ	ABG69920		Rabbit pl
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ALIGNMENTS

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. (HARB-) HARBOR-UCLA RES & EDUCATION INST. Antimicrobial peptide RP-4 SEQ ID NO:6. AAY57468 standard; peptide; 13 AA. 99WO-US003350. 98US-00025319 25-FEB-2000 (first entry) Oryctolagus cuniculus. 18-FEB-1998; 17-FEB-1999; WO9942119-A1 26-AUG-1999. AAY57468; RESULT 1
AAY57468
AC AAY5
XX AAY5
XX AAY1
XX AAL1
XX A

Yeaman MR, Shen AJ; WPI; 1999-527417/44.

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure; Page 108; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXXBA and its derivatives selected from XZBZBXXXBA BXZXB, XBBXZXBBX and BBXZBBXZ; and (b) as second peptide template XBBXZXBBXXBBX and BBXZBBXZ; and (b) group consisting of XBBXBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

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considered to have undesirable toxicity,

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Gaps

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Length 13; 0; Indels

Score 65; DB 5; I Pred. No. 0.00025;

100.0%; Scor. 100.0%; Pred. No. v. 0; Mismatches

Query Match
Best Local Similarity 100.
Matches 13; Conservative

Sequence 13 AA;

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neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                            Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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                                                                                                                                                                                                                                                          Rabbit platelet microbicidal protein, PMP-2, based peptide #4.
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100.0%; Pred. No. 0.00025;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 129; 221pp; English.
                                                                                                                                                                                         ' ABG69892 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple antibiotic resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                     25-AUG-2000; 2000US-00648816
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Best Local Similarity 100.vv
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                                                                                                              1 ARYRKFKNKILKS 13
                                                                                                                                 1 ARYRKFKNKILKS 13
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                                             Sequence 13 AA;
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Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                   Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                      Antimicrobial peptide RP-5 SEQ ID NO:7.
                                                                                                                                                                                                         Disclosure; Page 109; 166pp; English.
AAY57469 standard; peptide; 13 AA.
                                                                                                                      99WO-US003350
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                         25-FEB-2000 (first entry)
                                                                              Oryctolagus cuniculus.
                                                                                                                                                           Shen AJ;
                                                                                                                                                                         WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                      Sequence 13 AA;
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                                                                                                                                                            Yeaman MR,
                                                                        Synthetic.
             AAY57469;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbicotadal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial activity of

leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, a disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acid core sevensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungic and timicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial conventional and antimicrobials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbit platelet microbicidal protein, PMP-2, based peptide #5
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                             Score 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                     ABG69893 standard; peptide; 13 AA
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                             90.8%;
84.6%;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBRARB, BXZZSB, XBBXZBBX and BBXZBBXZ; and (b) as second peptide template XBBXXBBX, BXXBXXBB, and their derivatives selected from the group consisting of XBBXZBBX; where B = at least one positively charged amino acid, x at least one non-polar hydrophobic amino acid, z = at least one aromatic amino acid, and where B, and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal nections. The peptides overall effect cellular disruption and rapid apptosis of microbial cells. AAY57463 to AAY57557 represent sequences
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overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                       Score 59; DB 5; Length 13; Pred. No. 0.0027; 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                   AAY57466 standard; peptide; 13 AA.
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84.6%;
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Matches 11; Conserv
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euthocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial against bacteria and fungi, agents in combination with other specifically against bacteria and fungi, agents in combination with other conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in functions of leukocytes, as disinfectants or preservatives for use in functions of leukocytes, as disinfectants or preservatives for use in bloody techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short hard have been actual antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprissing a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, condinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of
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                                                                                                                                                                                                                                     Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                           Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
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                                                 ABG69890 standard; peptide; 13 AA
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                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                             mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200255554-A2
                                                                                                                                          21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                             ABG69890;
RESULT 6
                        ABG69890
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Sequence 13 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against conganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZEXENE and its derivatives selected from XZBEZEXENE and BRXZBEX, as second peptide template XBEXXXXBX, XBEXXXBX, and BRXZBBX; and (b) a second peptide template XBEXXXBX, BXZEXXB, SEBZEXBBX, and their derivatives selected from the group consisting of XBEXXBBX, and their derivatives selected from the group consisting of XBBXXBBX, and their derivatives selected from the are least one non-polar hydrophobic amino acid; z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of intercents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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     Length 13
 Score 54; DB 5;
Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                              Antimicrobial peptide RP-1-2R SEQ ID NO:41.
                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                      AAY57503 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US003350
   ch 83.1%;
1 Similarity 76.9%;
10; Conservative
                                                                                                                                                                                                                                                                              25-FEB-2000 (first entry)
                                                                             1 ARYRKFKNKILKS 13
                                                                                                             1 ARYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Teaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527417/44.
Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                          AAY57503;
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RESULT

셤 8

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83.1%; Score 54; DB 5; Length 18; 76.9%; Pred. No. 0.027; ive 2; Mismatches 1; Indels
        ABG69927 standard; peptide; 18 AA
                                                                                                                  25-AUG-2000; 2000US-00648816.
                                                                                                        24-AUG-2001; 2001WO-US041877
                            21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                        Query Match 83.1
Best Local Similarity 76.9
Matches 10; Conservative
                                                                      Oryctolagus cuniculus.
                                                                                                                                     Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                             mutant; mutein.
                                                                                     WO200255554-A2.
                                                                                               18-JUL-2002
                                                                            Synthetic.
                  ABG69927;
RESULT 8
     ABG69927
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AAY57505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The inversion relates to an antimutational peptide composition to the invention relates to an antimutational peptide composition to the invention relates to the invention relates to the invention at a 1-13 amino acid core sequence (derived from truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial agents that chance the antimicrobial in the conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents that enhance the antimicrobial the considered to have undesirable toxicity, immunogenicity and short beingogy techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short that based upon natural antimicrobial peptides that have potent and broad resistance. They exhibit lower inherent mammalian cell toxicities and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                      Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resistance. They exhibit lower inherent mammalian cell toxicities
                                                      Rabbit platelet microbicidal protein, PMP-2, based peptide #39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARB-) HARBOR-UCLA RES & EDUCATION INST.
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                      Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52; DB 2; Length 18;
Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                              Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 59; 166pp; English.
AAY57505 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG69929 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%;
                                                                                                                                                                                                                                             99WO-US003350
                                                                                                                                                                                                                                                                     98US-00025319
                                                                                                                                                                                                                                                                                                                                                                                            against bacteria and fungi.
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ARYKKFKKKFLKS
                                                                                                                                                              Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                          Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                                                                                                                                                                                                             17-FEB-1999;
                                                                                                                                                                                                                                                                      .8-FEB-1998;
                                                   25-FEB-2000
                                                                                                                                                                                       WO9942119-A1
                                                                                                                                                                                                                 26-AUG-1999
                                                                                                                                                Synthetic.
                         AAY57505;
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ABG69929
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Rabbit platelet microbicidal protein, PMP-2, based peptide #41.
                                                                                                      (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                      Example; Page 72; 221pp; English
                                                                                  24-AUG-2001; 2001WO-US041877.
                                                                                            25-AUG-2000; 2000US-00648816.
    21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.9°
Matches 10, Conservative
                                                 Oryctolagus cuniculus.
                                       mutant; mutein.
                                                               WO200255554-A2.
                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
                                                                        18-JUL-2002.
                                                                                                               Yeaman MR,
                                                     Synthetic.
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Shen AJ;

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXEBAB and its derivatives selected from XZBBZBXEBAB, BXXZRSB, XBBXZBBAB and BBXZBBXZ; and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBB, BXXBXB, XBBXZBBZ, and consisting of XBBXBBX, XBBXXBB, BXXBXB, BXBBXXBB, and activative of XBBXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AMST7463 to AAYS7757 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                          Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.9%; Score 50; DB 2; Length 14; 90.0%; Pred. No. 0.1; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                Antimicrobial peptide RP-3 SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 108; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG69891 standard; peptide; 14 AA.
                                                      AAY57467 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US003350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00025319
                                                                                                                                                                         25-FEB-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                AAY57467;
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RESULT 11
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ID ABG(
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DT 21-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid corre sequence (derived from 150 amino acid a containing a 7-13 amino acid corre sequence (derived from PWP-1 and PWP-2, platelet microbicidal protein), and retromers.

Truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungions; and (2) antimicrobial peptides for potentiating antimicrobial agents are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobial peptides are useful as individual antimicrobial agents conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in foods and commercies and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicity immunogenicity and considered to have inherent mammalian cell toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                     Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 0.06;
1; Mismatches 2; Indels
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80.0%; 76.9%;

1 ARYRKFKNKILKS 13 |||:||| | ||| ARYKKFKKKFLKS 13

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New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting
Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                      (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                          Disclosure; Page 129; 221pp; English.
                                                                                                                                                                                                          multiple antibiotic resistance.
                                                                                                                      25-AUG-2000; 2000US-00648816.
                                                                                                     24-AUG-2001; 2001WO-US041877
                                           Oryctolagus cuniculus
                                                                                                                                                       Yeaman MR, Shen AJ;
                                                                                                                                                                        WPI; 2002-590659/63
                          mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 AA;
                                                                   WO200255554-A2
                                                                                    18-JUL-2002
                                                   Synthetic.
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-6150 amino acide scontaining a 7-13 amino acide foors esquence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and recromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial agents described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial agents that enhance the dungi. The leukocytes against organisms such as bacteria and fungi. The cantimicrobial peptides are useful as individual antimicrobial agents that enhance the antimicrobial agents that enhance the antimicrobial agents that chance the antimicrobial or conventional antimicrobials, agents that enhance the antimicrobial or foods and cosmetics and as agents to improve efficiency of conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular complexed to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic creatstance. They exhibit lower inherent mammalian cell toxicitys in plasma and complement sequence is a rabbit pWm based antimicrobial peptides.
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Pred. No. 0.1;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 90.0
Matches 9; Conservative
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ABG69895 standard; peptide; 13 AA.
                                                                                                                                                                                                                                        (first entry)
                                                                                 1 ARYRKFKNKILKS 13
                                    Best Local Similarity 69.2
Matches 9; Conservative
Sequence 13 AA;
                                                                                                                                                                                                                                        21-OCT-2002
                                                                                                                                                                                                            ABG69895;
                           Query Match
                                                                                                                                                      RESULT 14
                                                                                                                                                                  ABG69895
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                                                                                                                                                                                                                                                                                                                          AAY57471 standard; peptide; 13 AA
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AAY57471;

RESULT 13
AAY57471
ID AAY57,
XX
AC AAY57.

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the present invention describes an administratory produce with the corganisms such as bacteria and fungi. The AP comprises: (a) a peptide corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBEXXBEX and its derivatives selected from XZBBZBXBEX BXXXBX XBEXXBX ABXXBEX BX ABBXXBBX and BBXZBBX; and (b) a second peptide template XBBXXBBX, BXXBXB, XBBXXBBX, and the group consisting of XBBBBX and their derivatives selected from the group consisting of XBBBX and their derivatives selected from the corp. The peptide template amino acid; Z = at least one aromatic amino acid. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial calls. AAYS7453 to AAYS7557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                    Antimicrobial, metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.8%; Score 48; DB 2; Length 13; 69.2%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                 HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                   Antimicrobial peptide RP-7 SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 110; 166pp; English
                                                                                                                                                                                                                                                                                                            98US-00025319.
                 (first entry)
                                                                                                                                                           Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                     Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant; mutein.
                                                                                                                                                                                                                                                                                                            18-FEB-1998;
                                                                                                                                                                                                                                                                          17-FEB-1999;
                                                                                                                                                                                                 WO9942119-A1
                   25-FEB-2000
                                                                                                                                                                                                                                      26-AUG-1999
                                                                                                                                          Synthetic.
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms and the as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXEXBX and BBXZBBXZ; and (b) a second peptide template XEXE, BXZXXXB, XBBXZXBX and BBXZBBXZ; and (b) are second peptide template XBBXX and their derivatives selected from the group consisting of XBBXXBBX, XBBXXBX, XBBXXXB, and their derivatives selected from the group consisting of XBBXXBBXXBXXBX, and their derivatives can non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal nections. The peptides overall effect cellular disruption and rapid applysis of microbial activity of apoptosis of microbial cells. ANYSTGST represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial; platelet microbiccidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial peptides for potentiating antimicrobial agents active
Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
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72.3%; Score 47; DB 2; Length 18;
Best Local Similarity 69.2%; Pred. No. 0.43;
Matches 9; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 106; 166pp; English.
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                                                                                                                                                                                                                                                                                                             99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                      98US-00025319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   against bacteria and fungi
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                                                                                                                     Oryctolagus cuniculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200255554-A2.
                                                                                                                                                                                                                                                                                                                                                                      18-FEB-1998;
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                                                                                                                                                                                                                                                26-AUG-1999
                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG69889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The interior learners to an antimitation of propertion of against corganisms such as bacteria and fungi comprising a peptide of 5. 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a matimicrobial peptide composition and retromers. The possible structures are fully described in the specification. Also or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial against bacteria and fungi, agents in combination with other specifically against bacteria and fungi, agents in combination with other conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in fooder and second to more and an agents to improve efficiency of more and an agents to improve efficiency of more and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally the perior and an agents to improve efficiency of molecular perior and an agents to improve efficiency of molecular perior and an agents to improve efficiency of molecular perior and antimicrobial peptides of prior art have generally the perior and an agents to a perior and an agents to a perior art have generally the perior and an agents to a perior and an agents to a perior and an adequate the antimicrobial antimicrobial and antimicrobial ant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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3; Mismatches
                                                                                                                                                                                                                                                                                                                                         (HARB-) HARBOR-UCLA RES & EDUCATION INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 130; 221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple antibiotic resistance
                                                                                                                                                                                                                    24-AUG-2001; 2001WO-US041877
                                                                                                                                                                                                                                                                                25-AUG-2000; 2000US-00648816
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1 ALYKKWKONKLLKS
      Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                     Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-590659/63
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                                                                                           WO200255554-A2
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                                                                                                                                                 18-JUL-2002.
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AAY57465;

Query Match

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Gaps

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99WO-US003350 98US-00025319

Shen AJ;

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(HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                   17-FEB-1999;
                                                                                      18-FEB-1998;
                  26-AUG-1999.
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                                                                                                                                                                                                                                                                                              The invention trainers to an antimutational peptide comparising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
PWP-1 and PMP-2, platelet microbiocidal protein), and retromers,
truncations, extensions, combinations, funions and their derivatives. The
possible structures are fully described in the specification. Also
conclusions, extensions are fully described in the specification. Also
core sequence selected from truncations active against organisms such as
bacteria and fungi comprising a peptide composition for direct activity
or for potentiating antimicrobial agents active against organisms such as
core sequence selected from truncations of the peptides described above,
and retromers, extensions, combinations of the peptides described above,
and retromers, extensions, combinations of the peptides described above,
and retromers, extensions, combinations of the peptides described above,
and imicrobial peptides for potentiating antimicrobial activity of
antimicrobial peptides are useful as individual antimicrobial agents,
specifically against bacteria and fungi, agents in combination with other
conventional antimicrobials, agents that enhance the antimicrobial
conventions of leukocytes, as disinfectants or preservatives for use in
floods and cosmetics and as agents to improve efficiency of molecular
conventions of leukocytes, as disinfectants or preservatives for use in
the floods and cosmetics and as agents to improve efficiency of molecular
considered to have undesirable toxicity, immunogenicity and short
are based upon natural antimicrobial peptides of the present invention
are based upon natural antimicrobial peptides that have potent and broad
spectrum activity against pathogens exhibiting multiple antibiotic
conversemence. They exhibit lower inherent mammalian cell toxicitys and overcome problems of toxicity, immunogenicity, and shortness of defectiveness due to biodegradation, retaining activity in plasma and
covercome problems of toxicity, immunogenicity, and shor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                        New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                     invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 5; Length 18;
Pred. No. 0.43;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
                                                                    (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                  Claim 24; Page 71; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY57501 standard; peptide; 19 AA.
24-AUG-2001; 2001WO-US041877.
                                   25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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Oryctolagus cuniculus.
                                                                                                                                      WPI; 2002-590659/63.
                                                                                                         Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXXZXB, XBBXZXBX and BBXZBBXZ; and (b) a second peptide template XBBXX BXXXBXB, XBBXZXBBX, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and XBBXXXBBX, where B = at least one positively charged amino acid; and where B, X and Z amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal controphils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AM57463 to AAY57557 represent sequences to see the antimicrobial activity of sections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AM57463 to AAY57557 represent sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                              Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 2; Length 19;
Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptide OC-RP-1 SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                          Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY57499 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shen AJ;
WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY57499;
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to an antimicrobial peptide composition for use

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distriction relates to an antimicrobial peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
PWP-1 and PWP-2. platelet microbicidal protein), and retromers,
truncations, extensions, combinations, fusions and their derivatives. The
possible structures are fully described in the specification. Also
included are (i) an antimicrobial peptide composition for direct activity
or for potentiating antimicrobial peptide composition for direct activity
or for potentiating antimicrobial peptide of 13-74 containing an amino acid
core sequence selected from truncations of the peptides described above,
and retromers, extensions, combinations and fusions; and (2)
antimicrobial peptides for potentiating antimicrobial activity of
leukocytes against organisms such as bacteria and fungi. The
antimicrobial peptides are useful as individual antimicrobial agents,
specifically against bacteria and fungi, agents in combination with other
antimicrobials, agents that enhance the antimicrobial
conventional antimicrobials, agents the thance, potentiate or restore efficacy of
conventional antimicrobials, agents to improve efficiency of
conventions of leukocytes, as disinfectants or preservatives for use in
conventions of leukocytes, are disinfectants or preservatives for use in
considered to have undesirable foxicity, immunogenicity
been considered to have undesirable foxicity, immunogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                             invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                           The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXZB, XBBXXZBB, and BBXZBBXZ; and (b) a second peptide template XBBXXBX, XBBXXBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXBBX, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXBBX, and consisting of XBBZBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and consisting of XBBZXBBX and their derivatives cone aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX57463 to AAX5757 represent sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                              Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit platelet microbicidal protein, PMP-2, based peptide #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 2; Length 19;
Pred. No. 0.46;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                        Disclosure; Page 58; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | |:||| |:|||
2 ALYKKFKKKLLKS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 69.2
Matches 9; Conservative
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                             WPI; 1999-527417/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 AA;
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RESULT 19 ABG69923

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                                    Gaps
                                   ;
                                                                                                                                                                                                                 Rabbit platelet microbicidal protein, PMP-2, based peptide #37
          Score 47; DB 5; Length 19; Pred. No. 0.46;
                                   2; Indels
                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                           ABG69925 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-2000; 2000US-00648816.
           72.3%;
                                                                                                                                                                                          21-OCT-2002 (first entry)
Query Match
Best Local Similarity 69.2.
Best Local 9; Conservative
                                                          1 ARYRKFKNKILKS 13
                                                                                 2 ALYKKFKKKLLKS 14
                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Teaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                       WO200255554-A2.
                                                                                                                                                                                                                                                                             mutant; mutein.
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                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                    ABG69925;
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New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

Yeaman MR, Shen AJ; WPI; 2002-590659/63.

Example, Page 71-72; 221pp; English

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core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents are useful as individual antimicrobial agents.

Specifically against bacteria and fungi, agents in combination with other attimicrobials, agents that enhance the antimicrobial activity of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in functions of leukocytes, as disinfectants or preservatives for use in commercies and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiocic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                         against organisms such as bacteria and fund comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above,
New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                           invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial, metapeptide, PMP-2, platelet microbicidal protein, antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 5; Length 19;
Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY57502 standard; peptide; 20 AA
                                                                                               Example; Page 72; 221pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ARYRKFKNKILKS 13
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nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1999;
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Shen AJ;

Yeaman MR,

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXZB, XBBXZXBBX and BMXZBBXZ; and (b) a second peptide template XBBXXXB, XBBXXXBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXXBX, BXXXBX, XBBXXXBB, and XBBXXBBX; where B = at least one positively charged amino acid; and where B, X and Z mino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX57463 to AAX5757 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                  Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.3%; Score 47; DB 2; Length 20; 69.2%; Pred. No. 0.48;
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                                                                                                        Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG69926 standard; peptide; 20 AA.
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ALYKKFKKKLLKS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 69.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY57496 standard; peptide; 25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.3%;
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New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                           The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against conganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXEBS and BBXZBBXZ; and (b) a selected from XZBZBXEBS, BXZXZB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XZBZXZB, XBBXZXBBX and their derivatives selected from the group consisting of XBBXZBBX, and their derivatives selected from the group consisting of XBBXBBX, BXXBXSB, BXZBXXB, XBBZXXBBX and their derivatively charged amino acid; X = t least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabbit platelet microbicidal protein, PMP-2, based peptide #32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.3%; Score 47; DB 2; Length 25; 69.2%; Pred. No. 0.6;
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                         Disclosure; Page 126; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 25 AA;
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                                            The invention features to an antimuticional peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,

truncations, extensions, combinations, funions and their derivatives. The possible structures are fully described in the specification. Also concluded are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungi. The antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial agents for potentiating antimicrobial agents.

Cole sepecifically against bacteria and fungi, agents in combination with other antimicrobial peptides are useful as individual antimicrobial agents that enhance the antimicrobial activity of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in footen and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in the benchmiques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short or are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, relating activity in plasma and coverceme problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, relating activity in plasma and a rabbit pwent and activity and shortness due to biodegradation, relati
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                               The invention relates to an antimicrobial peptide composition for use
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Pred. No. 0.48;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and DMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

WPI; 1999-527417/44.

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Gaps

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included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as active adamenta and fungi comprising a peptide of 13-74 contraining an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) and retromers, extensions, combinations and funsions; and (2) core sequence selected from truncations and fungi. The attimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents. The appendix and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic cresistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of a rabbit pWP based antimicrobial peptide 8888888888888888888888888888888

Sequence 25 AA;

DB 5; Length 25; 2; Indels Score 47; DB 5 Pred. No. 0.6; 2; Mismatches 72.3%; Query Match
Best Local Similarity 69.2%,
Conservative 1 ARYRKFKNKILKS 13 1 ALYKKFKKKLLKS 13 ઠ

ADL70275 standard; peptide; 33 AA. ADL70275; RESULT 25

20-MAY-2004 (first entry) Peptide antibiotide PT-1 Protide; antibiotide; antimicrobial; interleukin-8; Staphylococcus; infection.

Synthetic.

Location/Qualifiers Cleavage-site

15. .16
/note= "Cleaved by V8 protease"

WO2004017985-A1

04-MAR-2004.

20-AUG-2003; 2003WO-US026405.

20-AUG-2002; 2002US-00225562

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Brass EP Yeaman MR, Yount NY, Edwards JE,

New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory

Claim 1; SEQ ID NO 1; 103pp; English

condition.

The present sequence is that of Protide-1 (PT-1), a peptide antibiotide with distinct effector and activator domains. PT-1 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for staphylococcus V8 protease. PT-1 was designed to be cleaved into 2 construct effectors in the presence of V8 protease. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of V8 protease produced by Staphylococcus aureus. Thus, PT-1 can adesigned to exert optimal antimicrobial activity in the context of infections due to staphylococcus aureus. Thus, PT-1 can adesigned to exert optimal antimicrobial activity in the context of infections due to staphylococcus aureus. Thus, PT-1 can synthesised by solid-phase synthesis. It is an example of context-activated protides of the invention that have 2 or context effectors with individual distinct biological functions and one or more effectors with individual distinct biological functions and one or more effectors upon context activation. The biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad in a produced processes are useful in the diagnosis, prophylaxis and therapy of a broad in a produce and a produced produced in the diagnosis, prophylaxis and therapy of a broad in the diagnosis.

Sequence 33 AA;

Gaps ö 72.3%; Score 47; DB 8; Length 33; 69.2%; Pred. No. 0.79; Indels 2; Mismatches Local Similarity 69.2 les 9; Conservative Query Match Best Loca Matches

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1 ARYRKFKNKILKS 13 | |:||| |:||| 16 ALYKKFKKKLLKS 28

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Gaps

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RESULT 26 AAY57497

AAY57497 standard; peptide; 35 AA.

AAY57497;

(first entry) 25-FEB-2000

Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

Oryctolagus cuniculus. Synthetic

WO9942119-A1.

26-AUG-1999

99WO-US003350. 17-PEB-1999; 98US-00025319 18-FEB-1998; (HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 1999-527417/44.

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi

Disclosure; Page 126; 166pp; English

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives aselected from XBBZXBXB. BXZXZB. WBXZXSBX and BBXZBBXZ, and (b) a second peptide template XBBX and their derivatives selected from transparent and consisting of XBBXBBX, XBBXXBBX, XBBXXBBX, and (b) group consisting of XBBXBBX, XBBXXBBX, XBBXXBB, and

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New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X = at least one aromatic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells AAYS7463 to AAYS7557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabbit platelet microbicidal protein, PMP-2, based peptide #33
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Pred. No. 0.84;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                  used in the exemplification of the present invention
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1 ALYKKFKKKLLKS 13
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Best Local Similarity
                                                                                                                                                                                                                                                                                                       Sequence 35 AA;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above,

and retromers, extensions, combinations and fusions; and (2) antinicrobial peptides for potentiating antinicrobial activity of leukocytes against organisms such as bacteria and fungi. The antinicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials.

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functions of leukocytes, as disinfectants or preservatives for use in foods and cosmerics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, recaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                      5; Length 35;
                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protide; antibiotide; antimicrobial; interleukin-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Cleaved by C3 convertase"
                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brass EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                      Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL70276 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2002; 2002US-00225562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-2003; 2003WO-US026405
                                                                                                                                                                                                                                                                      72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                               1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                                                                                                                                    | |:||| |:|||
1 ALYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide antibiotide PT-2.
                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yount NY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-226740/21
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                   Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2004017985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL70276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADL70276
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example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of Protide-3 (PT-3), a peptide antibiotide antimicrobial peptide effector and activator domains. PT-3 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors in the presence of thrombin. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of thrombin. but equivalent to or exceeding that of RP-1 in the presence of thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thus, PT-3 exerts optimal antimicrobial activity in the context of thrombin as would be present in the setting of vascular injury or infection. PT-3 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more diffectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                       ö
                                                                                                                                                                  DB 8; Length 36;
                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protide; antibiotide; antimicrobial; interleukin-8.
                                                                                                                                                                Score 47; DB 8;
Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brass EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18. 19
/note= "Cleaved by thrombin"
                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 3; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yount NY, Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                ADL/10277 standard; peptide; 37 AA
                                                                                                                                                              72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-2002; 2002US-00225562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-2003; 2003WO-US026405
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                Query Match
Best Local Similarity 69.27
These 9; Conservative
                                                                                                                                                                                                                                        1 ARYRKFKNKILKS 13
                                                                                                                                                                                                                                                           | |:||| |:|||
19 ALYKKFKKKLLKS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide antibiotide PT-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-226740/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004017985-A1.
                                                                                                                               Sequence 36 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                 ADL70277;
                                                                                                                                                                                                                                                                                                                             RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of Protide-4 (PT-4), a peptide antibiotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protide; antibiotide; antimicrobial; interleukin-8; cytostatic.
                                                                                                                             ö
                                                                          Length 37;
                                                                                                                          2; Indels
                                                                          DB 8;
                                                                       Score 47; DB 8;
Pred. No. 0.89;
2; Mismatches
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/note= "Cleaved by MMP-9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edwards JE,
                                                                                                                                                                                                                                                                                                                                                     ADL70278 standard; peptide; 39 AA
                                                                     72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2003; 2003WO-US026405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-2004 (first entry)
                                                                                                                                                                          1 ARYRKFKNKILKS 13
                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide antibiotide PT-4.
                                                                                                                                                                                                               21 ALYKKFKKKLLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-226740/21
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004017985-A1
                       Sequence 37 AA;
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Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                       Matches
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Score 47; DB 8; Length 39; Pred. No. 0.94;

72.3%;

Best Local Similarity

Query Match

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide contentining a 7-13 amino acide core sequence (derived from 150 amino acide contentining a 7-13 amino acide core sequence (derived from pWP-1 and PWP-2, platelet microbial protein), and recromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial agents or potentiating antimicrobial agents or potentiating antimicrobial agents or potentiating antimicrobial agents from the secret specifically against bacteria and fungi, agents in combination with other antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents to improve efficiency of foods and cosmetics and as agents to improve efficiency of foods and cosmetics and as agents to improve efficiency of ben considered to have undesirable toxicity, immunogenicity and short of spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicity and short overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity and shortness of effectiveness due to biodegradation, retaining activity in plasma and cosmetics and even because of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
Gaps
                                                                                                                                                                                                                                                                                                                         Rabbit platelet microbicidal protein, PMP-2, based peptide #102
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Indels
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Mismatches
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                                                                                                                                                                                            ABG69990 standard; peptide; 40 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-2000; 2000US-00648816
                                                                                                                                                                                                                                                                                 21-OCT-2002 (first entry)
                                          1 ARYRKFKNKILKS 13
                                                                22 ALYKKFKKKLLKS 34
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant; mutein.
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                                                                                                                                                 Matches
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acida containing a 7-13 amino acid core sequence (derived from 150 amino acida corts and peptide of 5-
150 amino acida containing a 7-13 amino acid core sequence (derived from truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents to antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance the antimicrobial companients and as agents to improve efficiency of molecular or foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short to be an considered to bave undesirable toxicity, immunogenicity and short care based upon natural antimicrobial peptides that have potent and broad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                  Rabbit platelet microbicidal protein, PMP-2, based peptide #104.
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                                                                     0.96;
                                                                                         Mismatches
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                                                    Score 47;
Pred. No.
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                                                                                         2
                                                                                                                                                                                                                                                             ABG69992 standard; peptide; 40
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                                                    72.3%;
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                           1 ARYRKFKNKILKS 13
                                                                                                                                                                1 ALYKKFKKKLLKS 13
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus.
                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200255554-A2.
                   Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                     21-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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crivity or for potentiating antifactobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting containing an amino acid sequence selected from the group consisting selected from XZBBZKBXB, BXZXZB, XBBXZXBX, and its derivatives selected from the group consisting of xBBXBXBX, BXXXZBX, XBBXZXBX, and BBXZBBXZ; and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBX, XBBXXBXB, XBBXXBBX, BXXBXXB, XBBXXBB, and XBBZXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid cused in the exemplification of the present invention
spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for potentiating-antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               platelet microbicidal protein;
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                                                                                                                                                                                     ö
                                                                                                                                                 Length 40;
                                                                                                                                                                                 2; Indels
                                                                                                                                                                0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial peptide RP-1-10F SEQ ID NO:42.
                                                                                                                                                 ОВ
                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                               Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                               AAY57504 standard; peptide; 18 AA
                                                                                                                                               72.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                          1 ALYKKFKKKLLKS 13
                                                                                                                                                                                                                     1 ARYRKFKNKILKS 13
                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus
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                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                             Sequence 40 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                     AAY57504;
                                                                                                                                                                                     Matches
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Score 45; DB 2; Length 18; Pred. No. 0.95;

69.2%; 69.2%;

Best Local Similarity

Query Match

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The invention relates to an antimatorobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from the period are (i) parability and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also consider are (i) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as bacteria and fungi. The containing an amino acid conventional apprides are useful as bacteria and fungi. The peptides for conventional antimicrobials, agents that enhance the antimicrobial with other antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in the considered to have undesirable toxicity, immunogenicity and short been considered to have undesirable toxicity, immunogenicity and short conservatives adminicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad espectrum activity against leaves inherent mammalian cell taxicity experience. The periods and considered to have undesirable mammalian cell taxicity in the present invention are based upon natural antimicrobial apprides that thave potent and broad espectrum activity against periods inherent mammalian cell taxicities and diversions of functions of functions of functions of functions are based upon natural antimicrobial and manual and antimicrobial and antimi
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                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an antimicrobial peptide composition for use
Gaps
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  Indels
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  Mismatches
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                                                                                                                                                                                                                         ABG69928 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                            (first entry)
                                                 1 ARYRKFKNKILKS 13
                                                                                                1 ALYKKFKKFLKS 13
  9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant; mutein.
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  Matches
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXZB, XBBXXZBX and BMXZBXZ; and (b) a second peptide template XBBXXXBX, BXXXBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXXBX, XBBXXXBB, and XBBXXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AMX57463 to AAX57757 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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Pred. No. 2.1;
2; Mismatches 2; Indels
                                                   Length 18;
                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                           Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
                                                                                 1; Mismatches
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                                                 Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 58; 166pp; English.
                                                                                                                                                                                                                                      AAY57500 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00025319
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                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                      1 ALYKKFKKKFLKS 13
                                                                                                                     1 ARYRKFKNKILKS 13
                                                               Local Similarity 69.2
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shen AJ;
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Best Local Similarity
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                 Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                          AAY57500;
                                               Query Match
                                                                                   Matches
                                                                                                                                                                                                        RESULT 35
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-7 containing an amino acid core sequence selected from truncations and fusions; and (2) and retromers, extensions, combinations and fusions; and (2) and retromers peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The artimicrobial peptides are useful as individual antimicrobial agents, agents that enhance the antimicrobial antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial for unctions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular conventions and commissional peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity immunostical inconsidered to have undesirable toxicity, immunostical immunostical inconsidered to have undesirable toxicity, immunostical im
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
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                                                                                                                                                                                                                                                Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.
                                                                                                                                                                                                 Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
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                             ABG69924 standard; peptide; 18 AA.
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                                                                                                                                          21-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                     ABG69924;
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DB 5; Length 18;

Score 43; DB Pred. No. 2.1;

66.2**%**; 66.7**%**;

Query Match Best Local Similarity

Sequence 18 AA;

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Gaps

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8; Conservative 1 ARYRKFKNKILK 12 | |:||| |:|| 1 ALYKKFKKKLLK 12

Matches

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2000US-0231242F

2000US-0231243F

2000US-0231414F

2000US-0232144F

2000US-0232081F

2000US-0232081F

2000US-0232081F

2000US-0232398F

2000US-0232398F

2000US-0232398F

2000US-0232401F

2000US-0232401F

2000US-023364F

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2000US-023364F

2000US-023365F

2000US-023365F

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2000US-023365F
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2000US - 0236303P

2000US - 0237039P

2000US - 0237039P

2000US - 0237039P

2000US - 023703P

2000US - 0239937P

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2000US - 0246528P

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2000US-0235444P
2000US-0235834P
2000US-0235834P
2000US-023537P
2000US-0235367P
2000US-0235367P
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2000US-0249207P.
2000US-0249208P.
2000US-0249209P.
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
14-SEP-2000;
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25-SEP-2000;
26-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; fimuluosuppressive; antiinflammatory; anti-HIV; antibacerial; vulnerary; antiparakinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabelic; antilucer; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
     Gaps
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     Indels
                                                                                                                                                                                                                                                                                  Human nervous system related polypeptide SEQ ID NO 3441
     ;
 Mismatches
                                                                                                                                                                    ABB14784 standard; protein; 74 AA
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02-MAR-2000; 2000US-0.18664P.
02-MAR-2000; 2000US-0.18664P.
19-MAR-2000; 2000US-0.189123P.
19-MAY-2000; 2000US-0.189123P.
19-MAY-2000; 2000US-0.209467P.
20-JUN-2000; 2000US-0.219135P.
20-JUN-2000; 2000US-0.219135P.
20-JUL-2000; 2000US-0.215135P.
20-JUL-2000; 2000US-0.214886P.
211-JUL-2000; 2000US-0.214880P.
211-JUL-2000; 2000US-0.214880P.
26-JUL-2000; 2000US-0.214890P.
26-JUL-2000; 2000US-0.21489P.
26-JUL-2000; 2000US-0.21496P.
26-JUL-2000; 2000US-0.22518P.
26-JUL-2000; 2000US-0.225214P.
26-JUL-2000; 2000US-0.225214P.
26-JUL-2000; 2000US-0.225214P.
26-JUL-2000; 2000US-0.225214P.
26-JUL-2000; 2000US-0.225214P.
26-JUL-2000; 2000US-0.225214P.
26-JUL-2000; 2000US-0.225268P.
26-JUL-2000; 2000US-0.225268P.
26-JUL-2000; 2000US-0.225268P.
27-MUG-2000; 2000US-0.225268P.
27-MUG-2000; 2000US-0.22575P.
27-MUG-2000; 2000US-0.22575P.
27-MUG-2000; 2000US-0.22575P.
23-MUG-2000; 2000US-0.22575P.
23-MUG-2000; 2000US-0.22575P.
23-MUG-2000; 2000US-0.225778P.
30-MUG-2000; 2000US-0.225928P.
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2000US-0229345P
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   8; Conservative
                                      1 ARYRKFKNKILK 12
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ALYKKFKKKLLK 12
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01-SEP-2000; 2
01-SEP-2000; 2
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ABB14784

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ABB14 ABB14

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   Matches
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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 27152; 1399pp + Sequence Listing; English
              Human polypeptide SEQ ID NO 27152
                                                                                                                                                                                                                                                                        26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                             28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 63.0.
Local 7; Conservative
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7 YKKFKNKKFKA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI93191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 60 AA;
                                                                                                                                                                                             WO200164835-A2.
                                                                                                                                                      Homo sapiens.
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25-JUL-1994
                                                                                                                                                                                                                                 07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR45673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR45673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB1678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The mucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) aradiovastes such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA013260 standard; protein; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barash SC, Ruben SM;
                              17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024924P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-025931P.
                                                                                                                                                                                                                             05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0256719P.
                                                                                                                                                                                                                                                                                                           08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
                                                                                                                                                                                                                                                                                                                                                                 08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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58.3%;
                                                                                                                                                                                                                                                                                            36-DEC-2000; 2000US-0251479P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity be...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | | | : | : | : | | | 33 KYRKLRNQIIKS 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-541565/60.
N-PSDB; ABA11110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
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The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, call proliferation or call differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity infinibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNIP heparin binding fragment.
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06-NOV-2001 (first entry)

RESULT 38
AAO13260
ID AAO13;
XX
AC AAO13;
XX

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Gaps

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Length 16; 1; Indels

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The present sequence represents a heparin-binding sequences, derived from a human cationic protein, having lipopolysaccharide binding and anticoagulant activity. The polypeptide is designated CAP18. Amino acids 134-170 of CAP18 represent a reactive nitrogen inhibitory protein (RNIP). The CAP18 polymucleotide is useful for producing cationic proteins. The TAP18 polymetide is useful for reacting and diagnosing lipopolyaaccharide-associated conditions such as gram negative sepsis, and/or coagulation-related disorders, such as disseminated intravascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBKBK and its derivatives selected from XZBBZBXBKB, BXZXB, XBBXZXBBX and BBXZBBXZ; and (b) as second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, XBBXXBBX, XBBXXBBX, where B = at least one positively charged amino acid; X = at least one aromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an antimicrobial peptide (AP) for direct
                       Novel human cDNA encoding cationic proteins having lipopolysaccharide binding and anticoagulant activity, useful for treating and diagnosing gram negative sepsis and disseminated intravascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 3;
Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial peptide RP-8 SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 111; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY57472 standard; peptide; 18 AA.
                                                                                                              Disclosure; Col 26; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US003350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial peptides for against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
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5 RLRKFRNKI 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527417/44.
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                   coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY57472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of CAP18 C-terminal RNIP was compared to that of a number of heparin binding proteins to determine residues important for binding to lipopolysaccharides and inhibiting LPS-mediated activation of macrophage, as well as interfering with the clotting cascade to inhibit coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cationic protein; lipopolygaccharide binding; anticoagulant;
CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis;
coagulation-related disorder; disseminated intravascular coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                   proteins - are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in conditions of disseminated intravascular coagulation. See also AAR45667-81. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heparin-binding sequence from a human cationic protein CAP18.
                                                                                                                                                                                                                                                                                                                                               Sequences encoding mammalian cationic antibacterial protein homologous to human and rabbit CAP18 sequences and have lipo:polysaccharide binding and anti-coagulation activity.
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Pred. No. 20;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 50; 112pp, English
                                                                                                                                                                                                                                                      Hirata M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB07905 standard; peptide; 16 AA
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93WO-US006731.
94US-00313681.
96US-00691280.
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                                                                                          93WO-US006731
                                                                                                                                   92US-00916761
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Best Local Similarity 77. o
7; Conservative
                                                                                                                                                                                                         (PANO-) PANORAMA RES INC.
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                                                                                                                                                                                                                                                      JW, Wright SC,
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WO9402589-A1
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                                                                                        15-JUL-1993;
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                                             03-FEB-1994
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AAB0

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AAB70648 to AAB70675 represent antimicrobial peptides (I), of which AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine SAB70648 to AAB70664, AAB70675 are derived from the lupine activity peptide, and AAB70655 to AAB70673 are derived from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic, antimicrobial and antiviral activities, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (I) are useful for inhibiting microbial growth in an environment capable of sustaining such agrowth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibiting the growth of drug-resistant microbial strains such as
Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas
                amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. ANY57463 to ANX57557 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antimicrobial peptides useful as antibiotics for inhibiting growt and proliferation of microbes, and for treating microbial infections.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovine; SWAP29; lupine; RCAP 18; cathelicidin; antimicrobial; bactericidal; antibiotic; antiviral; microbial growth inhibitor; proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; burkholderia cepacia; Alcaligenes; Xanthomonas.
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                                                                                                                                                                       56.9%; Score 37; DB 2; Length 18; 54.5%; Pred. No. 23; 1; Indels ive 4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          AAB70667 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 103; 137pp; English.
  and where B, X and Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-2000; 2000WO-US022781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0149886P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                      3 YRKFKNKILKS 13
                                                                                                                                                                                                                                                                             3 YKKWKNKLKRS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tack BE, Mccray P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-234911/24.
                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2001
                                                                                                                                       Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                AAB70667;
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                      RESULT 42
AAB70667
                                                                                                                                                                                                                                                                                                                                                                                            8888888
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-

150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derivatives from 150 amino acids containing an articolar acids fusions and their derivatives. The possible structures are fully described in the specification. Also conformations are fully described in the specification. Also core sequence selected from truncations of the peptide activity or for potentiating antimicrobial apents active against organisms such as bacteria and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of specifically against bacteria and fungi, agents in combination with other specifically against bacteria and fungi, agents in combination with other conventional antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in foods and commetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have present invention are based upon natural antimicrobial peptides that have present invention are based upon natural antimicrobial peptides that have generally considered to have undesirable to effective and as agents to improve an effect of the effective and as agents to improve of the present sequence is a rabbit pub based antimicrobial peptides of the present sequence is a rabbit pub based antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                Rabbit platelet microbicidal protein, PMP-2, based peptide #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to an antimicrobial peptide composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 130; 221pp; English.
                                                                                                                  ABG69896 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-AUG-2000; 2000US-00648B16
                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates
2 RLRKFRNKI 10
                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                                                      mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200255554-A2.
                                                                                                                                                                                                                    21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                    ABG69896;
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Sequence 18 AA;

Gaps

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Score 37; DB 4; Length 18; Pred. No. 23; 1; Mismatches 1; Indels

56.9%;

Query Match
Best Local Similarity 77.8
Matches 7; Conservative

Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:19.

(first entry)

15-MAY-2001

Ovine; SWAP29; lupine; RCAP 18; cathelicidin; antimicrobial; bactericidal; antibitotic; antiviral; microbial growth inhibitor; proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; Burkholderia cepacia; Alcaligenes; Xanthomonas.

Oryctolagus cuniculus.

WO200112668-A1.

22-FEB-2001

Lehrer

Travis SM,

Mccray P, Welsh M,

Tack BE,

WPI; 2001-234911/24.

(IOWA) UNIV IOWA RES FC (REGC) UNIV CALIFORNIA.

18-AUG-2000; 2000WO-US022781.

99US-0149886P.

18-AUG-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease in an organism which comprises one or more types of polypeptide which have an alpha-helix structure and/or thionine component. The composition of the invention demonstrates antibacterial and antifungal activities and may be useful for preventing a disease in an organism, for generating cultivated plants and in providing resistance to plant tissue against fungi such as Pyricularia and na specudomonas etc. The composition has high antimicrobial activity at low concentration. The current sequence is that of the rabbit CAP18 peptide fragment of the
                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial polypeptide composition for a plant pathogen, comprises one or more types of thionine and/or a polypeptide having an alpha helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel polypeptide composition for preventing
                                                                                                                                                                                                          alpha-helix; thionine; antibacterial; antifungal; plant;
fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
Pseudomonas; antimicrobial; rabbit; CAP18.
                       Gaps
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Score 37; DB 5; Length 18; Pred. No. 23; 1; Indels 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Length 20;
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Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; SEQ ID NO 6; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                           structure, as an active ingredient.
                                                                                                                       ADK70765 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                               (TOYW ) TOYOTA CHUO KENKYUSHO KK.
                                                                                                                                                                                     Rabbit CAP18 peptide fragment 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.9%;
 56.9%;
54.5%;
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                                                                                                                                                                (first entry)
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Best Local Similarity 77.8
7, Conservative
                       Conservative
                                                       3 YKKWKNKLKRS 13
                                             3 YRKFKNKILKS 13
                                                                                                                                                                                                                                                       Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-102620/11.
N-PSDB; ADK70783.
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                           JP2003204794-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 AA;
                                                                                                                                                                  06-MAY-2004
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                                                                                                                                                                                                                                                                                               22-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                            ADK70765;
                                                                                                 RESULT 44
ADK70765
                       Matches
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                                                                                                                                              AAB70648 to AAB70675 represent antimicrobial peptides (I), of which AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic, antimicrobial and antiviral activities, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (I) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistent microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas
New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 4; Length 21;
Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 16, 2005, 08:38:29 Job time : 54.1293 secs
                                                                                           Claim 1; Page 103; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.9%;
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Best Local Similarity 77...
77. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RYRKFKNKI 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 AA;
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Gaps ö

1; Indels

2 RYRKFKNKI 10 | |||:||| 5 RLRKFRNKI 13 AAB70666 standard; peptide; 21 AA.

RESULT 45

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AAB70666

AAB70666 ID AAB7 XX, AC AAB7

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 54.8017 Seconds (without alignments) 121.475 Million cell updates/sec Run on:

US-09-648-816B-4 64

Title: Perfect score: Sequence:

1 ARYKKFKKKLLKS 13

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

145419 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	de			SUMMAKIES	
Score		Query Match Length	DB	ID	Description
4	0 62.5	. 62	2	Q6MRG6	Q6mrg6 bdellovibri
m	7 57.8	3 25	7	Q7R7R2	
'n	7 57.8	3 54	7	Q9UC64	Q9uc64 homo sapien
	6 56.2	54	7	69NON3	Q9nqn3 homo sapien
ñ	6 56.2	9 62	-	YB45 METJA	Q58545 methanococc
	6 56.2	70	~	Q636 <u>2</u> 0	Q636z0 bacillus ce
	5 54.7	7 58	~	064196	064196 bacteriopha
ĕ	5 54.7	7 58	~	034850	034850 bacillus su
		, 62	7	Q6L2F0	Q612f0 picrophilus
ň	4 53.1	34	~	050694	O50694 borrelia bu
m	4 53.1	54	~	Q7VAR3	Q7var3 prochloroco
m	4 53.1	. 55	7	QBRDF8	
m	4 53.1	1 57	~	Q7NHA1	-
33.	5 52.3	53	~	Q8F1S1	
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m	3 51.6	5 49	N	Q7V1V2	_
m	3 51.6	5 49	~	Q7VCB8	
'n	3 51.6	54	N	О 86Н39	
m	3 51.6	9 60	~	Q9LJ46	
m	3 51.6	9 60	7	921190	
m	3 51.6	5 62	N	Q91801	
m	3 51.6	5 67	~	Q737N5	Q737n5 bacillus ce
'n	3 51.6	5 73	~	Q8NZHS	Q8nzh5 streptococc
m	3 51.6	5 73	~	Q7CMT8	
m	3 51.6	74	7	Q7P6D0	Q7p6d0 fusobacteri
m	2 50.0	32	-	CAR1 ECHCA	O9prp9 echis carin
m		41	7	Q8F3 <u>N</u> 7	Q8f3n7 leptospira
m		49	2	Q72WW2	Q72ww2 bacillus ce
Ä		'n	~	Q8F2Z2	
Ä	2 50.0	57	~	Q7R8G1	Q7r8g1 plasmodium
m	2 50.0	58	Н	CECC ANOGA	Q8muf3 anopheles g

25 AA.

PRT;

PRELIMINARY;

RESULT 2 Q7R7R2 ID Q7R7R2

	Q65wt3 oryza satīv Q8gr44 enterococcu Q9pid2 campylobact	Q8r6m0 thermoanaer Q81df8 bacillus ce	Q83903 ovine adeno O908w3 rhodomonas			Q6ms10 mycoplasma Q9b8f8 heterodoxus	
Q65MF3 O35041	Q65WT3 Q8GR44 RS21_CAMJE	QBR6MO QBldf8	Q83903 Q9G8W3	Q91FM3	071114	Q6MS10 Q9B8F8	
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61	65 70	2,0	72	37.5	33	5.48 5.3	
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ALIGNMENTS

							,	ionales;							Lanz C.,		4	vorus rrom a						teriovorus							strain							0; Gaps 0;	
	AA.		update)	annotation update)	(Flp1 protein).			eria; Bdellovibr					SIB 9529;		M., Baar	ın A., Meyer F.,	a transfer of the state of	vibrio bacterio					aid M.:	Rdellovibrio bacteriovorus	2	DBJ databases.					independent B. bacteriovorus		JUBU databases.			3A5B CRC64;	3 2; Length 62;	; 2; Indels	
	PRT; 62 A		Last	, Last annotatio	protein (Flp1 pilus subunit) (Flp1 protein)	les=Bd0119;		Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales	vibrio.			•	STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB		sinus A., Epping	Evans K.J., Goesmann A.,	 	"A predator unmasked: lile cycle or bdellovibrio bacterlovorus					Appel B. Linscheid M.:	cluster of		to the EMBL/GenBank/DDBJ databases				ppel B.;	t independent B.		e EMBL/Genbank/UDBJ databases			; 75E6A7530E13BA5B	; Score 40;	<pre> ; Pred. No. 25; 3; Mismatches</pre>	
	PRELIMINARY;	(TrEMBLrel.	(TrEMBLrel.		al protein (Flp1	Name=flp1; OrderedLocusNames=Bd0119;	Bdellovibrio bacteriovorus.	Proteobacteria;	ionaceae; Bdello	=959;		ROM N.A.	00 / DSM 50701 /	52164; DOI=10.11	Rendulic S., Jagtap P., Rosinus A.,	Keller H., Lambert C., Eva	Sockett R.E., Schuster S.C.;	r unmasked: Ille	genomic perspective.";	3:689-692(2004).	A N MOS	50701.	uch E.					ROM N.A.	,00	Schwudke D., Strauch E., Appel B.;	diversity in hos		Submitted (AUG-2004) to the party by the submitted (Aug-2004)	1609: CAR47773.1:		Æ		Similarity 58.3% 7; Conservative	
RESULT 1 DEMRG6	Q6MRG6	05-JUL-2004	05-JUL-2004	25-OCT-2004	Hypothetical	Name=flp1;	Bdellovibri	Bacteria; F	Bdellovibri	NCBI TaxID=959;	Ξ	SEQUENCE FROM N.A.	STRAIN=HD10	PubMed=1475	Rendulic S.	Keller H.,	Sockett R.E	A predator	genomic per	Science 303	SECTIENCE FEOM N &	CTDY TOTAL	Schwidke D.	"Putative	DSM 50701."	Submitted (SEP-2003)	[3]	SEQUENCE FROM N.A.	STRAIN=HI100;	Schwudke D.,	"Sequence c	HI100.";	Submitted (AUG-2	EMBL: A.1584609:		SEQUENCE		Best Local Sim Matches 7;	
RES	8		DŢ	텀	OE:	N C	SO	ပ္ပ	ပ	ŏ	RN	ЯP	RC	2	Æ	%	\$ 5	2 5	K.	7 2	5 0	4 6	Z Z	Ē	RT	RL	RN	RP	Z C	R	2 E	¥ ;	3 G	2 2	ä	S	a	ďΣ	

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                                                                                                                                                                                                                                                                                                                 69NON3;
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Q58545;
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YB45_METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                  Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parasite Plasmodium yoelli yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                        Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 2; Length 25;
Pred. No. 33;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6033 MW; COB560236BF1B14A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7D03F492B4ADA65F CRC64;
                          01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gupta S.K., Hassel T., Singh J.P.;
Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995).
HSSP; P02776; 1F9Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 AA.
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GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0000855; P:immune response; IEA.
InterPro; IPR002473; C-X-C/InterIkn 8.
InterPro; IPR001811; Chemokine ILB.
                                                                                                                                                                                                                                                                                       STRAIN=17XNL;
PubMed=12368865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
EMBL; AABL01002785; EAA20001.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95372366; PubMed=7644496;
                                                                                                     Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00048; ILB; 1.
PRINTS; PR00436; INTERLEUKINB.
PRINTS; PR00437; SMALLCYTKCXC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AA; 3157 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UC64;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 88.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 KKFKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKFKKKELK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 AA;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                              NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00199;
SEQUENCE 54 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carucci D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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STRAINS-JAL-1 / DSW 2661 / ATCC 43067;

MEDLINE-96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woses C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
Length 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams S.;
submitted (APP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL135544; CAB96731.1; -.
SEQUENCE 54 AA; 6389 MW; 611C1972916FCA61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
DJ71N10.1.2 (Novel protein (Putative isoform 2)).
Name=dJ71N10.1,
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 2; I
Pred. No. 1.1e+02;
2; Mismatches 1;
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(Rel. 39, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                        54 AA.
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                                          1; Mismatches
  Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein MJ1145 precursor.
OrderedLocusNames=MJ1145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.2%;
70.0%;
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  57.8%;
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Matches 7; Conservative
                                            8; Conservative
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                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                     3 YKKPKKKLLKS 13
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KKLKKKLVRS 40
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                                                                                                                               44 YKKIIKKLLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Gaps

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Length 58;

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Score 35; DB 2; Le
Pred. No. 1.7e+02;
3; Mismatches 2;
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54.7%; (milarity 54.5%; 1
Conservative 3;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                    2 RYKKFKKKLLK 12
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6 RYEELKKKTIK 16
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     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=66797;
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Karamata D.;
                                                                                                                                                                                                                                                                              Score 36; DB 1; Length 65; Pred. No. 1.3e+02; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.2%; Score 36; DB 2; Length 70; 66.7%; Pred. No. 1.4e+02; Live 3; Mismatches 0; Indels
                                                                                                                                                                                                Hypothetical protein MJ1145.
1DD7EF92E847F51F CRC64;
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PIR; T12949; T12949.
Hypothetical protein.
SEQUERICE 58 AA; 7071 MW; 8175150844F41668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                           Complete proteome; Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 AA.
  or send an email to license@isb-sib.ch)
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                                                          EMBL; U67557; AAB99155.1; -. PIR; H64442; H64442.
                                                                                                                                                                                                                                                                                 56.2%;
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                                                                                                                                                                                                                             65 AA; 7693 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 69.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group-specific protein. ORFNames=BTZK3444;
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es 6; Conserv
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                                                                                                                    TIGR; MJ1145; -.
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SEQUENCE
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064196;
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Q63620;
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Matches
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KUNDER F., OGGRAWATEN N., MOSEZET I., Albertini A. M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursider L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

A Brois S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Britz C., Fujita M., Pujita Y., Fura S., Galizzi A., Galleron D. T.,

Britz C., Fujita M., Fujita Y., Fura S., Galizzi A., Galleron N.,

Riberpi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

A Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,

Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,

Kumano M., Kurita K., Lapidus A., Liu H., Masuda S., Mauel C.,

A Haller C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,

Razarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,

Razarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,

Rock M., Noone D., O'Reilly M., Portetelle D., Porwollik S.,

Rey M., Reynolds S., Rieger M., Rivolta C., Roccha E., Rocche B.,

Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,

Shin B.S., Soldo B., Sorokin A., Tacconi B., Tarakan T., Tarkahashi H.,

Nassarotti A., Viari A., Wambutt R., Wadler E., Wedler H.,

Westarotti A., Viari A., Wambutt R., Wamane C., Yamane C., Yamane C., Yamane C., Yawane C.
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"The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 1.7e+02;
3; Mismatches 2; Indels
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                         Name=yotN; Synonyms=yokJ; OrderedLocusNames=BSU19820;
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Gaps

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Indels

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Dufresne A. Salanoubat M., Partensky F., Artiquenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Robert C., Rogozin I.B., Rolf, T.I., Hess W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wolf Y.I., Hess W.R.;
"Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome.";
Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
EMBL; AE017165; AAQ00438.1; -.
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EMBL; AE012981; AAM23381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
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Last annotation update)
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Pred. No. 1.5e+02;
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                          60.0%;
                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                               Predicted protein.
OrderedLocusNames=Pro1394;
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                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
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37 KIKKRRKKLLKN 48
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                                                                                                       3 YKKPKKKLLK 12
                                                                                                                                                      10 YKKIKNELIK 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prochlorococcus.
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                          Best Local
Matches
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STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
STRAIN=B8065943; Pubm6d=9403685; DOI=10.1038/37551;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
Salzberg S.L., Hanson M., van Yugt R., Palmer N., Adams M.D.,
Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
Artiach P., Bowman C., Garland S.A., Pulji C., Cotton M.D., Horst K.,
Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=DSM 9790 / ATCC 700027;
PubMed=15184674; DOI=10.1073/pnss.0401356101;
FubMed=15184674; DOI=10.1073/pnss.0401356101;
FubMed=15184674; DOI=10.1073/pnss.0401356101;
Schepers B., Dock C., Antranikian G., Liebl W.;
"Genome sequence of Picrophilus torridus and its implications for life
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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                                                                                                                                                                                                                                                                                                                                                  Archaea, Buryarchaeota, Thermoplasmata, Thermoplasmatales, Picrophilaceae, Picrophilus.
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Pred. No. 1.8e+02;
2; Mismatches 1; Indels
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EMBL, AE017861, AAT4852.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 62 AA, 7321 MW; 48FD2563ACBBESBF CRC64;
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                                                                                                                                                         62 AA
                                                                                                                                                                                                           Created)
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PIR; E70239; E70239.
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                                                                                                                                                                                                                                                                                   Hypothetical protein.
OrderedLocusNames=PT00267;
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Matches 6; Conservative
                                                                                                                                                         PRELIMINARY;
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41 AHYKEYKKK 49
                             RYEELKKKTIK
                                                                                                                                                                                                                                                                                                                                     Picrophilus torridus.
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Gaps

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53.1%; Score 34; DB 2; Length 55; 6630 MW; 021B696DC0922F8B CRC64; Query Match ä

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Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W., Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A., Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22598143; PubMed=12712204; DOI=10.1038/nature01597; Ren S.-X., Fu G., Jiang K.-G., Zeng R., Miso Y.-G., Xu H., Zhang X.-G., Zeng R., Miso Y.-G., Xu H., Jiang Y.-X., Xu M., W. G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F. Jiang Y.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F., Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W., Yso Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A., Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4)
Bacteria, Cyanobacteria, Prochlorales, Prochlorococcaceae;
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                                                                                                                       "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing.";
EMBL; AEOI1467; AMN50255.1; -.
Complete protecome 53 AA; 6713 MW; F8CC4B5B79A52C40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing.";
                                                                                                                                                                                                                                                                                                                                          Score 33.5; DB 2; Length 53;
Pred. No. 2.8e+02;
1; Mismatches 1; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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70.0%; Pred. No. 2.6e+02;
tive 1; Mismatches 2;
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Best Local Similarity 64...
Best Local 9, Conservative
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Best Local Similarity 70.0
Best A 70.00
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NCBI_TaxID=59919;
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Q8F0P7
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GO; GO:000735; P:structural constituent of ribosome; IRA.

GO; GO:000412; P:protein biosynthesis; IRA.

RM InterPro: IPR001911; Ribosomal S21; T.
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MEDL/NR=2259143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
                                          Gaps
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OrderedLocusNames=LA3057;
Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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Prodom; PR00551; Ribosomal S21; 1.
TIGRFAMS; TIGR0030; S219; 1.
PROSITE; PS01181; RIBOSOMAL S21; 1.
COMPLETE PS01181; RIBOSOMAL S21; 1.
COMPLETE PSO1081; RIBOSOMAL S21; 1.
SEQUENCE 57 AA; 6869 MW; E9E94BB992682807 CRC64;
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         Pred. No. 2.4e+02;
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Gloeobacter violaceus
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MEDLINE=22977040; PubMed=14621292;
         75.0%;
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30S ribosomal protein S21.
                                      6; Conservative
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17 KRFKKKIQKA 26
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46 YKRFSKKL 53
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3: Indels

Score 33; DB 2; I Pred. No. 3.5e+02;

0; Mismatches

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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Elchinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
                                                                                                                                                                                                                                         Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: AROS3204.1; -.
Hypothetical protein.
SEQUENCE 54 AA; 6247 MW; 65A29B646CGE8DD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             51.6%;
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                                                                                                                                                      Nature 418:79-85(2002).
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Best Local Similarity
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIR=SARG / CCMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
Dufreene A., Salanoubat M., Parteneky F., Artiguenave F., Axmann I.M.,
Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
Scanlan D.J., Tandeau de Mareac N., Weissenbach J., Wincker P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphotorrophic genome."; Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
EMBL; AE017163; AAP99867.1; -.
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           MEDLINE-2285569; PubMed=12917642; DOI=10.1038/nature01947; Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb B.A., Zinser E.R., Chisholm S.W.; nucleand divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation."
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Bacteria, Cyanobacteria, Prochlorales, Prochlorococcaceae,
                                                                                                                                                                                                                                                                                                     Score 33; DB 2; Length 49;
Pred. No. 3.1e+02;
3; Mismatches 1; Indels
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Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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Pred. No. 3.1e+02;
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                                                                                                                                                                                           Nature 424:1042-1047(2003).
EMBL; BX572092; CAB19210.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 49 AA; 5560 MW; 307AEDCA185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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(TrEMBLrel. 25, I
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=Pro0823;
                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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RKFKKRKLRS 29
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les 6; Conserv
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Best Local Similarity
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SEQUENCE 49 AA;
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01-OCT-2003
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CYCE8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids; eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; APO00736; BABO2599.1;
SEQUENCE 60 AA; 6937 MW; 6FD18DCB8C9C222F CRC64;
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Pred. No. 3.8e+02;
3; Mismatches 2; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                          Last sequence update)
Last annotation update)
60 AA.
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Bacillus thuringiensis (Subsp. konkukian)
                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20363099; PubMed=10907853;
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SKARARARASS

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Hayashi H., Hattori M., Hamada S.;
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
                                      Pubmed=14960714; DOI=10.1093/nar/gkh258;

Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
Shores K.A., Fouts D.E., Tourasse N.J., Angluoli S.V., Kolonay J.F.,
Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987; reveals metabolic
adaptations and a large plasmid related to Bacillus anthracis pXOI.";
Nucleic Acids Res. 32:977-988(2004).

ITGR: BCE2612; --
TIGR: BCE2612; --
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MEDLINE=2213808; Pubmed=1212206; DOI=10.1073/pnas.152298499;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S., Parkins L.D.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.,
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein SP90263 (Hypothetical protein SpyM3_1604).
OrderedLocusNames=SP80263, SpyM3_1604;
Streptcoccus pyogenes (serotype M3).
Bacteria, Firmicutes; Lactobacillales; Streptcoccaceae;
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Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
                                                                                                                                                                                                                                                                                                                                                                                             Length 67;
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Pred. No. 4.6e+02;
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InterPro; IPR001387; HTH 3.
InterPro; IPR010982; Lambda_like_DNA.
SMART; SM00530; HTH 3; 1.
PR0SITR; PS0943; HTH CROL! 1.
COMplete proteome; Hypothetical protein.
SEQUENCE 73 AA; 8376 MW; 8D8499BB0791CAD5 CRC64;
                                                                                                                                                                                                                                                                                                                                     67 AA; 8274 MW; 0C0855EC4F081A71 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 2; Le
Pred. No. 4.3e+02;
3; Mismatches 0;
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EMBL; AE014167; AAM80211.1; -.
GO; GO:0003677; F:DNA binding; IEA.
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Genome Res. 13:1042-1055(2003).
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62.5%;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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36 KYKRPKEK 43
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                       Complete proteome SEQUENCE 67 AA;
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                                                                                                                               Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R. Richardson P., Rubin E., Tice H., Longmire J., Lucas S., Okinaka R. Complete genome sequence of Bacillus thuringiensis 97-27."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, ABCINTSS; ARTS9981.1:

Complete proteome; Hypotherical protein.

SEQUENCE 60 AA, 7430 MW; 061BDEC4ECB3D6C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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MEDLINE=96198088; PubMed=8626421; DOI=10.1074/jbc.271.11.6273;
Puzianowska-Kuznicka M., Shi Y.B.;
"Nuclear factor I as a potential regulator during postembryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                             51.6%; Score 33; DB 2; Length 60; 62.5%; Pred. No. 3.8e+02; ive 3; Mismatches 0; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=222523;
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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Last annotation update)
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Last annotation update)
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. 4e+02;
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 271:6273-6282(1996).
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60.0%;
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OrderedLocusNames=BCE2612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
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29 KYKRFKEK 36
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
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                       NCBI_TaxID=180856;
                                                                            SEQUENCE FROM N.A.
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                                                                                                                STRAIN=97-27;
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RESULT 21
(991801)
DD AC (99180)
DT (01-NO)
DT (01-NO)
DD (01-NO)

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RESULT 22 Q737NS DD Q737N AC Q737N DT 05-JU DT 05-JU DE HYPOLI GN Order OS Baccie OX NCBI

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Gaps

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Yamada D., Sekiya F., Morita T.; "Isolation and characterization of carinactivase, a novel prothrombin activator in Echis carinatus venom with a unique catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                        28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 46, Last annotation update)
Carinactivase-1 (RC 3.4.24-.) (CA-1) (Fragment).
Echis carinatus (Saw-scaled viper).
Echis carinatus (Saw-scaled viper).
Ichidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Viperinae; Echis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 271:5200-5207(1996).
-!- FUNCTION: Calcium-dependent prothrombin activator.
-!- COFACTOR: Binds 1 zinc ion and 1 calcium ion per subunit (By
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PROSITE; BS00142; ZINC PROTEASE; PARTIAL.
Calcium; Direct procesin sequencing; Hydrolase; Metal-binding;
Metalloprotease; Prothrombin activator; Zinc; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96214956; PubMed=8617803; DOI=10.1074/jbc.271.9.5200;
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STRAIN=SEGO1 / Seroyroup Icterohaemorrhagiae / Serovar lai,
MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
                                                   Score 33; DB 2; Length 74;
Pred. No. 4.7e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 1; Length 32;
Pred. No. 3.1e+02;
EMBL; AABF01000039; EAA24308.1; -. SEQUENCE 74 AA; 8890 MW; 8984BCCSEA1BE1BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SIMILARITY: Belongs to the peptidase M12B family
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001590; Peptidase_M12B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AA; 3749 MW; 1A1B1496A3D26449 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                         32 AA.
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                                                   Match 51.6%;
Local Similarity 70.0%;
les 7; Conservative
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                                                                                                                                                                                                                                                         STANDARD;
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1 SRKQKFDKKFIK 12
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                                                                                                                              4 KKFKKKLLKS 13
                                                                                                                                                                21 KKYKKTĽSKS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mechanism."
                                                                                                                                                                                                                                                        CAR1 ECHCA
Q9PRP9;
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                                                                                                                                                                                                                     RESULT 26
CAR1_ECHCA
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                                                                         Best Loc
Matches
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Matches
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Q8F3N7
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                                                                                                                                                                                                                                                                                                                                                                                                               Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Rapur V., Daly J.A., Veasy L.G., Musser J.M.; Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N.; Submitted (JAN-2003) to the BBL/GenBank/DDBJ databases - I. CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MGASB232;
MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2; Length 73;
Pred. No. 4.6e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                         Streptococcus pyogenes (Serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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EMBL, AE010098; AAL98422.1; -
GO, GO.000377; F.DNA binding; IEA.
INCEPPO: IPRO01387; HTH 3.
INCEPPO: IPRO01982; Lambda_like_DNA.
Pfam; PRO11381; HTH 3; 1.
SWART; SWOGS30; HTH XRE; 1.
PROSITE; PSS0943; HTH_CROCI; 1.
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                                                                                                                                                                                   Created)
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                        Hypothetical protein spyM18_1923.
OrderedLocusNames=spyM18_1923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
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                  1 ARYKKFKKKLLKS 13
                                                     32 ARYEKDTKKLRRA 44
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les 7; Conservative
                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 73 AA;
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=FNV1324;
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Q7P6D0;
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Matches
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Q7P6D0
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25 KYKKURKULL
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Matches 6; Conserv
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CECC ANOGA
ID CECC ANOGA
AC Q8MUF3;
                                                                                                                                                                                                                                                  SEQUENCE
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Matches
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Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F., Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Xin H.-F., Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W., Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A., Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P.; man pathogenic features of Leptospira intercogans revealed by whole-genome sequencing.", Nature 422:888-893[2003].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=14960714; DOI=10.1093/nar/gkh258; Rasko D.A., Ravel J., Ockstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.; "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus and alarge plasmid related to Bacillus and blasmid blasmid and                                                                                                                                                                                                                                                                                                              Gaps
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
MEDLINE=22599143; PubMed=12712204; DOI=10.1038/nature01597;
                                                                                                                                                                                                                                                                 Score 32; DB 2; Length 41; Pred. No. 3.9e+02; 5; Mismatches 1; Indels
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Pred. No. 4.7e+02;
0; Mismatches 3; Indels
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Bacillus cereus (strain ATCC 10987).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome, Hypothetical protein. SEQUENCE 49 AA; 5923 MW; C5320B83F9F1FB2D CRC64;
                                                                                                                                                                                                      Complete proteome.
SEQUENCE 41 AA; 5213 MW; 3558C58CA5B722AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OrderedLocusNames=LA2619;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                   Best Local Similarity 45.
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RFFRFKKILE 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=222523;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=173;
                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q72WW2;
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Q72WW2
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Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-P., Wan M., Huang H.-L., Qiang B.-H., Yin B.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."; Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman D.M., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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NCBL_TaxID=73239;
                                                                                                                                                                                                                                "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing."; Nature 422:888-893(2003). EMBL; AR011429; AAM49818.1; -.
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Pred. No. 5.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 32; DB 2; Length 55; 45.5%; Pred. No. 5.2e+02; rive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0D127E9C69FBCAD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               55 AA; 6952 MW; CB125F86B70E93F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12368865; DOI=10.1038/nature01099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.

EMBL, AABL01002616; EAA19653.1; -.

Hypothetical protein.

NON_TER 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Last 01-MAR-2004 (TrEMBLrel. 26, Last Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium yoelii yoelii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 45.5
les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRRFKNEILHS 46
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SEQUENCE FROM N.A.
STRAIN=ATCC 14580;
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                                                                                                                                                                                                                                                                                                                                                                     YfjT protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168;
                                                                                                                                              SEQUENCE
                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                  RESULT 33
                                                                                                                                                                                                                                                                                             035041
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                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                 -1- FUNCTION: Cecropins have lytic and antibacterial activity against several Gram-positive and Gram-negative bacteria (By similarity).
several Gram-Dostion Secreted (By similarity).
-1- SUBCELLULAR LOCATION: Cecreted (By similarity).
-1- SIMILARITY: Belongs to the cecropin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cecropin C.
Valine amide (G-58 provides amide group)
(Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                               Anopheles gambiae (African malaria mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;

"The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";

J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                     SEQUENCE FROM N.A. Zheng X.-L., Zheng L.; Renomic organization and regulation of three cecropin genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 1; Length 58;
Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein yfjr. Names-BL00826; Names-Pfjr; ORFNames-BL03087, BL100826; Bacillus licheniformis DSM 13. Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                           Anopheles gambiae.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20CBD2CFC96B1D88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 28, Last sequence update) (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          Amidation; Antibiotic; Insect immunity; Signal
           (Rel. 44, Last sequence update) (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                           EMBL; AF525673; AAM82612.1; -.
InterPro; IPR0100875; Cecropin.
InterPro; IPR010631; Mos_cecropin.
Pfam; PF06759; Mos Cecropin; 1.
PROSITE; PS00268; ČECROPIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                      Potential
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 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 AA; 6203 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 75.0
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                                    Cecropin C precursor.
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25 RFKKFLKK 32
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PubMed=15383718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Q65MF3
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MEDINE-9804403; Pubmed-93843/7; DOI=10.1038/36/86;

Kunst R., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borrise R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.P., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entiz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., And Grin S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., And Hibert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Kumano M., Kurita K., Lapidus A., Liul H., Masuda S., Mauel C., Kobayashi Y., Koetter P., Konigstein G., Krogh S., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Rodna N., Mellado R.P., Mizuno M., Moestl D., Nakai S., R. Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan B., Pujic P., Purnelle B., Rapoport G., Rose M., Sadie Y., Sachor T., Schowska A., Seror S.J., Serror P., Schin B.S., Soldo B., Sorokin A., Tacconi E., Takashashi H., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takashashi H., Tamakatu K., Takeuchi M., Tanakoshi A., Tanakata T., Terpstra P., Takeuchi M., Tanakoshi A., Tanakata T., Terpstra P., Vasincoc K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Wedler H., Vanner E., Wohler E., Weiller B., Noshikawa H.F., Zumstein E., Weiller B., Weiler P., Winters P., Wint
                                                                                                                                                                            Berka R.M.;
"Complete genome sequence of the industrial bacterium Bacillus
licheniformis and comparisons with closely related Bacillus species.";
Genome Biol. 5:R77-R77(2004).
EMBL; AE017333; AAU39761.1;
EMBL; CP000002; AAU22413.1;
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The complete genome sequence of the Gram-positive bacterium Bacillus
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Zaretsky I
G., Olsen I
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Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen Rammussen M.D., Ardersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 32; DB 2; Length 61; 62.5%; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AA; 7294 MW; D7C8462ECFF7B8A6 CRC64;
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01-JAW-1998 (TrEMBLrel. 05, Created)
01-JAW-1998 (TrEMBLrel. 05, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=yfjT; OrderedLocusNames=BSU07970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aypothetical protein.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
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Hypothetical protein; Plasmid.
NON TER 1 1
SEQUENCE 67 AA; 8174 MW; 9B8904D03C80857F CRC64;
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16 YRKFKKQV 23
                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          CAMJE
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QBR6M0;
                                                                                                                                                                                                                                                                                             RESULT 36
RS21_CAMJE
ID RS21_C
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Matches
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QBR6M0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Cheng C.-H., Chung C.-I., Han S.-Y., Haisao S.-H., Ching C.-I., Han S.-Y., Haisao S.-H., Haing J.-N., Hau G.-H., Hung G.-J., Kau P.-I., Lee M.-C., Leu H.-L., Wu H.-P., Shaw J.-F., In Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F.;
"Oryza sativa RAC Polibliz genomic sequence.";
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AC137004, Aut4280-11. .
SEQUENCE 65 AA, 7579 MW; ZEFAB593226711FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Bhrhartoideae, Oryzeae, Oryza.
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STRAIN-K.4;
Doi K., Eguchi T., Iwatake A., Shima J., Ohmomo S., Ogata S.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB092692; BAC20321.1; -
                                                                                                                                                                                                Score 32; DB 2; Length 61;
Pred. No. 5.8e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 32; DB 2; Length 65; 45.5%; Pred. No. 6.2e+02; ive 5; Mismatches 1; Indels
                Sekiguchi J., Yamamoto H., Uchiyama S., Fajar A.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z99108; CAB12626.1; -
EMBL; D83967; BAA23390.1; -
PIR; CG9807; CG9807.
Complete proteome.
SEQUENCE 61 AA; 7269 MW; 9C558D441CD0B27B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Unknow proctein.
Name=P0615D12.12;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis (Streptococcus faecalis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AA
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                                                                                                                                                                                                       50.0%;
                                                                                                                                                                                                                            Best Local Similarity 62.5
Matches 5; Conservative
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nes 5; Conservative
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52 WRKFRVKILKN 62
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51 AKYERFKK 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=39947;
       STRAIN=AC327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=orf1;
                                                                                                                                                                                                       Query Match
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065WT3

AC 065WT3

AC 065WT3

DT 25-OC

DT 25
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Q8GR44
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
MAINTES-20150912; Mungall K.L., Keelley J.M., Churcher C.M., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jasham D., Chillingworth T., Moule S., Pallen M.J., Penn C.W., Guail M.A., Raijandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
Nature 403:665-668(2000)
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
10S ribosomal protein S21.
Name=rpsU; OrderediocusNames=Cj0370;
Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteraceae; Campylobacterer.
NGEL TAXID=197;
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Pred. No. 6.6e+02;
3; Mismatches 0; Indels
   Length 67;
Score 32; DB 2; Length 67;
Pred. No. 6.4e+02;
5; Mismatches 2; Indels
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ProDom; PRO0551; Ribosomal S21; 1.
TIGREAMS; TIGR00030; S319; 1.
PROSITE; PSO1181; RIBOSOMAL S21; FALSE NEG.
Complete proteome; Ribosomal protein.
SEQUENCE 70 AA; 8673 MW; A26FA2317333E0F7 CRC64;
                                                                                                                                                                                                                                                                                                                                             70 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 AA.
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HAWAR; MF 00358; -; 1.
InterPro; IPR001911; Ribosomal S21.
Pfam; PF01165; Ribosomal S21; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL139075; CAB74206.1; -.
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Local Similarity 62.5%;
les 5; Conservative
   h 50.0%;
Similarity 41.7%;
5; Conservative
                                                                                                                              1 ARYKKFKKKLLK 12
                                                                                                                                                                     S ANYQRYKKRVEK 16
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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MEDLINE-95297141; PubMed-7778275;
Vrati S., Boyle D., Kocherhans R., Both G.W.;
"Sequence of ovine adenovirus homelogs for 100K hexon assembly, 33K,
pVIII, and fiber genes: early region E3 is not in the expected
                                                                                                                                                                                                                                                                                                                                                                                         Xu Z.Z., Hyatt A., Boyle D.B., Both G.W.; "Construction of ovine adenovirus recombinants by gene insertion or deletion of related terminal region sequences."; Virology 230:62-71(1997).
                                                                            Ovine adenovirus type 7.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Atadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=OAV287;
MEDLINE-OAV287;
MABLINE-TO 6.4 (1998.9136;
MARTIA A., Both G.W.;
"Identification of transcripts and promoter regions of ovine
                                                                                                                                                                                                                                                                                                                                                                               WEDLINE=97271311; PubMed=9126262; DOI=10.1006/viro.1997.8452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 2; Length 71;
Pred. No. 6.7e+02;
0; Mismatches 1; Indels
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Vrati S.V., Brookes D.B., Boyle D.B., Both G.W.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Both G.W.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0019013; C:viral nucleocapsid; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR008393; Adenovirus PX.
Pfam; PF05629; Adeno PX; I.
SEQUENCE 71 AA; 7776 MW; 109EE3C84503AD2A CRC64;
                    Last sequence update)
Last annotation update)
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Last annotation update)
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  Created)
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(TrEMBLrel. 16, I
(TrEMBLrel. 24, I
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01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /irology 245:128-141(1998).
                                                                                                                                                                                                                                                                                              Virology 209:400-408(1995).
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Matches 6; Conservative
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                                                                                                                 NCBI_TaxID=114430;
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01-MAR-2001 (
01-JUN-2003 (
Orf72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22668415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kaparral V., Bhatteacharyya A., Reznik G., Mikhailova N., Lapidus A., Grechkin Y., Bhatteacharyya A., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.C.; Gerome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                         Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yang H.; A complete sequence of the T. tengcongensis genome."; Genome Res. 12:689-700(2002).

Genome Res. 12:689-700(2002).

InterPro: IPR002296; DUF951.

Pfam; PF06107; DUF951; 1.
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                                                                                              Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                      MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
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Pred. No. 6.6e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria: Firmicutes; Bacillales; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE017005; AAP09372.1; -.
Complete protecome; Hypothetical protein.
SEQUENCE 70 AA; 7890 MW; 2846567CFBBS1F9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AA; 7987 MW; 348EADE5DDF319DA CRC64;
Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 6.6e+02;
5; Mismatches 2;
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                    (TrEMBLrel. 21, (TrEMBLrel. 26,
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46.2%;
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EMBL; AE017005; AAP09372.1;
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                                                                              OrderedLocusNames=TTE2782;
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51 AKFEKSIKKILKT 63
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KFRKKMIK 10
                                                           Hypothetical protein
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MEDLINE=91118242; PubMed=1475907;
Sonntag K.C., Darai G.,
"Characterization of the third origin of DNA replication of the genome of insect iridescent virus type 6.";
Virus Genes 6:333-342(1992).
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MEDLINES-9435841; PubMed=8073636;

Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;

Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;

"Chilo iridescent virus encodes a putative helicase belonging to a distinct family within the 'DEAD/H' superfamily: implications for the evolution of large DNA viruses.";

Virus Genes 8:151-158(1994)
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"Insect iridescent virus type 6 encodes a polypeptide related to the largest subunit of eukaryotic RNA polymerase II.";
J. Gen. Virol. 75:1557-16949.
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BEDLINE-29125233, PubMed=9926400; DOI=10.1023/A:1008017820941;

Muller K., Tidona C.A., Bahr U., Darai G.;

"Identification of a thymidylate synthase gene within the genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=94292906; PubMed=8021587;
Schnitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
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"Identification of the primary structure and the coding capacity
the genome of insect iridescent virus type 6 between the genome
coordinates 0.310 and 0.347 (7990 bp).";
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MEDLINE=98141693; PubMed=9482589; DOI=10.1023/A:1007932620930;
                                                                                                  Gray M.W.;
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Pred. No. 6.8e+02;
1; Mismatches 2; Indels
                                                                         SEQUENCE FROM N.A.

Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL, AF288990; AAG17734.1; -
GO; GO:0005739; C:mitochondrion; IEA.
    Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
NCBI _TaxID=52970;
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Virus Genes 17:243-258(1998).
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Viruses; dsDNA viruses,
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Mitochondrion.
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"Identification of genes encoding zinc finger proteins, non-histone chromosomal HMG protein homologue, and a putative GTP phosphohydrolase in the genome of Chilo iridescent virus."; Nucleic Acids Res. 22:156-166(1994).
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Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the first complete DNA sequence of an invertebrate iridovirus: coding strategy of the genome of Chilo iridescent virus.";
Virology 286:182-196(2001).
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MEDLINE=87321126; PubMed=2820141;
Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
Schnitzler P., Darai G.,
Molecular cloning and physical mapping of the genome of insect
"Molecular cloning and physical mapping of the genome of insect
iridescent virus type 6: further evidence for circular permutation of
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Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6.";
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MEDLINE=86174607; PubMed=3959991;
Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
"Insect iridescent virus type 6 induced toxic degenerative hepatitis
Bahr U., Tidona C.A., Darai G., "The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391; similarities in coding strategy between insect and vertebrate iridoviruses.";
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                                                                                                                                                                                                                                                                                                                                 virus 6: evidence for circular
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MEDLINE=92360401; PubMed=8492091;
Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
Identification of the gene encoding the major capaid protein of
insect iridescent virus type 6 by polymerase chain reaction.";
J. Gen. Virol. 74:873-879(1993).
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MEDLINE=99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
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MEDLINE=94167241; PubMed=8121799;
Schnitzler, Hug M., Handermann M., Janssen W., Koonin E.V.,
Delius H., Darai C.;
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                                                                                                                                                                                                                                                                              Delius H., Darai G., Fluegel R.M.;
"DNA analysis of insect iridescent vir
permutation and terminal redundancy.";
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                                                                                                                                                                Virus Genes 15:235-245(1997).
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Virology 160:66-74(1987).
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
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STRAIN=South Stradbroke Island;
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Best Local Similarity 53.0.
Local 7; Conservative
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5 AHIKKLROKLEKS 17
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STRAIN=2603 V/R / Serctype V;
STRAIN=2603 V/R / Serctype V;
STRAIN=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Tettelin H., Maaignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., Radone D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Inacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Ranado D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
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EMBL; AE014191; AAM98917.1;
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Pred. No. 4.4e+02;
4; Mismatches 2; Indels
                                                                Length 74;
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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                   284DC4CA8FEEFFC1 CRC64;
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Lactoboacillus delbrueckii (subsp. lactis).
                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro, IPR002453; Beta tubulin.
PROSITE; PS00228; TUBULIN B AUTOREG; UNKNOWN_1.
                                                            Score 32; DB 2;
Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 AA
                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 4797;
Langenheim J.F., Ulrich R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein SAG0009.
                                                              54.5%;
                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 23, TrEMBLrel. 23, TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 AA; 4058 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.48;
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  EMBL; AF303741; AAK82162.1;
SEQUENCE 74 AA; 9009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27,
                                      Query Match
Query Match
Best Local Similarity 54.55,
Best Local Similarity 54.55,
                                                                                                                                                                                                                                                                                                                                                                                                                      OrderedLocusNames=SAG0009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 45.9
Matches 5; Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                       2 YKKMLKKAIKN 12
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                                                                                                                                               3 YKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. SEQUENCE 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=216466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=29397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAG0009; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                      01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2004
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08E2H9
AC 08E2H9
DT 01-MA
DT 
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EMBL, AF496436; AAQ07124.1; -. 600 GOO03677; F.DNA blinding; IEA. GO; GO:00001567; F.two-component response regulator activity; IEA. GO; GO:0000156; F.two-component signal transduction system (p. . .; IEA. GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M., "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PGIT, the causative agent of contagious bovine pleuropneumonia
                                                                                                                                                                                                                                                                                                                                                      Gaps
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Neoptera; Paraneoptera; Phthiraptera; Amblycera; Boopidae;
                                                                                                                                                                                                                                                                                   Score 31; DB 2; Length 39;
Pred. No. 5.6e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 2; Length 48;
Pred. No. 6.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CBPP).";
Genome Res. 14:221-227(2004).
EMBL: BX842645; CAE77581.1; -.
CCMplete proteome.
SEQUENCE 48 AA; 5834 MW; AE11017CDCD190A0 CRC64;
                                                                                                                                                                                                        NON TER 1 1 = --
SEQÜENCE 39 AA; 4406 MW; F8BDF562AFF9C0E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=MSC_0972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 AA.
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                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=14762060; DOI=10.1101/gr.1673304;
                                                                                                             InterPro; IPR009059; bi resp regltr C.
InterPro; IPR001867; Trans_reg_C.
ProDom; PD000329; Trans_reg_C; 1.
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                                                                                                                                                                                                                                                                                            48.4%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma mycoides (Subsp.
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WEDLINE=21219197; PubMed=11319269;
Shao R., Campbell N.J., Barker S.C.;
*Numerous gene rearrangements in the mitochondrial genome of the wallaby louse, Heterodoxus macropus (Phthiraptera).";
Mol. Biol. Evol. 18:858-865(2001).
Bibl., AP370939; AAG32657.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
SEQUENCE 53 AA; 6747 MW; 477FF6B040BDC6AB CRC64;
                                                                                                                                                                                          Query Match 48.4%; Score 31; DB 2; Length 53; Best Local Similarity 75.0%; Pred. No. 7.5e+02; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                      3 YKKFKKK 10
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42 YSKFDKKL 49
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Search completed: May 16, 2005, 08:30:22 Job time : 57.8017 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 58.2931 Seconds (without alignments) 92.887 Million cell updates/sec Run on:

US-09-648-816B-5 Title: Perfect score:

1 KLYRKFKNKLLKLK 14 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

1066881 Total number of hits, satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* 1: geneserm1000c.t geneseqp1980s:* geneseqp1990s:* geneseqp2004s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	% Query	•	:	SUMMAKIES		
Σį	atch	Match Length DB	B	ID	Description	-
Ä	100.0	14	~	AAY57467		Antimicro
Н	100.0	14	ហ	ABG69891		Rabbit pl
	80.0	14	~	AAY57470	-	Antimicro
	80.0	14	Ŋ	ABG69894		Rabbit pl
	71.4	13	7	AAY57468		Antimicro
	71.4	13	'n	ABG69892	-	Rabbit pl
	9.89	13	~	AAY57471		Antimicro
	9.89	13	Ŋ	ABG69895	-	Rabbit pl
	67.1	18	~	AAY57500		Antimicro
	67.1	18	~	AAY57465		Antimicro
	67.1	18	Ŋ	ABG69924	-	Rabbit pl
	67.1	18	ß	ABG69889		Rabbit pl
_	57.1	19	7	AAY57501		Antimicro
•	67.1	19	7	AAY57499	-	Antimicro
_	67.1	19	വ	ABG69923		Rabbit pl
•	67.1	19	ß	ABG69925	-	Rabbit pl
_	67.1	20	~	AAY57502	-	Antimicro
•	67.1	20	Ŋ	ABG69926		Rabbit pl
	67.1	25	~	AAY57496		Antimicro
_	57.1	25	ហ	ABG69920		Rabbit pl
	67.1	33	œ	ADL70275	Ad170275 Pe	Peptide a
	67.1	35	~	AAY57497		Antimicro
	67.1	35	Ŋ	ABG69921	Abg69921 Ra	Rabbit pl
	67.1	36	8	ADL70276		Peptide a
_	67.1	37	æ	ADL70277	Ad170277 Pe	Peptide a

	Aar13936 Cationic Aay57508 Antimicro
ADL/10278 ABG69990 ABG69992 AAK57469 AAK57472 AAK57466 AAK57466 AAK57503 AAK57504 AAK57504 AAG69927 AAG13260 AAO11260 AAO11267 AAO11297 AAO11297	AAR13936 AAY57508
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	23 2 18 2
677 677 677 677 677 677 677 677 677 677	55.7 54.3
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 6 6 6 6	339
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	44 45

ALIGNMENTS

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. (HARB-) HARBOR-UCLA RES & EDUCATION INST. Antimicrobial peptide RP-3 SEQ ID NO:5. AAY57467 standard; peptide; 14 AA 99WO-US003350. 98US-00025319 (first entry) Oryctolagus cuniculus. WO9942119-A1 17-FEB-1999; 18-FEB-1998; 25-FEB-2000 26-AUG-1999 Synthetic. AAY57467;

Shen AJ; Yeaman MR,

WPI; 1999-527417/44.

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure; Page 108; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB. BXZXBX XBBXZXBBX and BBXZBBXZ; and (b) as second peptide template XBBXZXBB, XBBXZXBBX and BBXZBBXZ; and (b) group consisting of XBBXBBX, BXXBXXB, XBBZXXBB, and XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X = at least one aromatic amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 anino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations and fungical above,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbit platelet microbicidal protein, PMP-2, based peptide #3
                                                                                                                                                                                                                                     DB 2; Length 14;
                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                 100.0%; Score 70; DB 2; I 100.0%; Pred. No. 0.00022;
                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 129; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG69891 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple antibiotic resistance.
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                                                                                                                                                                                                                                                                                                                                                                                       1 KLYRKFKNKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLYRKFKNKLLKLK 14
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                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutant; mutein.
                                                                                                                                                         Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG69891;
                                                                                                                                                                                                                                 Query Match
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LD ABG69
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been considered to have undesizable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                          Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                   .
0
                                                                                                                            Length 14;
                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used in the exemplification of the present invention
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                                                                                                                           100.0%; Score 70; DB 5; I 100.0%; Pred. No. 0.00022;
                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide RP-6 SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 109; 166pp; English.
                                                                                                                                                                                                                                                     AAY57470 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00025319
                                                                                                                                                                        1 KLYRKFKNKLLKLK 14
                                                                                                                                                                                            1 KLYRKFKNKLLKLK 14
                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-527417/44.
                                                                                                                                      Similarity
                                                                                                       Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14 AA;
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                                                                                                                                                                                                                                                                          AAY57470;
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Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY57468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core sequence selected from fruncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The estimate of the antimicrobial peptides are useful as individual antimicrobial agents has reserved at minicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as dishifectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular cology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short all-lives due to biodegradation. The peptides of the present invention spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Rabbit platelet microbicidal protein, PMP-2, based peptide #6
                    Score 56; DB 2; Length 14; Pred. No. 0.038;
                                                                     1; Indels
                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 130; 221pp; English.
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                                                                                                                                                                                                                                                                                               ABG69894 standard; peptide; 14
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                    80.0%;
78.6%;
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1 KLYKKWKKGLLKLK 14
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                  Query Match
Best Local Similarity 78.6
Matches 11; Conservative
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXZBXB and BRXZBBX; and (b) as second peptide template XBXXBXXBXB and BRXZBBX; and (b) as second peptide template XBBXXBB, BXXXXBX, BBZXBBX; and (b) as second peptide template XBBXXBBX, BXXBXXBB, and their derivatives selected from the group consisting of XBBXXBBX, XBBXXBB, and their derivatives selected from the XBBXXBBXXBBXXBBX; where B = at least one positively charged amino acid; z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other canno acids. The peptides can be used to treat bacterial and fungal neutrophils. The peptides overall effect cellular distribution and rapid applesis of microbial cells. ANYSTAST tepreseent sequences
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overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                       1; Indels
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                                                                                                                                                                                                    Score 56; DB 5;
Pred. No. 0.038;
2; Mismatches
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Pred. No. 0.32;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial peptide RP-4 SEQ ID NO:6.
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90.0%;
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Best Local Similarity 78.6%;
Matches 11; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 50 amino acids containing a 7-13 amino acid core sequence (derived from 50 amino acids combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also core sequence selected from truncations of the peptides described are (1) an antimicrobial apents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungio. The antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents.

Specifically against bacteria and fungi, agents in combination with other antimicrobial agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial convention of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular conventional antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and socratic spectrum activity against pathogens exhibiting multiple antibiotic covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, relaining activity in plasma and complex of the peptides of the present sequence is a rabbit pwp addictiving antimicrobial peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                 Rabbit platelet microbicidal protein, PMP-2, based peptide #4.
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                                                                                                                                                                                     ABG69892 standard; peptide; 13 AA
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                         3 YRKFKNKILK 12
YRKFKNKLLK 12
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ABG69892
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                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                            Indels
                                                               1; Mismatches
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Score 50;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial peptide RP-7 SEQ ID NO:9.
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                                                                                                                                                                                                                                                                                                                                       AAY57471 standard; peptide; 13 AA.
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   71.4%;
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   Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                     3 YRKFKNKILK 12
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                                                                                                                            3 YRKFKNKLLK
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Matches 9; Conserv
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2 LYRKFKNKLLK 12

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us-09-648-816b-5.rag

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide contentaning a 7-13 amino acide core sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid or retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungion; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials agents to improve efficiency of molecular fonds and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short that half-lives due to biodegradation. The peptides of the present invention are broader and proper are based upon natural antimicrobial peptides of that present invention are broadent and antimicrobial peptides of prior art have general to are based upon natural antimicrobial peptides of that present invention are been considered to bave undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that between the present invention are because the considered to bave undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that have present and broad are based upon natural antimicrobial peptides that persent and proper are based upon natural antimicr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and
                                                                                                                                                         Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 13;
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81.8%; Pred. No. 0.67;
ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 130; 221pp; English.
ABG69895 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2001; 2001WO-US041877
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Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                  mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200255554-A2
                                                                                                       21-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                       ABG69895;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXXZB, KBBXZXBBX and BBXZBBXZ, and (b) a second peptide template XBBXX BXXBXB, MBBXXBB, and consisting of XBBXBBX, XBBXXBB, BXXBXXB, MBBXXBB, and Consisting of XBBXBBX, XBBXXBBX, BXXBXXB, MBBXXBB, and Consisting of XBBXBBX, MBAXBBX, BXXBXXB, MBBZXXBB, and consisting of XBBZXBBX, BXXBXB, BXXBXB, and consisting of XBBZXBBX and their derivatives selected from the group consisting of XBBZXBBX, BXXBXB, BXXBXXB, and a least one annopolar hydropholic amino acid, z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of apoptosis of microbial cells. ANSTAGS to AANSTAGS represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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Pred. No. 1.3;
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                                                                                                                                                                                                         Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 58; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY57465 standard; peptide; 18 AA.
                                                                                                       AAY57500 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00025319
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81.8%;
                                                                                                                                                                            (first entry)
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2 LYKKWKONKLLK 12
                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-527417/44:
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1998;
                                                                                                                                                                              25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                            WO9942119-A1
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                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                                                                          AAY57500;
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                                                                    RESULT 9
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                                                                                        AAY57500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22225222
2622252
                                                                                                                                                                                                                                                                                                                                               The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms and that and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, XBBXZXBBX and BXZBBXZ; and (b) a second peptide template XZBXXXB, XBBXXXBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXXBX, BXXBXXB, XBBXXXBB, and XBBZXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = ar least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX737463 to AAX5757 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                           Antimicrobial peptides for potentiating antimicrobial agents active
                                                      Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 2; Length 18;
Pred. No. 1.3;
1; Mismatches 1; Indels
                                                                                                                                                                                                                      (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                Antimicrobial peptide RP-1 SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                             Claim 17; Page 106; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69924 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.8%;
                                                                                                                                                                                                                                                                                                     against bacteria and fungi.
         25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 67.1
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LYRKFKNKLLK 12
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LYKKFKKKLLK 12
                                                                                                    Oryctolagus cuniculus
                                                                                                                                                                                                                                             Shen AJ
                                                                                                                                                                                                                                                                   WPI; 1999-527417/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant; mutein.
                                                                                                                                                                                                18-FEB-1998;
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                                                                                                                             WO9942119-A1
                                                                                                                                                                         17-FEB-1999;
                                                                                                                                                    26-AUG-1999
                                                                                                                                                                                                                                             Yeaman MR,
                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG69924;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as or for potentiating antimicrobial agents active against organisms such as ore sequence selected from truncations and fusions; and (2) and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides are useful as individual antimicrobial agents, and minimicrobial peptides are useful as individual antimicrobial agents that enhance the antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial activity of antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial for conventional antimicrobials, agents to improve efficiency of conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial perides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short been considered to have undesirable toxicity, immunogenicity and short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example, Page 72; 221pp; English
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Oryctolagus cuniculus.
Synthetic.
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Best Local Similarity
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                                                                                                                             WO200255554-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       feaman MR,
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99WO-US003350

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Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                  Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
                                                                                                                Oryctolagus cuniculus.
                                                                                                                                                WO9942119-A1.
                                                                                                                                                                                                                 17-FEB-1999;
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                                                                                                                                                                                26-AUG-1999
                                                                                                  Synthetic
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Matches
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CC 150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,
CC PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,
CC truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 contraining an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions such as such as such and fungi. The law of the second antimicrobial agents that enhance the antimicrobial agents that enhance the antimicrobial activity of conventional antimicrobials, agents that enhance the antimicrobial or foods and cosmetics and as agents to improve efficiency of foods and cosmetics and as agents to improve efficiency of foods and cosmetics and as agents to improve efficiency of biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic confessed to biology techniques of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and every and shortness of defectiveness due to biodegradation, retaining activity in plasma and every and shortness of effectiveness due to biodegradation, retaining acti
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                                                                                                                                                                                                                                                                                                                             New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
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Pred. No. 1.3;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                Claim 24; Page 71; 221pp; English.
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                                                                                                                                                                                                                                                                                                                                                               multiple antibiotic resistance.
                                                                                                                                                                 24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                25-AUG-2000; 2000US-00648816.
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LYKKFKKKLLK 12
                                                                  Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                               WPI; 2002-590659/63
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                                                                                                                                                                                                                                                                feaman MR,
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AAY57501
ID AAY57
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DT 25-FE
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                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                           Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
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(HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                          Disclosure; Page 59; 166pp; English.
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81.8%;
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                                                                      Yeaman MR, Shen AJ;
                                                                                                                                            WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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autimicrobial peptides are useful as bacteria and fungi. The antimicrobial peptides are useful as individual autimicrobial against organisms such as bacteria and fungi, agents in combination with other specifically against bacteria and fungi, agents in combination with other autimicrobials, agents that enhance the autimicrobial conventional antimicrobials, agents that enhance the autimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                          against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of
                                                                                                                              New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
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bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                      The invention relates to an antimicrobial peptide composition for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.1%; Score 47; DB 5; Length 19; 81.8%; Pred. No. 1.4; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                               Example; Page 71-72; 221pp; English.
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                            Shen AJ;
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Best Local Similarity
Matches 9; Conserv
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                         Yeaman MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXBX, XBBXZBBX and BBXZBBXZ; and (b) a second peptide template XBBXXBX, XBBXXBXB, XBBXXBBX, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and XBBZXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. ANY5757451 tepresent sequences used in the exemplification of the present invention
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81.8%; Pred. No. 1.4;
tive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 58; 166pp; English.
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Best Local Similarity 81.8
Matches 9; Conservative
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                            26-AUG-1999
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RESULT 15 ABG69923

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against.

corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XEBEXEXE and its derivatives selected from XEBEZEXENS, BXXXZB, XBBXZXBA and BEXZBBXZ; and (b) a selected from XEBEZEXENS, BXXXZB, XBBXZXBA and BEXZBBXZ; and (b) a selected from XEBEZEXENS, Where B = at least one positivatives selected from the group consisting of XEBEXEX, XBBXXZBB, BXXXBX, BXXEXXB, SBEZXENS, and xBEZXENSY, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of apoptosis of microbial cells. ANSTAGS to AANSTAST represent sequences used in the exemplification of the present invention
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1; Mismatches
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                                                                                  17-FEB-1999;
                                                                                                                                       .8-FEB-1998;
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                                                                                                                                                                                                                                                      Teaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The inversion transfer to an antimitation between the inversion of a peptide of 5-150 amino acids containing a 7-13 amino acid comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2. platelet microbiocidal protein), and retromers, cremeions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also concluded are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides are useful as individual activity of antimicrobial peptides are useful as individual activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance potentiate or restore efficacy of conventional antimicrobials agents to improve efficiency of molecular fonds and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides of prior art have general and spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicity in an experience problems of toxicity, immunogenicity, and shortness of duration and antimicrobial activity and shortness of duration and antimicrobial activity and shortness of duration and antimicrobial activity and short in a prior art and activity and short in a prior art and activity and short in a prior art and activity an
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                                                                                                                                                                                                                                                                                 New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of effectiveness due to biodegradation, retaining activity in plasma and
serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 1.4;
1; Mismatches 1; Indels
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                                                                                                            (HARB-) HARBOR-UCLA RES & EDUCATION INST.
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                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 72; 221pp; English
24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.1%;
81.8%;
                                                       25-AUG-2000; 2000US-00648816
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Best Local Similarity 81.8
Matches 9; Conservative
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LYKKFKKKLLK 12
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                                                                                                                                                                 Yeaman MR, Shen AJ;
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98US-00025319
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 18-FEB-1998;
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                                                                                                                                                                                              The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers.

Truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) autimicrobial peptides for potentiating antimicrobial agents of leukocytes against organisms such as bacteria and fungi. The leukocytes against organisms such as individual antimicrobial agents that enhance the antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobial peptides are useful as individual antimicrobial agents of conventional antimicrobials, agents that enhance the antimicrobial for antimicrobials, agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in the foods and cosmercies and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short ball-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicity immunosicity and short infernations are based upon natural antimicrobial antimicrobial antimicropial antimicrobial antimicrobial antimicrobial antimicropial antimicrobial antimi
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                                                                                            New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 5; Length 20;
Pred. No. 1.5;
1; Mismatches 1; Indels
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                                                                                                                                                                   Example; Page 72; 221pp; English
                                                                                                                                 multiple antibiotic resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.1%;
81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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                   Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 AA;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXENS and BEXZBBX.

Selected from XZBBZNSRAS, BXZZSB, XBBXZXBX and BEXZBBXZ and (B) a second peptide template XBBXXB, WXBXXBBX and BEXZBBXZ, and (b) group consisting of XBBXZBBX, XBBXXBBX, BXXBXXB, XBBZXBB, and their derivatives selected from the group consisting of XBBZXBBX, Where B = at least one positively charged amino acid, x = at least one positively charged amino acid; x = at least one positively charged amino acid; x = at least one positively charged amino acidi. The peptides can be used to treat bacterial and fungal mino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAN57463 to AAN57557 represent sequences
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                                                                                                                                                       Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
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Pred. No. 1.9;
1; Mismatches 1
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(HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                      Disclosure; Page 126; 166pp; English.
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81.8%;
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                                                                                                        WPI; 1999-527417/44.
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Best Local Similarity
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                                                              The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide contening a 7-13 amino acide core sequence (derived from PMP-1 and PMP-2, platelet microbial protein), and rerromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as core sequence selected from truncations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesizable toxicity, immunogenicity and short because of the considered to have undesizable toxicity, immunogenicity and short because of the considered to have undesizable toxicity, and short and an against because of prior art have generally been considered to have undesizable toxicity, and short and an against and as agents to improve calling and an adversally been considered to have undesizable toxicity, and short and an adversally and short and a supposition of the adversally and short and an against and toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.1%; Score 47; DB 5; Length 25; 81.8%; Pred. No. 1.9; 1: Indels tive 1; Mismatches 1; Indels
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                                     Example; Page 70; 221pp; English.
multiple antibiotic resistance.
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LYKKFKKKLLK 12
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Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL70275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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The present sequence is that of Protide-1 (PT-1), a peptide antibiotide with distinct effector and activator domains. PT-1 contains a C-terminal antihing distinct effector and activator domains. PT-1 contains a C-terminal contains a periode effector (RP-1), an N-terminal chemokine-like peptide effector (Interleukin-8 domain) and an activator site specific for staphylococcus (N protease. PT-1 was designed to be cleaved into 2 distinct effectors in the presence of VB protease. In particular, it was casing deto exert antimicrobial activity less than that of RP-1 in the absence of VB protease produced by Staphylococcus aureus. Thus, PT-1 cwas designed to exert optimal antimicrobial activity in the context of infections due to staphylococcus aureus. Thus, PT-1 cwas designed to exert optimal antimicrobial activity in the context of infections due to staphylococcus cells elaborating the virulence factor VB protease. PT-1 was synthesised by solid-phase synthesis. It is an case effectors with individual distinct biological functions and one or more effectors with individual distinct biological functions and one or corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad trange of pathological conditions.
                                                                                              New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 8; Length 33; Pred. No. 2.4; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
Brass EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                             Claim 1; SEQ ID NO 1; 103pp; English.
Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY57497 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.1%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US003350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 81.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LYRKFKNKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 LYKKFKKKLLK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus
Yount NY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-527417/44.
                                              WPI; 2004-226740/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-1999
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Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                               condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY57497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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cor for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of elevicoytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, apents that enhance, potentiate or restore efficiacy of conventional antimicrobials, agents that enhance, potentiate or restore efficiacy of conventions of leukocytes, as disinfectants or preservatives for use in thuctions of leukocytes, as disinfectants or preservatives for use in comparation and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and effectiveness due to biodegradation, managemicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

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                                  The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XXBZBXBXB and its derivatives selected from XZBBZBXBXB and its derivatives as second peptide template XBXZXBX xBXXXBBX and BBXZBBXZ; and (b) a second peptide template XBBXX and their derivatives selected from the XBBZXXBBX, where B = at least one positively charged amino acid, x at least one aromatic amino acid, and where B, X and Z may be separated by one or more other
                                                                                                                                                                                                                                                    amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 2; Length 35;
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                    used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
Disclosure; Page 126; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG69921 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                                 67.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                 81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||:||| ||||
LYKKFKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LYRKFKNKLLK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200255554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG69921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Gaps

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5; Length 35; 1; Indels

Score 47; DB : Pred. No. 2.6; 1; Mismatches

67.1%; 81.8%;

Query Match
Best Local Similarity 81.0.
Pest Local 9; Conservative

Sequence 35 AA;

2 LYRKFKNKLLK 12

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The present sequence is that of Protide-2 (PT-2), a peptide antibiotide with distinct effector and activator domains. PT-2 contains a C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                         New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                                                          Protide; antibiotide; antimicrobial; interleukin-8.
                                                                                                                                                                                                                               /note= "Cleaved by C3 convertase"
                                                                                                                                                                                                                                                                                                                                                                              Brass EP;
                                                                                                                                                                                                                                                                                                                                                      (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 2; 103pp; English.
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            Yount NY, Edwards JE,
                                                            ADL70276 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                      20-AUG-2003; 2003WO-US026405
                                                                                                                                                                                                                                                                                                                              20-AUG-2002; 2002US-00225562
                                                                                                           (first entry)
                                                                                                                                  Peptide antibiotide PT-2.
2 LYKKFKKKLK 12
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-226740/21.
                                                                                                                                                                                                                                                        WO2004017985-A1.
                                                                                                                                                                                                                     Cleavage-site
                                                                                                          20-MAY-2004
                                                                                                                                                                                                                                                                              04-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                              Yeaman MR,
                                                                                                                                                                                  Synthetic.
                                                                                     ADL70276;
                                     RESULT 24
                                                   ADL7027
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity

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New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting

Example; Page 71; 221pp; English.

multiple antibiotic resistance.

antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2 distinct effectors in the presence of C3 convertase. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of C3 convertase. Thus, PT-2 was designed to exert optimal antimicrobial activity in the context of activation of one of the in the presence of C3 convertase. Thus, PT-2 was designed to exert optimal antimicrobial activity in the context of activation of one of the context-activated protides of the invention that have 2 or example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions. 88888888888888888888

Sequence 36 AA;

ö 8; Length 36; 1; Indels Score 47; DB Pred. No. 2.7; 1; Mismatches 67.1**%**; 81.8**%**; Query Match
Best Local Similarity 81.0 20 LYKKFKKKLLK 30 2 LYRKFKNKLLK 12 셤 ઠે

ADL70277 standard; peptide; 37 AA.

20-MAY-2004 (first entry) Peptide antibiotide PT-3. ADL70277; RESULT 25
ADL70277
AC ADL70277
AC ADL70277
AC ADL7027
AC ADL702
AC

Protide; antibiotide; antimicrobial; interleukin-8. Synthetic

WO2004017985-A1

Cleavage-site

18. .19
/note= "Cleaved by thrombin"

Location/Qualifiers

04-MAR-2004

20-AUG-2003; 2003WO-US026405.

20-AUG-2002; 2002US-00225562.

(HARB-) HARBOR-UCLA RES & EDUCATION INST

Brass EP; Yeaman MR, Yount NY, Edwards JE,

WPI; 2004-226740/21

New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.

Claim 1; SEQ ID NO 3; 103pp; English.

The present sequence is that of Protide-3 (PT-3), a peptide antibiotide with distinct effector and activator domains. PT-3 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors in the presence of thrombin. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of thrombin,

but equivalent to or exceeding that of RP-1 in the presence of thrombin. Thus, PT-3 exerts optimal antimicrobial activity in the context of thrombin as would be present in the setting of vascular injury or infection. PT-3 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions. 888888888888888

Sequence 37 AA;

Gaps ö 67.1%; Score 47; DB 8; Length 37; 81.8%; Pred. No. 2.7; 1; Indels 1; Mismatches Best Local Similarity 81.6 Matches 9; Conservative 2 LYRKFKNKLLK 12 22 LYKKFKKKLLK 32 Query Match 8

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Gaps

ADL70278 standard; peptide; 39 AA.

ADL70278;

(first entry) 20-MAY-2004

Peptide antibiotide PT-4.

Protide; antibiotide; antimicrobial; interleukin-8; cytostatic.

Synthetic

/note= "Cleaved by MMP-9" Location/Qualifiers Cleavage-site

WO2004017985-A1

04-MAR-2004

20-AUG-2003; 2003WO-US026405

20-AUG-2002; 2002US-00225562.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Brass EP; Edwards JE, Yount NY, Yeaman MR,

WPI; 2004-226740/21.

New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.

Claim 1; SEQ ID NO 4; 103pp; English.

with distinct effector and activator domains. PT-4 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for matrix metalloproteinase MMP-9, which is produced to dissolve the tissue in front of the growing blood vessel tip to allow for its continued tissue invasion. PT-4 was designed to be cleaved into 2 distinct effectors in the presence of MMP-9. In particular, PT-4 exerts antimoplastic and/or antimicrobial activity less than that of RP-1 in the absence of MMP-9, but equivalent to or exceeding that of RP-1 in presence of MMP-9, Thus, PT-4 exerts optimal antimoplastic and/or antimicrobial activity in the context of new blood vessel formation. PT-4 is an example of context-activated protides of the invention that have 2 The present sequence is that of Protide-4 (PT-4), a peptide antibiotide

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        against organisms such as bacteria and fungi comprishing a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, placelet microbiocidal protein), and retromers. truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional attimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabbit platelet microbicidal protein, PMP-2, based peptide #102
                                                                                                                                                                                                  ö
                                                                                                                                                         Length 39,
                                                                                                                                                                                                  1; Indels
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8
                                                                                                                                                           Score 47; DB 8
Pred. No. 2.9;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            ABG69990 standard; peptide; 40 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-2001; 2001WO-US041877
                                                                                                                                                                              81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                       2 LYRKFKNKLLK 12
                                                                                                                                                                                                                                                           23 LYKKFKKKLLK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-590659/63.
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                      Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                   ABG69990;
                                                                                                                                                                                                  Matches
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against organisms such as bacteria and fungi comprising a peptide of 5-150 mino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers. The truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The
                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides of the present invention spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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1; Mismatches
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                                                                                                                                                                                                                                                                                    Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG69992 standard; peptide; 40 AA.
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                                                                                                                                                                                                                                                                                  Query Match 67.1%;
Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    2 LYRKFKNKLLK 12
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2 LYKKFKKKLLK 12
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antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobial, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular boilogy techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57469 standard; peptide; 13 AA.
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Best Local Similarity 81.0.,
Conservative
7, Conservative
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                                                                                                                                                                                                                                                                                                                                      Sequence 40 AA;
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gainst organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 core settle structures are fully described in the specification. Also
150 core sequence are fully described in the specification. Also
151 core sequence selected from truncations of the peptides described above,
152 core sequence selected from truncations of the peptides described above,
153 core sequence selected from truncations and fundions; and (2)
154 containing an amino acid
155 core sequence selected from truncations and fundions; and (2)
156 core sequence selected from truncations and fundion; and (2)
157 core sequence selected from truncations and fundion; and (2)
158 core sequence selected from truncations and fundion; and (2)
159 core sequence selected from truncations and fundion; and (2)
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150 core sequence selected from truncations and fundion; and (2)
150 core sequence selected from truncations and fundion; and (2)
150 core sequence selected from truncations and fundion; and (2)
150 core sequence selected from truncations and fundion; agents in combination with other antimicrobials, agents that enhance the antimicrobial
150 functions of leukocytes, as disinfectants or preservatives for use in
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amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. ANYS7463 to AAXS7557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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                                                                                                                                                                             Length 13;
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Pred. No. 2.9;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69893 standard; peptide; 13 AA.
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                                                                                                                                                                             62.9%;
70.0%;
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                                                                                                                                                           Query Match
Best Local Similarity 70.0°
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                                                                                                                                    Sequence 13 AA;
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crivity or for potentiating antimicrobial agents active against represent corpusing such as bacteria and fungi. The AP comprises: (a) a peptide corpusing an amino acid sequence selected from the group consisting containing an amino acid sequence selected from the group consisting selected from XZBBZBXBXB and its derivatives selected from the group consisting a second peptide template XBBXXXBB, XBBXXBBX and BBXZBBX; and (b) a second peptide template XBBXXBBX, BXBXXBB, MBXBXXBB, and XBBZXBBX, MBY BXBXXBB, BXBXXBB, and composition of XBBZXBBX, MBY and zero positively charged amino acid; x = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY5757 represent sequences used in the exemplification of the present invention
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foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inharent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                Score 44; DB 5; Length 13;
Pred. No. 2.9;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY57472 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                62.9%;
70.0%;
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Best Local Similarity 70.vv,
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                                                                                                                                                                                                                             Sequence 13 AA;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acide core sequence (derived from 150 amino acide containing a 7-13 amino acid core sequence (derived from 150 amino acides containing a combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or included are (1) an antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) archimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, against bacteria and fungi, agents in combination with other antimicrobials, against bacteria and fungi, agents in conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short the based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad
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                                                                                              Gaps
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                                                     DB 2; Length 18;
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Pred. No.
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                                                                                                                                                                                                                                                                       ABG69896 standard; peptide; 18 AA.
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                                                     62.9%;
80.0%;
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                                Query Match
Best Local Similarity 80.0
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                                                                                                                                    1 KLYRKFKNKL
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                  Sequence 18 AA;
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Mismatches

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Matches

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and consisting of XBBXBBX, XBBXXBBX, BXXBXXB, AZBBXXB, and consisting of XBBZBBX, XBBXXXBX, BXXBXXB, AZBBXXB, and consisting of XBBZBBX, XBBXXBBX, BXZBXB, and consisting of XBBZBBY, XBBXXBBX, BXZBXB, and consisting of XBBZBBY, XBBXXBBX, BXZBXB, and consisting of XBBZBBBY, XBBZXBB, and consisting an incomplete and consisting complete and consisting and consisting and consisting and consisting application of the present invention
spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                     DB 5; Length 18;
                                                                                                                                                                     0; Indels
                                                                                                                                                                   2; Mismatches
                                                                                                                                     Score 44; D
Pred. No. 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial peptide RP-2 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 107; 166pp; English
                                                                                                                                                                                                                                                                                                                        AAY57466 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00025319.
                                                                                                                                  62.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                    1 KLYRKFKNKL 10
                                                                                                                                                                                                                       1 KLYKKWKNKL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-527417/44.
                                                                                                    Sequence 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                         AAY57466;
                                                                                                                                                                                                                                                                                       RESULT 33
AAY57466
                                                                                                                                                                                                                                                                                                                        888888
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Score 43; DB 2; Length 13; Pred. No. 4.2;

61.4%; 80.0%;

Query Match Best Local Similarity Sequence 13 AA;

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The invention relaters to an animalization peptide of 5-
diginate organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
PMP-1 and PMP-2. platelet microbiocidal protein), and retromers,
truncations, extensions, combinations, fusions and their derivatives. The
possible structures are fully described in the specification. Also
conclusions, extensions, combinations and their derivatives. The
possible structures are fully described in the specification. Also
core sequence selected from truncations of the specific activity
or for potentiating antimicrobial peptide of 13-74 containing an amino acid
core sequence selected from truncations of the specified above,
and retromers, extensions, combinations of the specified above,
and retromers, extensions, combinations and fusions; and (2)
antimicrobial peptides for potentiating antimicrobial activity of
antimicrobial peptides are useful as individual antimicrobial agents,
specifically against bacteria and fungi, agents in combination with other
antimicrobial antimicrobials, agents that enhance the antimicrobial
conventional antimicrobials, agents to improve efficiency of
functions of leukocytes, as disinfectants or preservatives for use in
conventional antimicrobial peptides of prior art have generally
been considered to have undesirable toxicity, immunogenicity and short
convention artivity against pathogens exhibiting multiple antibiotic
conversione problems of toxicity, immunogenicity, and shortness of duration
covercome problems of toxicity, immunogenicity, and shortness of duration
covercome problems of toxicity, immunogenicity, and shortness of duration
covercome problems of toxicity, immunogenicity, and shortness of serum. The present sequence is a rabbit pube based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 128; 221pp; English.
                                                                                                                                                        ABG69890 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                   21-OCT-2002 (first entry)
3 YRKFKNKLLK 12
                                          3 YKKFKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                     mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200255554-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .8-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                        ABG69890;
                                                                                                                RESULT 34
                                                                                                                                     ABG69890
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Sequence 18 AA;
                                                                                                                                                                                    WO9942119-A1.
                                                                                                                                                                                                                             17-FEB-1999;
                                                                                                                                                                                                                                                  18-FEB-1998;
                                                                                                                                                                                                       26-AUG-1999
                                                                                                                                                    Synthetic.
                                                      AAY57504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG69928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 37
ABG69928
ID ABG69:
XX
AC ABG69
DT 21-OC
            RESULT 36
                       AAY57504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, XBBXXZBB, and BMXZBXZ, and (b) a second peptide template XBBXXXB, MEMEXXBB, and selected from the group consisting of XBBXBBX, XBBXXBB, BXXBXXB, MEMEXXBB, and XBBZXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid, Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. ANY57463 to AAN5757 represent sequences
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                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                            Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.4%; Score 43; DB 2; Length 18; 80.0%; Pred. No. 5.8; 1; Indels ive 1; Mismatches 1; Indels
                      DB 5; Length 13;
                                          1; Indels
                      Score 43; DB :
Pred. No. 4.2;
                                                                                                                                                                                                        Antimicrobial peptide RP-1-2R SEQ ID NO:41.
                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 59; 166pp, English.
                                                                                                                                         AAYS7503 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                       99WO-US003350.
                     61.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                            98US-00025319
                                                                                                                                                                                   (first entry)
                               Local Similarity 80.0
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                                                                           |:||| ||||
3 YKKFKKULK 12
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3 YKKFKKKLLK 12
                                                                3 YRKFKNKLLK 12
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                                                                                                                                                                                                                                                                       Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                     Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
tes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                      17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                            18-FEB-1998;
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                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                              AAY57503;
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                      Query Match
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Matches
                                          Matches
                                                                                                                    RESULT 35
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activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBEXKB and its derivatives selected from XZBBZBEXB. BXZXB. BXXZXB. XBBXZXBBX and BBXZBBXZ; and (b) as second peptide template XBBXZXBB XBXXBBX and BBXZBBXZ; and (b) group consisting of XBBXBBX, BXXBBX, XBXZXBB, and XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7461 to AAYS757 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                        Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in the exemplification of the present invention
                                                                                                                                                                                                           Antimicrobial peptide RP-1-10F SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 2
Pred. No. 5.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG69928 standard; peptide; 18 AA.
AAY57504 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US003350
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                                                                                                                                       25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LYRKFKNKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYKKFKKKFLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeaman MR, Shen AJ;
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Best Local Similarity
Matches 8; Conserv
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rabbit;

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; 1

Rabbit platelet microbicidal protein, PMP-2, based peptide #39

21-OCT-2002 (first entry)

ABG69927;

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Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
Rabbit platelet microbicidal protein, PMP-2, based peptide #40.
                                                                                                                         (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                            Example; Page 72; 221pp; English
                                                                                              24-AUG-2001; 2001WO-US041877.
                                                                                                           25-AUG-2000; 2000US-00648816.
                                                Oryctolagus cuniculus
                                                                                                                                      Yeaman MR, Shen AJ;
                                                                                                                                                   WPI; 2002-590659/63
                                   mutant; mutein.
                                                                    WO200255554-A2
                                                                                 18-JUL-2002
                                                      Synthetic.
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overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide Sequence 18 AA;

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Gaps
                            ö
   Score 43; DB 5; Length 18;
Pred. No. 5.8;
                           2; Indels
                           1; Mismatches
   61.4%;
Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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LYRKFKNKLLK 12 ||:||| | || LYKKFKKKFLK 12

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ABG69927 standard; peptide; 18 AA. RESULT 38 ABG69927

The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide contenting a 7-13 amino acide core sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and recromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as becteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial agents, specifically against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficancy of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in foods and commercies and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of prior art have generally became activity against pathogens exhibiting multiple antibiotic sesitation are based upon natural antimicrobial peptides of prior art have generally resistance. They exhibite lower imherent mammallan cell toxicities and divisition are based upon natural antimicrobial peptides of prior art have generally convertome problems of toxicity immunogenicity, and short and and and approach and antimicrobial peptides of prior art have generally and short inherent mammallance. They exhibite lower inherent mammallance and and antimicrobial participation are passed upon the pathogens exhibiting and approach and and and and and a New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

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(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Teaman MR, Shen AJ; WPI; 2002-590659/63

24-AUG-2001; 2001WO-US041877. 25-AUG-2000; 2000US-00648816.

Oryctolagus cuniculus. Synthetic.

WO200255554-A2. 18-JUL-2002

mutant; mutein.

overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide peptide composition for the prevention and treatment by organisms, such as bacteria and fungi, exhibiting invention relates to an antimicrobial peptide composition for use Example; Page 72; 221pp; English multiple antibiotic resistance. # antimicrobial
fections caused

ö Gaps ö Score 43; DB 5; Length 18; Pred. No. 5.8; 1; Mismatches 1; Indels 61.48; 80.08; 8; Conservative |:||| |||| YKKFKKKLLK 12 3 YRKFKNKLLK 12 Best Local Similarity Sequence 18 AA; Query Match Matches ઠે

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RESULT 39

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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019310) that exhibit activity elating to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and
                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 27189; 1399pp + Sequence Listing; English
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87.5%; Pred. No. 68;
ive 1; Mismatches
Human polypeptide SEQ ID NO 27189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY57505 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                              26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000; 2000US-00515126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.1
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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20 RLYRKFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-514838/
N-PSDB; AAI93228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 71 AA;
                                                                                                                                                                                                                 WO200164835-A2
                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9942119-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY57505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X M X S S X M M X B X H X Y X I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA01310) that exhibit activity elating to prytokine, cell proliferentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or irratment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequented for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 27152; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.4%; Score 43; DB 4; Length 60; 72.7%; Pred. No. 19; 2; Indels ive 1; Mismatches 2; Indels
                                                                                              AAO13260 standard; protein; 60 AA
                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 27152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA013297 standard; protein; 71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LYRKFKNKLLK 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI93191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164835-A2
                                                                                                                                                                                         06-NOV-2001
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                                                                                                                                             AA013260;
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Gaps

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Indels

RESULT 40
AA013297
ID AA013:
XX
AC AA013:
XX
DT 06-NO'

Matches

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Shen AJ;
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19-FEB-1991;
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 Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR13930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                           The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBZBXBXB, BXZXXB, XBBXZXBX and BRXZBBXZ; and (b) a second peptide template XBBXXXB, BXXXBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXXBX, XBBXXXBB, and consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and consisting of XBBZBBX, XBBXXBBX, BXXBXXB, AZBBX, and consisting of XBBZABBX and their derivatives one aromatic amino acid, and where B = at least one positively charged amino acid; X = amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AXF57463 to AAF5757 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial, platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                       Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabbit platelet microbicidal protein, PMP-2, based peptide #41
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 2; Length 18;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                         Disclosure; Page 59; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG69929 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                    55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-AUG-2000; 2000US-00648816.
                      99WO-US003350
                                             98US-00025319
                                                                                                                                                  against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YRKFKNKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YKKFKKKFLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus.
                                                                                                                WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
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                      17-FEB-1999;
                                             18-FEB-1998;
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26-AUG-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69929;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-

150 amino acids containing a 7-13 amino acid core sequence (derived from the particle and PMP-2.) platelet microbical all protein), and retromers,

CRP1-1 and PMP-2.) platelet microbicalal protein), and retromers,

truncations, extensions, combinations in the specification. Also consible structures are fully described in the specification. Also concentrating antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the covers against organisms such as bacteria and fungi, and (2) antimicrobial peptides for potentiate or restore efficacy of specifically against bacteria and fungi, agents in combination with other specifically against bacteria and fungi, agents in combination with other conventional antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in foods and commetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short considered to bave undesirable toxicity, immunogenicity and short or seet based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicity and short or resistance. They exhibit molecular inherent mammalian cell toxicity and short ore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                     New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                     invention relates to an antimicrobial peptide composition for use
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25;
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                                                                                                                                                                                                                                                                      Example, Page 72; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90US-00484020.
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Matches 7; Conservative
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3 YKKFKKKFLK 12
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26-NOV-1991 (first en
WPI; 2002-590659/63.
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Gaps

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, AAR13936 standard; protein; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 44; 64pp; English
                                                           Claim 17; Page 44; 64pp; English
                                                                                                                                                                                                                                                                                                           (BRIM ) BRISTOL-MYERS SQUIBB CO.
    (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                  8; Conservative
                                                                                                                                             1 KLYRKFKNKLLK 12
                                                                                                                                                                                                                          Cationic oligopeptide #7
                                                                                                                                                        3 KLYKKLLKKLLK 14
                                                                                                                                                                                                                                                                                                                       Darveau RP, Blake JJ,
               Darveau RP, Blake JJ,
                                                                                                                                                                                                                                                                                                                                 WPI; 1991-281214/38.
                          WPI; 1991-281214/38
                                                                                                                       Query Match
Best Local Similarity
                                                                                                             Sequence 20 AA;
                                                                                                                                                                                                                                                                                 23-FEB-1990;
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                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                               AAR13936;
                                                                                                  field.)
                                                                                                                                   Matches
                                                                                                                                                                         RESULT 44
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activity or for potentiating antimicrobial agents active against containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXXB and its derivatives selected from XZBBZBXBXB. BXZXB, XBBXXXBXB and its derivatives selected from XZBBZBXBXB BXZXBX BXXZXBX AND SXZBBXZBX and bear ascoond peptide template XBBXXXBXXB, XBBXXXBBX and BBXZBBXZ; and (b) a second peptide template XBBXX BXXXBXB, XBBXXXBBX, and (b) group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rappid apoptosis of microbial cells. AAYS7463 to AAYS7557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                       Score 39; DB 2; Length 23; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 18;
                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in the exemplification of the present invention
                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial peptide nRP-1:cRP-13 SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 2
Pred. No. 37;
1; Mismatches
                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 60; 166pp; English.
                                                                                                                                                                                                                                                                                            AAY57508 standard; peptide; 18 AA
                                                       55.7%;
nilarity 66.7%;
Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial peptides for against bacteria and fungi
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                                                                                                                                             1 KLYRKFKNKLLK 12
                                                                                                                                                                                    KLYKKLLKKLLK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-527417/44.
                                                         Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                   Sequence 23 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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Matches
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                                                                                                                                                                                                                                                                      This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphablical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13929 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphahalical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13937. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                             Compsns. for treating infections sensitive to beta-lactam antibiotics -
comprise beta-lactam antibiotic and cationic oligopeptide, useful against
Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compans. for treating infections sensitive to beta-lactam antibiotics -
comprise beta-lactam antibiotic and cationic oligopeptide, useful against
Enterobacteriaceae, Pseudomonas aeruginosa etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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91US-00655321.
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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 75.8793 Seconds (without alignments) 121.475 Million cell updates/sec Run on:

US-09-648-816B-3 87

1 ALYKKFKKKLLKSLKRLG 18 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

145419 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O8txt3 methanopyru	Q7rqr9 plasmodium		Q636z0 bacillus ce	_	Q8xmb6 clostridium	P10856 mus musculu			Q9bv95 homo sapien					Q6ngj2 corynebacte	Q8e0a5 streptococc	Q8e5y2 streptococc			Q91iu9 sin nombre			-		-	P62122 gossypium h	P62124 hordeum vul	'n	m	P62121 nicotiana t	P17305 bos taurus
SUMMAKIES	· a	OSTXT3	Q7RQR9	Q9UC64	029830	Q745E7	Q8XMB6	STP1 MOUSE	Q812C3	Q9X1A6	Q9BV95	Q9H058	Q6MRG6	Q7R7R2	Q9KUX1	Q6NGJ2	QBEOA5	Q8E5Y2	Q91IU7	Q911U8	Q911U9	Q911V0	Q91FM3	Q9S9B5	RL30 THEMA	RL41_ARATH	RL41 GOSHI	RL41_HORVU	RL41_ORYSA	RL41 PEA	RL41_TOBAC	STP1_BOVIN
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	Query Match Length	69	47	54	70	73	20	54	24	69	41	42	62	25	31	37	64	64	67	63	67	67	74	31	67	25	25	25	52	. 25	25	54
a	Query Match	50.0	47.1	47.1	47.1	46.0	44.8	44.8	44.8	44.8	43.7	43.7	43.7	42.5	42.5	42.5	42.5	42.5	42.5	٠	•	42.5	42.5	42.0	42.0	41.4	41.4	41.4	41.4	41.4	41.4	41.4
	Score	43.5	41	41	41	40	39	39	39	39	38	38	38	37	37	37	37	37	37	37	37	37	37	36.5	36.5	36	36	36	36	36	36	36
	Result No.	,	7	٣	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31

QTROR9 PRELIMINARY; PRT; 47 AA.
QTROR9;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.

RESULT 2
Q7RQB9
ID Q7RQB
AC Q7RQB
DT 01-M
DT 01-M
DT 01-M
DE HYPOO

P02317 rattus norv P22613 ovis aries Opngm3 homo sapien Q7var3 prochloroco Q8r855 thermoanaer O15571 entemoeba h Q91801 xenopus lae Q65wt3 oryza sativ Q7x4e4 julube witc Q7x4e4 cherry leth	
STP1_RAT STP1_SHEEP Q9NGN3 Q9NGN3 Q9R855 Q18571 Q91801 Q65WT3 Q7X4E2 Q7X4E4	Q8F1S1 Q63CRS Q7RKXS
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	35.5 35.5
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## ALIGNMENTS

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raceae; AV19	Gaps	
topy)	1,	
OBTITION PRELIMINARY; PRT; 69 AA.  OBTITION -2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 26, Last annotation update) Predicted nucleic-acid-binding protein containing an archaeal-type C2H2 Znfinger. COTABLE TARENT COTABLE SHANGS7; Methanopyrus kandleri. Archaea; Buryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae; Methanopyrus kandleri. Archaea; Buryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae; McBI TAXID=2320; [1] STRAIN=AV19 / DSM 6324 / JCM 9639; NCBI TAXID=2320; [1] STRAIN=AV19 / DSM 6324 / JCM 9639; NCBI TAXID=2320; [1] STRAIN=AV19 / DSM 6324 / JCM 9639; NCBI TAXID=21927647; Pubmed=11930014; DOI=10.1073/pnas.032671499; STRAIN=AV19 / DSM 6324 / JCM 9639; NCBI TAXID=21927647; Pubmed=11930014; DOI=10.1073/pnas.032671499; STRAIN=AV19 / DSM 6324 / JCM 9639; ARDINES-21927647; Pubmed=11930014; DOI=10.1073/pnas.032671499; STRAIN=AV19 / DSM 6324 / JCM 9639; ARDINES-21927647; Pubmed=11930014; DOI=10.1073/pnas.032671499; STRAIN=AV19 / DSM 6324 / JCM 9639; ARDINES-21927647; Pubmed=11930014; DOI=10.1073/pnas.032671499; STRAIN=AV19 / DSM 6324 / JCM 9639; ARDINES-21927647; Pubmed=11930014; DOI=10.1073/pnas.032671499; STRAIN=AV19 / DSM 6324 / JCM 9639; ARDINES-21927647; Pubmed=11930014; DOI=10.1073/pnas.032671499; ARDINES-21927644-4649(2002). GO: GO: 00005634; C: nucleus; IEA. GO: GO: 00005634; C: nucleus; IEA. GO: GO: 0000576; F: zincleic acid binding; IEA. COMPATE; PROOUSE; ZINC_ENGRE C2H2; I. PROSITE; PSO0028; ZINC_ENGRE C2H2; I. COMPATE; PSO0028; ZINC_ENGRE C2H2_1; I. PROSITE; PSO0028; ZINC_ENGRE C2H2_2; I.	Length 69; Indels	
ning ming ning yra] yyra] yyra] ( Y.) anog	2; 3;	
ied) sequence update) annotation update) annotation update) cotein containing a ri; Methanopyrales karova K.S., Polus Belova G.I., Arav v. R.L., Wolf Y.I., im S.A.; in S.A.;	.5; DB .72; cches	
T. 1  OBTITAL  OBTITA	Score 43.5; Pred. No. 72; 4; Mismatches	18 63
MBLrel. 21, Cre MBLrel. 26, Las MBLrel. 26, Las Mclarel. 26, Las C-acid-binding S-acid-binding M-acid-binding M	50.0%; 55.6%; ive	RIG RRG
rel. 21, rel. 21, rel. 21, rel. 26, cid-bind KN0577; ri. ota; Met evaya K. Shakaya K. Shakaya K. C. C. V, K e of hyp chaeal n I.B., k e of thy chaeal ucleus; ucleus; ucleus; ucleic a lor. 10.5	50. 55.	KSLF   :  KKMF
T. 1  OBTXT3  OBTXT3  OBTXT3  OBTXT3  OBTXT3  OBTXT3  OL-JUN-2002 (TrEMBLrel. 21, Create ol-JUN-2002 (TrEMBLrel. 26, Last sol-MAR-2004 (TrEMBLrel. 26, Last sol-MAR-2004 (TrEMBLrel. 26, Last sol-MAR-2004 (TrEMBLrel. 26, Last sol-Marchaea nucleic-acid-binding proceedations was subject to the subject of the	>	LYKKFK-KKLLKSLKRLG      :  :    
(T3)  (T3)  (TM-2002 (Tr  (TM-2002 (Tr  (TM-2004 (Tr  ficted nucle  2 Zn-finger.  readousham nanopyrus.  ranopyrus.	th Simi	2 LYK     46 LYK
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28 TXT T T T T T T T T T T T T T T T T T	Oue Bes Mat	දු පු

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Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin E., Tice H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li.L., Banantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AE017227, AASO2469.1; -
GO, GO:0003700; Fitnanscription factor activity; IEA.
GO; GO:0006355; Piregulation of transcription, DNA-dependent; IEA.
InterPro; IPR001967; Homeodomain_like.
InterPro; IPR001647; HTTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corymebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1770,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 2; Length 73;
Pred. No. 2.5e+02;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 2; Length 70; Pred. No. 1.7e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000001; AAU16820.1;
SEQUENCE 70 AA; 7813 MW; A83ACD3261D3E795 CRC64;
                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AA; 7780 MW; C1CFF6DE094D7B2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=MAP0152c;
                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                70 AA.
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                                                                                                                          Created)
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50 ALYKHFGSKRELLEARSRTG
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Local Similarity 50.0%;
hes 10; Conservative
                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Group-specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 63.6%;
7; Conservative
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                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 KFKKKLLKSLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KFRKKMIKSLQ 13
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                    ORFNames=BTZK3444;
Bacillus cereus ZK
                                                                                                                                                                                                                                                              NCBI_TaxID=288681;
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                              063620
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                                           RESULT 4
Q63620
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                                                                                                                                                                                                                                                                                                                                       "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."; Nature 419:121-519 (2002).

-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                 Carlton J.M., Angiuoli S.V., Suh B.B., Koolj T.W., Pertea M., Sinda J.C., Emolaeva M.D., Suh B.B., Koolj T.W., Pertea M., Sinda J.C., Emolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Shetreon J.D., Pop M., Koack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedgah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Vanningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Yan Janse C.J., Waters A.P., Smith H.O., White O.R., Carucci D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotza, Metarama, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 2; Length 47;
Pred. No. 1.2e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 2; Length 54;
Pred. No. 1.3e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AABLO1000271; EAA19856.1; -.
Hypothetical protein.
SEQUENCE 47 AA; 5719 MW; 1DA2D9E6D5B2B2C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0436; INTERLEUKINB.
PRINTS; PRO0437; SMALLCYTKCXC.
SMART; SMO0199; SCY; 1.
SEQUENCE 54 AA; 6033 MW; COB560236BF1B14A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gupta S.K., Hassel T., Singh J.P.;
Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995).
HSSP; P02776; 1F9Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR002473; C-X-C/Interlkn 8.
InterPro; IPR001811; Chemokine_IL8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.1%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KKFKKKLLKSLKR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 KKKKKKYIKAIKR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 61.9
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 75.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 LYKKIIKKLLES 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                  FROM N.A.
                        Eukaryota; Alveol
NCBL_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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**Q9UC64** 

RESULT 3 Q9UC64

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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 AA.
  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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28 YEECKEKLIPFLKKVG 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.8%;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001319; TP1.
Pfam; PF02079; TP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD010292; TP1; 1. PROSITE; PS00541; TP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 RKYRKSVLKSRKR 42
                                                                               EMBL; S80846; AAB21244.2;
EMBL; X12521; CAA31039.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KKFKKKLLKSLKR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 43.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.8 Matches 7; Conservative
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                                                                                                                                PIR; A40561; BGMS.
MGD; MGI:98784; Tnpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: In the elongating spermatids of mammals, the conversion of nucleosomal formatin to the compact, nonnucleosomal form found in the sperm nucleus is associated with the appearance of a small set of basic chromosomal transition proteins.

SUGCELLUAR LOCATION: Nuclear.

SUBCELLUAR SPECIFICITY: Testis.
SIMILARITY: Belongs to the nuclear transition protein 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Testis;
MEDLINE=88252150; PubMed=3382664; DOI=10.1016/0167-4781(88)90013-9;
Kleene K.C., Borzorgzadeh A., Flynn J.F., Yelick P.C., Hecht N.B.;
"Nucleotide sequence of a cDNA clone encoding mouse transition protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDIMED=1685480; MEDIME=29129951; PubMed=1685480; Yelick P.C., Kozak C., Kwon Y.K., Seldin M.F., Hecht N.B.; "The mouse transition protein 1 gene contains a B1 repetitive element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                  Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                        Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                            MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.8%; Score 39; DB 2; Length 50; 50.0%; Pred. No. 2.5e+02; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-070-1989 (Rel. 11, Created)
01-070-1989 (Rel. 11, Last sequence update)
05-070-2004 (Rel. 44, Last annotation update)
Spermatid nuclear transition protein 1 (STP-1) (TP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP001188; BAB80479.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 50 AA; 5894 MW; BAGC276FBC59D2F5 CRC64;
                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CPE0773.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and is located on chromosome 1.";
Genomics 11:687-694 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LYKKFKKKLLKSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYQNIKIKLKNSMKRI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      flesh-eater."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STP1 MOUSE
P10856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Tnp1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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ö ö Gaps Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. Gapa Chromosomal protein; DNA-binding; Nuclear protein; Nucleosome core; STRAIN=BN; Behboudi A., Roshani L., Montelius K., Rohme D., Klinga-Levan K., ö ö Score 39; DB 1; Length 54; Pred. No. 2.7e+02; 4; Mismatches 2; Indels 44.8%; Score 39; DB 2; Length 54; 43.8%; Pred. No. 2.7e+02; tive 6; Mismatches 3; Indels Stahl F.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases GO; GO:0000786; C:nucleosome; ISS.
GO; GO:000347; F:DNA binding; ISS.
GO; GO:0006342; P:chromatin silencing; ISS.
GO; GO:0009566; P:fertilization; ISS.
GO; GO:0009567; P:fertilization; ISS.
GO; GO:000012; P:single strand break repair; ISS.
GO; GO:000317; P:sperm motility; ISS.
GO; GO:0007290; P:spermatid nuclear elongation; ISS. 54 AA; 6276 MW; 333C1399698A02CF CRC64; 54 AA; 6312 MW; BOA145EA5F07B65E CRC64; 01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last amocation update) 01-MAR.2004 (TrEMBLrel. 26, Last amocation update) Gl to S phase transition protein I (Fragment).

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"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                                                         43.7%;
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9 YEKFPLELKKRLKKL 23
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                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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Les 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=959;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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QEMRG6
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rachards S., Worley K.C., Hale S., Garrinci P., Frange C.,
Richards S., Worley K.C., Hale S., Garrinci A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shovchenko Y., Bouffard G.G.,
Makebley B. W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                 STRAIN=MSBB // DSM 3109 / ATCC 43589;
MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
Melson K.E., Clayton M.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Pacterson J.D., Melson W.C., Ketchum K.A.,
McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L.,
Heidelberg J.F., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                 Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 2; Length 69;
Pred. No. 3.4e+02;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete protecome, Hypothetical protein.
SEQUENCE 69 AA; 8037 MW; AE7243AA781F36CF CRC64;
                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
69 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).
                                                       Created)
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                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.88;
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54 YERFKNELEKKAKRI 68
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                                                                                                                                                           OrderedLocusNames=TM1386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 46.7 tes 7; Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                  Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TM1386; -.
                                                                                                                                                                                                                                      NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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098795
AC 098879
AC 098879
DT 01-JUD
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Gaps
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PubMed=14752164; DOI=10.1126/science.1093027;
Pendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
Sockett R.E., Schuster, S.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The German cDNA Consortium;
Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
Pobo G., Han M., Wiemann S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AL512716; CAC21657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio.
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Pred. No. 3e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                 4; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Flp1 pilus subunit) (Flp1 protein)
Name=flp1, OrderedLocusNames=Bd0119;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; BC001370; AAH01370.1; -.
SEQUENCE 41 AA; 4779 MW; 8FC81D54F7DB7527 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AA; 4894 MW; 8F990905E3DB7527 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein DKF2p547D192 (Fragment).
                                                                                                                                                                  Score 38; DB 2; I
Pred. No. 2.9e+02;
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SEQUENCE FROM N.A.
STRAIN=EI TOR Nis961 / Serctype 01;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
Medlaberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Gill S.R., Nelson R.B., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Vanechaeva M.D., Vamachevan J.J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D., Nierman W.C., White O., Salaberg S.L., Smith H.O., Colwell R.R., McRalanos J.J., Venter J.C., Fraeer C.M.;
Mekalanos J.J., Venter J.C., Fraeer C.M.;
Monter J.C., Fraeer C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARBAIN-Blotype gravis / NCTC 13129;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
Cardeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
De Zoysa A., Chillingworth T., Cronin A., Dowd L., Fellwell T.,
Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
Whitehead S., Barrell B.G., Parkhill J.;
"The complete genome sequence and analysis of Corynebacterium
diphtheriae NCTC13129.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium diphtheriae.
Bacteria; Actinomycetales; Corynebacterines; Corynebacterium.
NCBI_TaxID=1717;
                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23DD36A83207F256 CRC64;
                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome, Hypothetical protein.
SEQUENCE 31 AA; 3718 MW; 23DD36A832C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome, Hypothetical protein.
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EMBL; BX248358; CAE50048.1; -.
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                                                                                                                                                        Created)
                                                                                                        PRT;
                                                                                                                                               01-0CT-2000 (TEMBLrel. 15, 01-0CT-2000 (TEMBLrel. 15, 101-0LN-2003 (TEMBLrel. 24, 14)

Hypotherical protein v6387.

OrderedLocusNames=VC0387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 406:477-483(2000).
EMBL; AE004126; AAF93560.1;
PIR; E82329; E82329.
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11 FYKFSQKTLASVKRI 25
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Best Local Similarity 46...
7; Conservative
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                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
16 KKFKKKELK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholerae.
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                                                                                                          Q9KUX1
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                                                                RESULT 14
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                                                                                          Q9KUX1
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Nature 419:512-519(2002).

-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=12368865; DOI=10.1038/nature01099;
Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.B., Riedmiller S.B., Peldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                STRAIN=DSM 50701;
Schwudke D., Strauch E., Appel B., Linscheid M.;
"Putative pilus encoding gene cluster of Bdellovibrio bacteriovorus
                                                                                                                                                                                                                                       STRAIN=HI100;
Schwudke D., Strauch E., Appel B.;
"Sequence diversity in host independent B. bacteriovorus strain
HI100.";
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NCBL_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.7%; Score 38; DB 2; Length 62; 63.6%; Pred. No. 4.3e+02; rive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.5%; Score 37; DB 2; Length 25; 88.9%; Pred. No. 2.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                        Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX842646; CAE77792.1; -.
EMBL; AJS84609; CAE47773.1; -.
EMBL; AJS84609; CAHA18528.1; -.
SEQUENCE 62 AA; 6806 MW; 7556A7530E13BA5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 AA; 3157 MW; 7D03F492B4ADA65F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TYEMBLrel. 26, Created)
01-MAR-2004 (TYEMBLrel. 26, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 AA
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EMBL; AABL01002785; EAA20001.1; -.
genomic perspective.";
Science 303:689-692(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium yoelii yoelii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 YKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 FKNFSKKLLKN 14
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                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Q7R7R2

8

RESULT 13

OTRTR
AC QTRTR
AC QTRTR
DT 01-MA
DT 0

Matches

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Gaps

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Length 64; Indels

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Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                    30D43BA7C375FD0E CRC64;
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Pred. No. 6.2e+02;
3; Mismatches 2;
                                                                                      MOI. Microbiol. 45:1499-1513(2002).
EMBL; AL766847; CAD46491.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.5%;
53.3%;
                                                                                                                                                                                                                                                                            64 AA; 7653 MW;
                                                                                                                                                                                                                                                                                                                                                   42.58;
                                                                                                                                                                                                                                                                                                                                                                                  ilarity 58.3%;
Conservative
                                                                                  invasive neonatal disease.";
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nes 8; Conservative
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51 KFTKELIKSTKK 62
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                                                                                                                                                                                         Sagalist; gbs0847; -.
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
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SEQUENCE 64 AA:
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                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches
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           SO WE REPART SO WE WAY
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MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
Masignain V., Cieglewicz M.J., Eisen J.A., Peterson S.N.,
Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
Madoff L.C., Wolf A.M., Bennan M.J., Brinkac L.M., Daugherty S.C.,
DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=NEM316 / Serctype III;
MEDLINE=22245108; PubMed=12354221;
Glaeer P., Ruemiok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae.";
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                  Length 37;
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                                                                                                                                                         Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
93D59B9F82F993BE CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical protein SAG6829.
OrderedLocusNames=SAG0829;
                                                                       42.5%; Score 37; DB 2; I
44.4%; Pred. No. 3.7e+02;
iive 5; Mismatches 5;
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Pred. No. 6.2e+02;
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12 ALYEICKGQAVKSMERCG 29
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       4201 MW;
                                                                                                                  Local Similarity 44.4%;
les 8; Conservative
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1es 7; Conservative
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51 KFTKELIKSTKK 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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       AA;
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       SEQUENCE
                                                                              Query Match
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108E5Y2
108E5Y2
AC Q8E5Y
AC Q8E5Y
DT 01-MA
DT 0
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08E0A5
10 Q8E0AA
AC Q8E0AA
DT 01-MAD
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MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsay R.,
Sanchez A.J., Nichol S.T., Artsob H.;
"Genetic and serotypic characterization of Sin Nombre-like viruses in
Canadian Peromyscus maniculatus mice.";
virus Res. 75:75-86(2001).
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MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsay R.,
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NCBI_TaxID=37705;
                                                                                                                                                                                                                                 Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus
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Drebot M.D.A. Jr., Artsob H.A.;
Submitted M.D.A.27201) to the EMBL/GenBank/DDBJ databases.
EMBL; AF380928; AAK59325.1; -1
NON TER 1
NON TER 67
SEQUENCE 67 AA; 7804 MW; 82C4488B74F209E3 CRC64;
                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Glycoprotein G1 (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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67 AA
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Best Local Similarity
Matches 8; Conserv
                                      SEQUENCE FROM N.A.
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STRAINs-Newfoundland;
STRAINs-Newfoundland;
MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
Drebot M.A., Gavrilovskaya I., Mackow E.R., Chen Z., Lindsay R.,
Sanchez A.J., Nichol S.T., Artsob H.;
"Genelic and serotypic characterization of Sin Nombre-like viruses in
Virus Res. 75:75-86(2001).
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Sanchez A.J., Nichol S.T., Artsob H.; "Genetic and serotypic characterization of Sin Nombre-like viruses Canadian Peromyscus maniculatus mice."; Virus Res. 75:75-86(2001).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Glycoprotein Gl (Fragment).
Sin Nombre virus.
Viruses, ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
NCBI_TAXID=37705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
NCBI_TaxID=37705;
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Pred. No. 6.5e+02;
3; Mismatches 4; Indels
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Dreboc M.D.A. Jr., Artsob H.A.;
Submitted M.D.A. 2010) to the EMBL/GenBank/DDBJ databases.
EMBL; AF380927; AAK59324.1; -.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF380926; AAK59323.1; -
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53.3%; Pred. No. 6.5e+02;
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MEDLINE=93118242; PubMed=1475907;
Sonntag K.C., Darai G.,
"Characterization of the third origin of DNA replication of the genome of insect iridescent virus type 6.";
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STRAIN=Alberta;
MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
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Sanchez A.J., Nichol S.T., Artsob H.;
"Genetic and serotypic characterization of Sin Nombre-like viruses in Canadian Peromyscus maniculatus mice.";
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Sonntag K.C., Schnitzler P., Koonin B.V., Darai G.;
Forllo iridescent virus encodes a putative helicase belonging to a
distinct family within the 'DEAD/H' superfamily: implications for
evolution of large DNA viruses.";
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF380925; AAK59322.1; -.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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MEDLINE=95213160; PubMed=7698884;
Sonntag K.C., Schnitzler P., Janssen W., Darai G.
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Chilo iridescent virus
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of an invertebrate Chilo iridescent virus.";

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REDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963; MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963; Jakob N.J., Muller K., Bahr U., Darai G.; "Analysis of the first complete DNA sequence of an invertebrationalysis of the genome of Chilo iridescent
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SEQUENCE FROM N.A.
MEDLINE=89073752; PubMed=3201750;
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Fischer M., Schnitzler P., Identification and characterization of the repetitive DNA element in
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MEDLINE=92196996; PubMed=1549908;
Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
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MEDILINE=993831793; PubMed=10456793; DOI=10.1023/A:1008072319875;
MEDILINE=9393831793; PubMed=10456793; DOI=10.1023/A:1008072319875;
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J. Virol. 49:609-614(1984).
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STRAIN=MSB8 / DSM 3109 / ATCC 43589;
MEDLINE=99287316; PubMed=10360571; DOI=10.1038/20601;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L.A., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
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MEDLINE=93100280; PubMed=1464588;
Bassi R., Soen S.Y., Frank G., Zuber H., Rochaix J.D.;
"Characterization of chlorophyll a/b proteins of photosystem I from
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Photosystem I light-harvesting complex chlorophyll A/B protein
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GO; GO:0009538; C:photosystem I reaction center; IEA.
GO; GO:0015979; P:photosynthesis; IEA.
InterPro; IPR003666; PSI_PsaF.
Pfam; PF02507; PSI_PsaF.
SEQUENCE 31 AA; 3512 MW; 178F840F75F0E9E1 CRC64;
iridovirus: coding strategy of the genome of Chilo iv
Virology 286:182-196(2001).
EMBL, AF303741; AAK82162.1; -.
SEQUENCE 74 AA; 9009 MW; 284DC4CA8FEEFFCI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36.5; DB; Pred. No. 3.7e+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
25-0CT-2004 (Rel. 45, Last annotation
50S ribosomal protein L30.
Name=rpmD; OrderedLocusNames=TW1482;
Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 YKKFKKKLLKSL-KRL 17
                                                                                                                                                                                         42.58;
                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydomonas reinhardtii."
                                                                                                                                                     Query Match
Best Local Similarity 46...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 62.5
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                               2 LYKKFKKKLLKSLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 24
RL30_THEMA
ID RL30_THEMA
AC Q9XIJI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chan A., Conway A.B., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J. B., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B., Kim C.J., Koo H.L., Kremenetskian I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Lin S.X., Liu S.X., Liu Z.A., Lurso J.S., Maith R., Marziali A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Militscher J., Rowley D., Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.L., Heidelberg J.F., Sutton G.G., Fleischmann R.D., Bisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; "Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=RPL41B; OrderedLocusNames=At3g08520; ORFNames=T8G24.5, T8G24_5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the ribosomal protein L30P family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=RPL41A; OrderedLocusNames=At1g56045; ORFNames=T6H22.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.0%; Score 36.5; DB 1; Length 67; 42.3%; Pred. No. 7.7e+02; ive 2; Mismatches 2; Indels 1
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STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B5B43F2CE43C54BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P62120; P35015;
01-FBB-1994 (Rel. 28, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
605 ribosomal protein L41.
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2; Mismatches
                                                                                                                                     genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000517; Ribosomal L30.
InterPro; IPR005996; Ribosomal L30.
Pfam; PF00327; Ribosomal L30; I.
TIGRFAM9; TIGR01308; TPMD bact; I.
PROSITE; PS00634; RIBOSOWAL L30; I.
Complete proteome; Ribosomal protein.
SEQUENCE 67 AA; 7667 MW; B5B43F2CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKLKIKLVKSPIGYSWDQKDTVKRLG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001798; AAD36548.1; -.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B72248; B72248.
HSSP; P74909; 1BXY.
TIGR; TM1482; -.
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RL41 ARATH
ID RL41
DT 01-FE
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Rabano H., Salberge S.L., Schwartz J.R., Shinn P. Southwick A.M.,

Bun H., Tallon L.D., Tambunga G., Toriumi M.J., Toon C.D.,

R. Utterback T., Van Aken S., Vaybeeg M. Vydeckada V.S., Walker M.,

M. D., W. G., Framer C.M., Van Aken S., Vaybeeg M. Wydeckada V.S., Walker M.,

R. Sequence and analysis of chromosome I of the plant Arabidopsis

R. Salannian M. Jamick K. R. K. Reger M. M. Assorge W. Unneed M. Salannian D. B. Salannian M. Jamick K. R. Reger M. M. Assorge W. Unneed M. M. Bene W. Determined B. Salannian M. Jamick K. R. Reger M. M. Assorge W. Unneed M. Whether B. Determined B. Determined B. Salannian M. Jamick K. R. Reger M. M. Assorge W. Unneed M. Whether B. Determined B. Determined B. Determined B. Jamick M. Reger M. M. Rabids M. Wandler-Nuck C. Reger M. M. Rabids M. Whether B. Determined B. De
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SEQUENCE FROM N.A.
                                                                                           NCBI_TaxID=4513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Deltapine 62;
STRAIN=cv. Deltapine 62;
MEDLINE=95062728; PubMed=7972506; DOI=10.1104/pp.105.4.1449;
Turley R.B., Ferguson D.L., Meredith W.R.;
"Isolation and characterization of a cDNA encoding ribosomal protein 141 from cotton (Gossypium hissutum L.).";
Plant Physiol. 105:1449-1450(1994).
-: SIMILARITY: Belongs to the ribosomal protein L41e family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                       Gaps
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Pred. No. 3.6e+02;
3; Mismatches 2; Indels
                                                                                                                                                    Score 36; DB 1; Length 25; Pred. No. 3.6e+02; 3; Mismatches 2; Indels
                                                                                                             9AD629D4293C039E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         RI41_GOSHI

ID R141_GOSHI

AC P62122; P35015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 60S ribosomal protein 141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EL41_HORVU STANDARD; PRT; 25 AA. P62124; P35015; CFEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) 60S ribosomal protein L41.
EMBL; AY058053; AAL24161.1; -. PIR; T49214; T49214. InterPro; IPR007836; Ribosomal L41. Pfam; PF05162; Ribosomal L41; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S38425; S38425.
InterPro; IPR007836; Ribosomal L41.
Pfam; PF05162; Ribosomal_L41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gossypium hirsutum (Upland cotton)
                                                                                                                                                         41.4%;
58.3%;
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                                                                                                             25 AA; 3428 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.3%;
                                                                                                                                Query Match
Best Local Similarity 50...
7; Conservative
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4 KWKKKRMRRLKR 15
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                                                                                                                                                                                                                                                KFKKKLLKSLKR 16
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                                                                                         Ribosomal protein.
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                                                                                                             SEQUENCE
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ID RL41 H(
AC P62124)
DT 01-FEB
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DE 60S rii
GN Name=RI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hordeum vulgare (Barley).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
Triticeae, Hordeum.
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STRAIN-CY, Japonica / Nipponbare;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraer C.M.;
Coyza sativa chromosome 3 BAC OSJUBB0091J19 genomic sequence.";
Submitted (FEB-2001) to the FWBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the ribosomal protein L41e family.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                 "Barley L41 ribosomal protein from immature endosperm.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ribosomal protein L41e family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 25;
Pred. No. 3.6e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 AA; 3428 MW; 9AD629D4293C039E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ed. ORYSA STANDARD; PRT; 25 AA. B6125; P35015; O1-FEB-1994 (Rel. 28, Created) O1-FEB-1994 (Rel. 28, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) of standard protein L41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ001160; CAA04564.1; -.
InterPro; IPR007836; Ribosomal_L41.
Pfam; PF05162; Ribosomal_L41; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AC084320; AAK09215.1; -.
INICEPTO; IPR007836; Ribosomal L41.
Pfam; PF05162; Ribosomal_L41; Ī.
Ribosomal protein.
                                                                                                                                                                                                                                                                                STRAIN=cv. Bomi; TISSUE=Endosperm; Rasmussen S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.4%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S KFKKKLLKSLKR 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosomal protein.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STP1 BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=TNP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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STP1_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstandnuble European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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Pred. No. 3.6e+02;
3; Mismatches 2; Indels
                                                                   Length 25;
                                                                                                                         2; Indels
      9AD629D4293C039E CRC64;
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                                                         Score 36; DB 1; I
Pred. No. 3.6e+02;
3; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                              P62123; P35015;
01-FRB-1994 (Rel. 28, Created)
01-FRB-1994 (Rel. 28, Last sequence update)
01-FRB-1994 (Rel. 45, Last annotation update)
60S ribosomal protein L41.
                                                                                                                                                                                                                                                                                                                                                                                                        25 AA
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STRAIN=cv. Little Marvel; TISSUE=Root tip;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L47967; AAA79268.1; -.
InterPro; IPR007836; Ribosomal_L41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF05162; Ribosomal_L41; 1
   25 AA; 3428 MW;
                                                                   41.48;
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STRAIN=cv. SR1; TISSUE=Leaf;
Zhou X.-R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pisum sativum (Garden pea)
                               Query Match
Best Local Similarity 58...
7; Conservative
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4 KWKKKRMRRLKR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 58.3 (es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 KPKKKLLKSLKR 16
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KWKKKRMRRLKR 15
                                                                                                                                                                                     5 KFKKKLLKSLKR 16
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=RPL41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WOO H.H.;
                                                                                                                                                                                                                                                                                                                                        RESULT 29
REAL PEA
AC P62123; PE
DT 01-FEB-199
DT 01-FEB-199
DT 01-FEB-199
DT 25-OCT-20C
DE 60S ribose
CO Eukaryota,
CO This SWISS
CO This SWISS
CO This SWISS
CO This SWISS
CO Detween
CO Detween
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      SEQUENCE
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RL41_TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- SUBCELULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: Testis.
-1- SIMILARITY: Belongs to the nuclear transition protein 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequences and expression of cDNA clones for boar and bull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transition protein 1 and its evolutionary conservation in mammals."; Differentiation 40:184-190(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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MEDLINE=89378557; PubMed=2777004;
Kremling H., Luerssen H., Abham I.M., Klemm U., Tsaousidou S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim Y., Kremling H., Tessmann D., Engel W.; "Nucleotide sequence and exon-intron structure of the bovine transition protein 1 gene.";
                                                                                                                                                                                                                                      Score 36; DB 1; Length 25;
Pred. No. 3.6e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Spermatid nuclear transition protein 1 (STP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                25 AA; 3428 MW; 9AD629D4293C039E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             EMBL; U26255; AAA67297.1; -.
InterPro; IPR007836; Ribosomal_L41.
Pfam; PF05162; Ribosomal_L41; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93091245; PubMed=1457814;
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 58.3
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4 KWKKKRMRRLKR 15
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STP1 SHEEP
P22613;
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05-JUL-2004 (Rel. 44, Last annotation update)
Spermatid nuclear transition protein 1 (STP-1) (TP-1) (Testis-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley, TISSUE-Liver;
MEDLINE-89252920; PubMed=2524424; DOI=10.1016/0378-1119(89)90381-8;
Heidaran M.A., Kozak C.A., Kistler W.S.;
"Nucleotide sequence of the Stp-1 gene coding for rat spermatid
nuclear transition protein 1 (TP1): homology with protamine P1 and
assignment of the mouse Stp-1 gene to chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-75095670; PubMed=1112834;
Kistler W.S., Noyes C., Hsu R., Heinrikson R.L.;
"The amino acid sequence of a testis-specific basic protein that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kistler W.S., Noyes C., Heinrikson R.L.; "Partial structural analysis of a highly basic low molecular weight
                                                                                                                                                                                                                                                                                               protein; DNA-binding; Nuclear protein; Nucleosome core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE-Liver;
MEDLINE=88005793; PubMed=2820847;
Heidaran M.A., Kistler W.S.;
Hisolation of a cDNA clone for transition protein 1 (TP1), a major chromosomal protein of mammalian spermatids.";
Gene 54:281-284(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length 54;
Pred. No. 7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                            82C9452AD9134424 CRC64;
                                     GO; GO:0000786; C:nucleosome; ISS.
GO; GO:000542; P:chromatin silencing; ISS.
GO; GO:000542; P:chromatin silencing; ISS.
GO; GO:00009566; P:fertilization; ISS.
GO; GO:000012; P:sincleosome disassembly; ISS.
GO; GO:000012; P:single strand break repair; ISS.
GO; GO:00012; P:single strand break repair; ISS.
GO; GO:00012; P:single strand break repair; ISS.
GO; GO:000139; P:single strand break repair; ISS.
FILLEPPO; IPRO01319; TP1.
                                                                                                                                                                                                                                                                                                                                                                                                                     7.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated with spermatogenesis.";
J. Biol. Chem. 250:1847-1853(1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Testis;
MEDLINE=74167135; PubMed=4829397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                      41.4%;
53.8%;
EMBL; X16171; CAA34293.1; -.
                                                                                                                                                                                                                                                                                                                                                            54 AA; 6324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KKFKKKLLKSLKR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESTRIBLES 42
                                                                                                                                                                                                                                                   ProDom; PD010292; TP1; 1.
PROSITE; PS00541; TP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 53.8
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 12-54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                     Spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               basic protein)
                                                                                                                                                                                                                                                                                               Chromosomal
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STP1 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
protein from rat testis.";

Biochem. Biophys. Res. Commun. 57:341-347(1974).

-!- FUNCTION: In the elongating spermatids of mammals, the conversion of nucleosomal chromatin to the compact, nonnucleosomal form found in the sperm nucleus is associated with the appearance of a small set of basic chromosomal transition proteins.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Testis.
-!- SIMILARITY: Belongs to the nuclear transition protein 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, VARIANT GLY-27, PHOSPHORYLATION SITES SER-8; SER-35; SER-36 AND SER-39, AND MASS SPECTROMETRY.
MEDLINE=91249791; PubMed=2040274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Nuclear transition protein 1 from ram elongating spermatids. Mass spectrometric characterization, primary structure and phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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05-JUL-2004 (Rel. 44, Last annotation update)
Spermatid nuclear transition protein 1 (STP-1) (TP-1) (Protein T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cure alles (sneep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chirat F., Martinage A., Briand G., Kouach M., van Dorsselaer A.,
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 54;
Pred. No. 7.4e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 47 DAS -> SAD (in Ref. 3).
54 AA; 6264 MW; 333C152FD98A02CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0000786; C:nucleosome; ISS.
GO; GO:0000786; F:DNA binding; ISS.
GO; GO:0003642; P:chromatin silencing; ISS.
GO; GO:0009566; P:fertilization; ISS.
GO; GO:000917; P:single strand break repair; ISS.
GO; GO:000717; P:sperm motility; ISS.
InterPro; IPR001319; TP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        core; Spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 198:13-20(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M17096; AAA42260.1; -. PIR; A29095; BGRT. RGD; 3884; Tupl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X07284; CAA30264.1; -.
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Nuclear protein; Nucleosome
INIT_MET 0 0 0
CONFLICT 45 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02079; TP1; 1.
ProDom; PD010292; TP1; 1.
PROSITE; PS00541; TP1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 RKYRKSSLKSRKR 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sites of two variants.";
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Ovis aries (Sheep)
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PIR:

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=SARG / CCMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1732211100;
Dufreene A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
Makazvova K.S., Ostrowski M., Oztes S., Robert C., Rogozin I.B.,
Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome.";
Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
EMBL; AE017165; AAQ00438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J. Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of the T. tengcongensis genome.";

Genome Res. 12:689-700(2002).
                                                                                        Prochlorococcus marinus.
Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2; Length 54;
Pred. No. 7.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2; Length 61;
Pred. No. 8.3e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
SEQUENCE 54 AA; 6680 MW; 8E3F7AED122ABCD5 CRC64;
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Interpro; IPR010982; Lambda_like_DNA.
Complete proteome.
SEQUENCE 61 AA; 7096 MW; 1F7B325AB545F606 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBRB55;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
                        Last annotation update)
    01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.4%;
66.7%;
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Matches 7; Conservative
                                                               OrderedLocusNames=Pro1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 66.7
Matches 8; Conservative
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49 KKYKEKIKKILK 60
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                                            Predicted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                               Prochlorococcus.
                                                                                                                                                     NCBI_TaxID=1219;
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FUNCTION: In the elongating spermatids of mammals, the conversion of nucleosomal formatin to the compact, nonuncleosomal form found in the sperm nucleus is associated with the appearance of a small set of basic chromosomal transition proteins.

SUBCELLULAR LOCATION: Nuclear.

TISSUE SPECIFICITY: Testis.

SIMILARITY: Belongs to the nuclear transition protein 1 family.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal protein; Direct protein sequencing; DNA-binding;
Nuclear protein; Nucleosome core; Phosphorylation; Polymorphism;
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Pred. No. 7.4e+02;
3; Mismatches 3; Indels
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Pred. No. 7.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133544; CAB96731.1; -.
SEQUENCE. 54 AA; 6389 MW; 611C1972916FCA61 CRC64;
                                                                                                                                                                GO; GO:000766; C:nucleosome; ISS.
GO; GO:0003677; F:DNA binding; ISS.
GO; GO:0003677; F:DNA binding; ISS.
GO; GO:000566; P:fertilization; ISS.
GO; GO:000537; P:ncleosome disassembly; ISS.
GO; GO:000012; P:single strand break repair; ISS.
GO; GO:000012; P:sperm motility; ISS.
GO; GO:0007290; P:spermatid nuclear elongation; ISS.
InterPro; IPPR001319; TP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C -> G.
82C945304DCAFD24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DJ71N10.1.2 (Novel protein (Putative isoform 2)).
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Phosphoserine.
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01-OCT-2003 (TrEMBLrel. 25, Created)
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35 35
36 36
27 27
54 AA; 6344 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 RKYRKSSLKSRKR 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD010292; TP1; 1.
PROSITE; PS00541; TP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 KKLKKKLVRS 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Williams S.;
                                                                                                                                                 S16075; BGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=dJ71N10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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MOD RES
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Gaps

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RESULT 35 Q7VAR3

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Unknow protein.
Name-P0615D12.12;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee I.-M., Martini M., Marcone C., Zhu S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
C -1- SIMILARITY: Belongs to the ribosomal protein L15P family.
R MSL; ANT97695; AA42342.1; -.
R GO; GO:0005840; C:ribosome; IEA.
GO; GO:0005410; C:ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR001196; Ribosomal_L15.
R PROSTIE; PS00475; Ribosomal_L15; 1.
R Ribonucleoprotein; Ribosomal_Drotein.
M Ribonucleoprotein; Ribosomal_protein.
J NON TER.
J SEQUENCE 67 AA; 7559 MW; D99345196B939430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15023941; DOI=10.1099/ijs.0.02697-0;

Lee I.M., Martini M., Marcone C., Zhu S.F.;

"Classification of phytoplasma strains in the elm yellows group

(165rV) and proposal of 'Candidatus Phytoplasma ulmi' for the

phytoplasma associated with elm yellows.";

Int. J. Syst. Evol. Microbiol. 54:337-347(2004).
                                                                                                                                                                                                                                                                             Chow T. Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M., Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R., Chang Y.-T., Chang C.-H., Hang C.-I., Han S.-Y., Haiso S.-H., Haing J.-N., Hau C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Le Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W., Wu H.-P., Shaw J.-F.;

"Oryza sativa PAC P0615D12 genomic sequence.";

Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AC137004; AAJ44280.1; -.

SEQUENCE 65 AA, 7579 WW; 2EFAB59326711FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 65;
Pred. No. 8.8e+02;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.4%; Score 36; DB 2; Length 67; Best Local Similarity 58.3%; Pred. No. 9.1e+02; Matches 7; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jujube witches'-broom phytoplasma.
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; Candidatus Phytoplasma.
NCBI_TaxID=230569;
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ribosomal_protein L15 (Fragment).
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Similarity 50.0%;
6; Conservative
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51 LWRKFRVKILKN 62
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                    NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                             MEDITIE=97396144; PubMed=9245698; DOI=10.1006/bbrc.1997.7019; Tanaka T., Tanaka M., Mitsui Y.; Tanaka T., Tanaka M., Mitsui Y.; "Analysis of expressed sequence tags (ESTs) of the parasitic protozoa Entamoeba histolytica"; Biochem. Biophys. Res. Commun. 236:611-615(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=96198088; PubMed=8626421; DOI=10.1074/jbc.271.11.6273;
Puzianowska-Kuznicka M., Shi Y.B.;
"Nuclear factor I as a potential regulator during postembryonic organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2; Length 62;
Pred. No. 8.5e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.4%; Score 36; DB 2; Length 62; 50.0%; Pred. No. 8.5e+02; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shi Y.-B.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L43150; AAB38018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E20AD05F623137CA CRC64;
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                             Last sequence update)
Last annotation update)
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Last annotation update)
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Last sequence update)
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     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                  Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.
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01-OCT-2003 (TrEMBLrel. 25, La
Nuclear factor I-C2 (Fragment)
Name-nfil-C2;
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Best Local Similarity 53.8%;
Matches 7; Conservative
  01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-NOV-1998 (TrEMBLrel. 08,
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01,
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YKKHEKKMTKEEER
                                                                                        K18 antigen (Fragment).
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NCBI_TaxID=8355;
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les 7; Conserv
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                                                                                                                                                                          NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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SEQUENCE
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Q65WT3
ID Q65WT3
AC Q65WT3;
DT 25-OCT-;
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Q91801
ID Q9180
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Leu H.-L.,

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STRAIN=5601 (Serogroup Icterohaemorrhagiae / Serovar lai, MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597; Ren S.-X., Pu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H., Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F., Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F., Zhang Y., Zhu G.-P., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W., Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                       Lee I.-M., Martini M., Marcone C., Zhu S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ribosomal protein L15P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing."; Nature 422:888-931(2003). EMBL; AE011467; AAN50255.1; -.
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                                                                                                                                                                                                                           EMBL; AY197693; AAP42338.1; -... GO; GO:0005840; C:ribosome; IRA. GO; GO:0005735; F:structural constituent of ribosome; IEA. GO; GO:0006412; F:protein biosynthesis; IEA. InterPro; IPR01196; Ribosomal_L15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2; Length 67;
Pred. No. 9.1e+02;
3; Mismatches 2; Indels
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Last annotation update)
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Q63CR5;

25-OCT-2004 (TrEMBLrel. 28, Created)

25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
phytoplasma associated with elm yellows.";
Int. J. Syst. Evol. Microbiol. 54:337-347(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 AA.
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                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00256; L15; 1.
PR051TE; PS00475; RIBOSOMAL L15; 1.
Ribonucleoprotein; Ribosomal protein.
1.
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Query Match
Beet Local Similarity 58.30,
Beet Local Similarity 58.30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LYKKFKK---KLLKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 53 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=173;
                                                                                                                  STRAIN=CLY-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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ID O6
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DT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee I.M., Martini M., Marcone C., Zhu S.F.;
"Classification of phytoplasma strains in the elm yellows group (165rV) and proposal of 'Candidatus Phytoplasma ulmi' for the phytoplasma associated with elm yellows.";
Int. J. Syst. Evol. Microbiol. 54:337-347(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CLY-5;
PubMed=15023941; DOI=10.1099/ijs.0.02697-0;
Lee I.M., Martini M., Marcone C., Zhu S.F.;
"Classification of phytoplasma strains in the elm yellows group (16SrV) and proposal of 'Candidatus Phytoplasma ulmi' for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes, Mollicutes, Acholeplasmatales, Acholeplasmataceae, Candidatus Phytoplasma.
NCBI_TaxID=230568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cherry lethal yellows phytoplasma.
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
Acholeplasmataceae; Candidatus Phytoplasma.
NCBL TaxID=230567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 AA; 7603 MW; D99345196B952280 CRC64;
                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-ORT-2004 (TrEMBLrel. 26, Last annotation update)
Ribosomal protein L15 (Fragment).
Name-rpl15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 2; I
Pred. No. 9.1e+02;
                                                                                                                                                                                                   67 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=PY-In;
PubMed=15023941; DOI=10.1099/ijs.0.02697-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2003 (TrEMBLrel. 25, Created) 01-0CT-2003 (TrEMBLrel. 25, Last seq 01-0CT-2004 (TrEMBLrel. 26, Last ann Ribosomal protein L15 (Fragment).
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.4%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.3%,
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Peach yellows phytoplasma
                              |||||::|: | |
FKKKIIKNNKSL 28
PKKKLLKSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 FKKKIIKNNKSL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 PKKKLLKSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE
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Q7X4E6;
                                                                                                                                                                                                                              Q7X4E4;
                                                                                                                                                                                                   Q7X4E4
                                                                                                                                 RESULT 41

07X4B4

1D 07X4B4

1D 07X4B4

1D 07X4B4

1D 07X4B4

1D 07X4B4

1D 07X4B4

1D 01-0C

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0784E6
10784E6
AC 07784E
AC 07784E
DT 01-0C
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"Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Blidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                    Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin E., Tice H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.5; DB 2; Length 63;
Pred. No. 1e+03;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.2%; Score 35; DB 2; Length 20; 47.1%; Pred. No. 4.1e+02; Live 2; Mismatches 7; Indels
                                                                   Bacillus cereus ZK.
Bacteria, Firmicutes, Bacillales, Bacillus
                                                                                                                                                                                                                                                                   "Complete genome sequence of Bacillus cereus ZK.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000001; AAU18547.1; -
                                                                                                                                                                                                                                                                                                                                                             63 AA; 7225 MW; 90E8EAA236DF779C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA; 2477 MW; E649CBE384302759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=17XNL;
PubMed=12368865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
EMBL; AABLO1000770; EAA22261.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|: | | |::|| | 44 AMYRSY-TKLEKTIKRAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALYKKFKKKLLKSLKRLG 18
                                              Name=ccdC; ORFNames=BTZK1707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKKFKKKLLKSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 47.1
Matches 8; Conservative
                           protein ccdC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 63 AA: 72
                                                                                                            NCBI_TaxID=288681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                             SEQUENCE FROM N.A.
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                           Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 45
O7RXX5
AC Q7RXX
AC Q7RXX
AC Q7RXX
DJ 01-MA
DT 01-MA
RA Shall
RA Shall
RA Shall
RA Carlt
CCC -1-C
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SLYRIFKKKKKKKTXNL 18

Search completed: May 16, 2005, 08:30:19 Job time: 77.8793 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 54.1293 Seconds (without alignments) 92.887 Million cell updates/sec Run on:

US-09-648-816B-4 64 Title: Perfect score:

1 ARYKKFKKKLLKS 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

1066881 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 74 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_16Dec04:* 1: genesem1000geneseqp1980s:* geneseqp1990s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Antimicro	Rabbit pl	Antimicro	Antimicro	Rabbit pl	Rabbit pl	Antimicro	Rabbit pl	Antimicro	Rabbit pl	Peptide a	Antimicro	Rabbit pl	Peptide a	Peptide a	Peptide a	Rabbit pl	Rabbit pl	Antimicro						
	Description			-	_				_	~	•	_		-	_											
		Aay57466	Abg69890	Aay57503	Abg69927	Aay57505	Abg69929	Aay57465	Abg69889	Aay57501	Aay57499	Abg69923	Abg69925	Aay57502	Abg69926	Aay57496	Abg69920	Ad1702	Aay57497	Abg69921	Ad1702	Ad170277	Ad170278	Abg69990	Abg69992	Aay57468
SUMMAKIES	αI	AAY57466	ABG69890	AAY57503	ABG69927	AAY57505	ABG69929	AAY57465	ABG69889	AAY57501	AAY57499	ABG69923	ABG69925	AAY57502	ABG69926	AAY57496	ABG69920	ADL70275	AAY57497	ABG69921	ADL70276	ADL70277	ADL,70278	ABG69990 ·	ABG69992	AAY57468
	DB	2	Ŋ	7	Ŋ	7	Ŋ	0	Ŋ	7	N	Ŋ	ß	N	Ŋ	0	Ŋ	œ	N	ហ	œ	œ	œ	Ŋ	Ŋ	7
de	Length	13	13	18	18	18	18	18	18	19	19	19	19	20	. 20	25	52	33	35	35	36	37	39	40	40	13
	Query Match	100.0	100.0	100.0	100.0	93.8	93.8	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	89.1	84.4
	Score	64	64	64	64	9	9	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	57	54
	Result No.		7	٣	4	'n	9	7	00	o	10	11	12	13	14	15	16	17	. 18	19	20	21	22	23	24	25

	Abg69924 Rabbit pl Abg69928 Rabbit pl Aay57469 Antimicro Abg69893 Rabbit pl	-100	Abg69894 Rabbit pl Aar13927 Cationic Aaw10351 Antibacte	Aay57508 Antimicro Aay68001 Antibacte Abg69932 Rabbit pl	Aaw10352 Antibacte Aay68002 Antibacte Aay57467 Antimicro Abg69891 Rabbit pl
ABG69892 AAY57500 AAY57504	ABG69924 ABG69928 AAX57469 ABG69893	AAY57471 ABG69895 AAY57470	ABG69894 AAR13927 AAW10351	AAY57508 AAY68001 ABG69932	AAW10352 AAY68002 AAY57467 ABG69891
13 5 18 2 18 2				18 2 18 3 18 5	19 2 14 2 14 2 14 5
84 82.8 82.8	82.8 82.8 75.0	73.4	71.9 68.8 68.8	68.8 68.8 68.8	68.8 68.8 67.2 67.2
53 53	5 4 4 5 3 3 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 6 4 4	4 4 4 4 4 4	4 4 4 4 4 4 6 6
26 27 28	30 31 32	3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	36 37 38	39 4 40 11	4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5

## ALIGNMENTS

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. (HARB-) HARBOR-UCLA RES & EDUCATION INST. Antimicrobial peptide RP-2 SEQ ID NO:4. AAY57466 standard; peptide; 13 AA. 98US-00025319. 99WO-US003350. 25-FEB-2000 (first entry) Oryctolagus cuniculus Shen AJ; 18-FEB-1998; 17-FEB-1999; WO9942119-A1. 26-AUG-1999 Yeaman MR, Synthetic. AAY57466; AAY57466 

WPI; 1999-527417/44.

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure; Page 107; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZENENB and its derivatives selected from XZBENENBS, BXZXZB, XBEXZENBX and BEXZBEXZ; and (b) a second peptide template XBEX may account the group consisting of XBEXENBX, BXXENSB, XBEXZENB, and (b) as a cond peptide template XBEX bear of derivatives selected from the group consisting of XBEXENBX, BXXENSB, XBEXZENB, and (b) at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid core sequence (derived from 150 amino acida containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, runcations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also contained are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in thoology techniques. Antimicrobial peptides of prior art have generally
                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                     Gaps
                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
                                                                                                                     100.0%; Score 64; DB 2; Length 13; 100.0%; Pred. No. 0.0016; rive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 128; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                          ABG69890 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-2001; 2001WO-US041877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                            1 ARYKKFKKKLLKS 13
                                                                                                                                                                                                                                                   1 ARYKKFKKKLLKS 13
                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus.
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                                                                                Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200255554-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   ABG69890;
                                                                                                                                                                                                                                                                                                                RESULT 2
ABG69890
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been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                 Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                               ;
0
                                                                                                                       Length 13;
                                                                                                                                             0; Indels
                                                                                                                       Score 64; DB 5;
Pred. No. 0.0016;
                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                               Antimicrobial peptide RP-1-2R SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                             AAY57503 standard; peptide; 18 AA.
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                                                                                                                         100.0%;
100.0%;
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                                                                                                                                                                                       1 ARYKKFKKKLLKS 13
                                                                                                                                               13; Conservative
                                                                                                                                                                    1 ARYKKFKKKLLKS
                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527417/44.
                                                                                                                         Query Match
Best Local Similarity
                                                                                                    Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                    AAY57503;
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The invention relates to an antimicrobial peptide composition for the second and the composition of the invention relates to an antimicrobial protein), and retroners, the invention relates to combinations, fusions and their derivatives from possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of entimicrobial antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in considered to have undesirable toxicity, immunogenicity and short conventions and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibicitic resistance. They exhibit lower inherent mammalian cell toxicities and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an antimicrobial peptide composition for use
                                                                                                                Gaps
                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rabbit platelet microbicidal protein, PMP-2, based peptide #39
                                      Length 18;
Score 64; DB 2; Lengtn 19, Pred, No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG69927 standard; peptide; 18 AA
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                                      100.0%;
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Synthetic.
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                           Query Match
Best Local Similarity
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Matches
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ABG 9927

ID 69927

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXENB and its derivatives selected from XZBBZBXENB. BXZXZB, XBBXZXBB and its derivatives selected from the group consisting of XBBXBX, BXXZB, XBBXXZB, XBBXZBBX; and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBX, XBBXXBB, BXXBXB, XBBXXBB, and and consisting of XBBXBX, XBBXXBB, BXXBXB, BXBBXXB, and and activatives selected from the group consisting of XBBXXBBX, XBBXXBB, BXXBXB, BXBBXXB, and and activatives and where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX57463 to AAY57557 represent sequences used in the exemplification of the present invention
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overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                   Score 64; DB 5; Length 18; Pred. No. 0.0021; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HARB-) HARBOR-UCLA RES & EDUCATION INST
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                                                                                                                                                                                                                                                                                                                                        AAY57505 standard; peptide; 18 AA.
                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Les 13; Conservative
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Matches 12; Conserv
                                                                                Sequence 18 AA;
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12; Conservative

Matches

Score 60; DB 5; Length 18; Pred. No. 0.0093;

93.8%;

Query Match Best Local Similarity

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ARYKKFKKLLKS

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New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                            Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                              Rabbit platelet microbicidal protein, PMP-2, based peptide #41
                                                                                                                                                                                                                                                    (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                           ABG69929 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                        Example; Page 72; 221pp; English.
                                                                                                                                                                                                                   24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                   25-AUG-2000; 2000US-00648816
                                                                             (first entry)
1 ARYKKFKKFLKS 13
                                                                                                                                                        Oryctolagus cuniculus.
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                                                                                                                                                                                                  18-JUL-2002
                                                                                                                                                                                                                                                                     Yeaman MR,
                                                                                                                                                                Synthetic
                                                            ABG69929;
                          RESULT 6
ABG69929
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euthorytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial against bacteria and fungi, agents in combination with other specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in functions of leukocytes, as disinfectants or preservatives for use in bology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbicidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13.74 containing an amino acid and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of invention relates to an antimicrobial peptide composition for use

Sequence 18 AA

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against activity or for potentiating antimicrobial agents active against conganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXXZXB, XBBXXZBB, and BMXZBBXZ, and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBX, XBBXXBB, BXXBXB, XBBXXXBB, and their derivatives selected from the group consisting of XBBXBX, XBBXXBB, BXXBXXB, ARBZXXBB, and their dark one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells.AAX57451 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                           Antimicrobial; metapeptide; PMP-2; platelet microbicidal proteir antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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Pred. No. 0.028;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                          Antimicrobial peptide RP-1 SEQ ID NO:3.
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                                                                                                                      AAY57465 standard; peptide; 18 AA.
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ilarity 92.3%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-527417/44.
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les 12; Conserv
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                                                                                                                                                                                                                                                                                                                 Synthetic.
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1 ALYKKFKKKLLKS 13

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and retromers, extensions, combinations of the periods described above, and retromers, extensions, combinations of the solutions; and (2) antimicrobial peptides for potentiating antimicrobial activity of entimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or reserve efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular belongy techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 anino acids cortaining a 7-13 amino acid core sequence (derived from PMP-1, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                    Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                         Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.1%; Score 57; DB 5; Length 18; 92.3%; Pred. No. 0.028; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                               ABG69889 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 24; Page 71; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-AUG-2000; 2000US-00648816.
                                                                                                                                       (first entry)
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                  WO200255554-A2
                                                                                                                                         21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2002.
                                                                                            ABG69889;
RESULT 8
                           ABG69889
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXENEM and BRXZBRXING SELECTED FOR XZBBZBRXB, BXXZXBX, MBRXZBBX and BRXZBBXZ, and (b) selected from XZBBZBRXB, XBBXXBBX, WASZR, XBBXXBBX, WASZR, ABXZBBX, WASZR, MBXZBBX, BXXBXXBBX, and (b) group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXBB, and A Least one non-polar hydrophobic amino acid, Z at least one aromatic amino acid, and where B, and Z amy be separated by one or more other amino acid. The peptides can be used to treat bacterial and fungal neutrophils. The peptides also increase the antimicrobial activity of apoptosis of microbial effect cellular disruption and rapid apoptosis of microbial cells. AAVS7463 to AAVS7557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                  Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in the exemplification of the present invention
                                                                                                                                    Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 59; 166pp; English.
                                AAY57501 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                             99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                             98US-00025319
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92.3%;
                                                                                                25-FEB-2000 (first entry)
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                                                                                                                                                                                                                                        Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-527417/44.
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les 12; Conserv
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                                                                                                                                                                                                                                                                                                                                             17-FEB-1999;
                                                                                                                                                                                                                                                                        W09942119-A1
                                                                                                                                                                                                                                                                                                           26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeaman MR,
                                                                                                                                                                                                                      Synthetic
                                                                  AAY57501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
RESULT 9
                 AAY57501
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AAY57499 standard; peptide; 19 AA.

RESULT 10

25-FEB-2000 (first entry)

AAY57499;

AAYS7499 ID AAYS XX AAC AAYS XX DT 25-F

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Gaps ö

Synthetic

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The invention relates to an antimatorbial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from 150 maino acids containing a 7-13 amino acid core sequence (derived from 150 maino acids containing a 7-13 amino acid core sequence (derivatives from 150 maino acids combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also conformed are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance the tenantimicrobial antimicrobials, agents that enhance the antimicrobial activity of conventional antimicrobials, agents that enhance the antimicrobial for specifically against bacteria and fungi, agents in combination with other functions of leukocytes, as disinfectants or preservatives for use in foolay techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and comment in a rabbit in mammalian cell toxicity, immunogenicity, and shortness of effectiveness due to biodegradation, retaining activity in plasma and companies.
                                                                                                                                                                                                                                                                                                                                                                                                                           New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabbit platelet microbicidal protein, PMP-2, based peptide #37.
                                                                                                                                                                                                                                                     (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example, Page 71-72; 221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple antibiotic resistance.
                                                                                                                                           24-AUG-2001; 2001WO-US041877
                                                                                                                                                                                                   25-AUG-2000; 2000US-00648816
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92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 AA;
                          WO200255554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG69925;
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셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZZXEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXXZXB, XBBXZXBB and its derivatives accord peptide template XBBXXXB, BXXZXB, XBBXXXBB, and BBXZBBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXXBB, BXXBXXB, MSBZXXBB, and C a second peptide template ABBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and C at least one non-polar hydrophobic amino acid, Z at least one positively charged amino acid; X a mino acids and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AMST7463 to AAMST757 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                  Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; DB 2; Length 19;
Pred. No. 0.03;
0; Mismatches 1; Indels
                             Antimicrobial peptide OC-RP-1 SEQ ID NO:37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 58; 166pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      against bacteria and fungi
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                                                                                                                                                                                                      Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeaman MR,
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Query Match Matches

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Gaps

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DB 5; Length 19; 1; Indels

Score 57; DB 5; Pred. No. 0.03; 0; Mismatches

Synthetic

Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40.

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, runcations, extensions, combinations, funcions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial activity of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of prior art have generally because are based upon natural antimicrobial peptides of prior and and broad are based upon natural antimicrobial peptides and and peptides of the preservatives and ender the ender of an ender invention are based upon natural antimicrobial peptides and and peptides and ender invention are based upon natural antimicrobial peptides and and peptides and ender invention are based upon natural antimicrobial peptides and and peptides and ender invention are based upon natural antimicrobial peptides and ender ender invention and prave and state and ender ender and ender ender and ender ender and en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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Pred. No. 0.03;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 72; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nultiple antibiotic resistance.
                                                                                                                                                                                                                                                24-AUG-2001; 2001WO-US041877.
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92.3%;
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                                                                         Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-590659/63.
                         mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 AA;
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                                                                                                  Synthetic
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  EXXXE
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25-FEB-2000 (first entry)

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activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXXB and its derivatives selected from XZBBZBXBXB. BXZXB. BXXZXB. XBBXXZBX and its derivatives selected from the group consisting of CHAPTER SERVERS. SERVERSES and Chair derivatives selected from the group consisting of XBBXBXX. BXXXBXB, XBBXXXBBX, and (b) XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7461 to AAXS757 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                           Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 2; Length 20;
Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                  (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69926 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                 98US-00025319.
                                                                                                                                                                                                                  99WO-US003350
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92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ARYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ALYKKFKKKLLKS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 12; Conservative
                                                                                                               Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus.
Synthetic.
                                                                                                                                                                                                                                                                                                                    (eaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
                                                                                                                                                                                                                  L7-FEB-1999;
                                                                                                                                                WO9942119-A1
                                                                                                                                                                                                                                                   18-FEB-1998;
                                                                                                                                                                                 26-AUG-1999
                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and retromers, extensions, combinations and fusions; and retromers, extensions, combinations and fusions; and retromers, extensions, combinations and fusions; and antimicrobial apptides for potentiating antimicrobial activity of leukocytes against useful as individual antimicrobial agents, actually against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in functions of leukocytes, as disinfectants or preservatives for use in conventional antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PWP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                  The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above,
                                                                                                                                                                                                                                         peptide composition for the prevention and treatment of by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                       Example; Page 72; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57496 standard; peptide; 25
                                                                                                                                                                                                                                                                       multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.1%;
                                                                             24-AUG-2001; 2001WO-US041877
                                                                                                             25-AUG-2000; 2000US-00648816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ARYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ALYKKFKKKLLKS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 92.3
les 12; Conservative
                                                                                                                                                                                                           WPI; 2002-590659/63.
                                                                                                                                                                                                                                                        infections caused
                                                                                                                                                                                                                                         antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20 AA;
             WO200255554-A2
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                                             18-JUL-2002
                                                                                                                                                                              Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57496;
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IID AAY5
XX
AC AAX5
XX
DT 25-F
XX
XX
DB Anti
XW Anti
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Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

(eaman MR, Shen AJ; WPI; 1999-527417/44.

99WO-US003350 98US-00025319

.7-FEB-1999; 18-FEB-1998;

Oryctolagus cuniculus.

Synthetic

W09942119-A1.

26-AUG-1999

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activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXKB and its derivatives selected from XZBZBXKBXB and its derivatives as second peptide template XBXX MXXBX BXXXXBXB and BBXZBBXZ; and (b) a second peptide template XBXX MXXB BXXXBBX and BBXZBBXZ; and (b) group consisting of XBBXBXX BBXX BBXXXBBX, XBBXXXBB, and XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular distuption and rapid apoptosis of microbial cells. AAYS7463 to AAYS7557 represent sequences
                                                 The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rabbit platelet microbicidal protein, PMP-2, based peptide #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57; DB 2; Length 25;
Pred. No. 0.038;
0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                used in the exemplification of the present invention
Disclosure; Page 126; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG69920 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 89.1
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ARYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALYKKFKKKLLKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200255554-A2
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Edwards JE, Brass EP;

Yount NY,

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New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                             (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1; 103pp; English
                                                               20-AUG-2003; 2003WO-US026405
                                                                                               20-AUG-2002; 2002US-00225562
                                                                                                                                                                                           WPI; 2004-226740/21
   WO2004017985-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1998;
                                 04-MAR-2004
                                                                                                                                                               reaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY57497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                  The invention features to an antimulational peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, placelet microbiocidal protein), and retromers,
truncations, extensions, combinations, funions and their derivatives. The possible structures are fully described in the specification. Also concluded are (il) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungio. The antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial complexity of functions of leukocytes, as disinfectants or preservatives for use in conventional antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short of a pased upon natural antimicrobial peptides of that pased upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic or esistance. They exhibit lower inherent mammalian cell toxicity and shortness of duration of effectiveness due to biodegradation, relaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, realistances of secture of secure is a rabbit pwe and antimicrobial peptides are abased upon natural antimicrobial peptides that the present sequence is a rabbit pwe antimicrobial peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                             New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                           invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protide; antibiotide; antimicrobial; interleukin-8; Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; DB 5; Length 25;
Pred. No. 0.038;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15. .16
/note= "Cleaved by V8 protease"
                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL70275 standard; peptide; 33 AA.
                                                                                                                                                                                        Example; Page 70; 221pp; English
                                                                                                                                                               multiple antibiotic resistance.
25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.1%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ARYKKFKKKLLKS 13
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les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide antibiotide PT-1.
                                                             Feaman MR, Shen AJ
                                                                                             WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADL70275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 17
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The present sequence is that of Protide-1 (PT-1), a peptide antibiotide with distinct effector and activator domains. PT-1 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for staphylococcus VB protease. PT-1 was designed to be cleaved into 2 designed to exert antimicrobial activity less than that of RP-1 in the presence of VB protease. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of VB protease produced by Staphylococcus aureus. Thus, PT-1 was designed to exert optimal antimicrobial activity in the context of infections due to staphylococcus called phase synthesis. It is an example of context-activated protides of the invention that have 2 or nore corresponding activator sites that can each initiate or amplify the biological functions and one or more effectors with individual distinct biological functions and one or more effectors with individual distinct biological functions and one or more effectors with individual distinct biological functions and one or prological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 8; Length 33;
Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY57497 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.1%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US003350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALYKKFKKKLLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9942119-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY57497;
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Example; Page 71; 221pp; English.

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBZBXBXBX, BXXZXB, XBBXXXBX and BXZBBXZ; and (b) a second peptide template XBBXXXBX, BXXXBX, XBBXXXBS, and consisting of XBBXBXBX, XBBXXBX, BXXXBX, XBBZXXBB, and XBBXXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX757463 to AAX5757 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                      Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rabbit platelet microbicidal protein, PMP-2, based peptide #33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 2; Length 35;
Pred. No. 0.052;
0; Mismatches 1; Indels
              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                            Disclosure; Page 126; 166pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-AUG-2000; 2000US-00648816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ARYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 89.1
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen AJ;
                                                  Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-590659/63.
                                                                                     WPI; 1999-527417/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35 AA;
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                                                  Yeaman MR,
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Gaps

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and retromers, extensions, combinations and fusions; and (2)
antimicrobial peptides for potentiating antimicrobial activity of
antimicrobial peptides for potentiating antimicrobial activity of
antimicrobial peptides are useful as individual antimicrobial agents in combination with other
antimicrobial, agents that enhance, potentiate or restore efficacy of
conventional antimicrobials, agents that enhance the antimicrobial
cunctions of leukocytes, as disinfectants or preservatives for use in
thurstions of leukocytes, as disinfectants or preservatives for use in
conventional antimicrobial peptides of prior art have generally
been considered to have undesirable toxicity, immunogenicity and short
care based upon natural antimicrobial peptides of the present invention
are based upon natural antimicrobial peptides that have potent and broad
spectrum activity against pathogens exhibiting multiple antibiotic
resistance. They exhibit lower inherent mammalian cell toxicities and
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                                                               against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protide; antibiotide; antimicrobial; interleukin-8.
                                                     The invention relates to an antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16. .17
/note= "Cleaved by C3 convertase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 5;
Pred. No. 0.052;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brass EP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yount NY, Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL70276 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2003; 2003WO-US026405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.1%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 92.30.
Best Local 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide antibiotide PT-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ARYKKFKKKLLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004017985-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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The present sequence is that of Protide-2 (PT-2), a peptide antibiotide with distinct effector and activator domains. PT-2 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2 distinct effectors in the presence of C3 convertase. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of C3 convertase. Dut equivalent to or exceeding that of RP-1 in the presence of C3 convertase. Thus, PT-2 was designed to exert optimal activity in the context of activation of one of the inhalt orbial activity in the context of activation of one of the complement pathways that make up the complement system, which is part of the innate immune response to antigen exposure. PT-2 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad provides of protides are useful in the diagnosis, prophylaxis and therapy of a broad
                                 New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                     Claim 1; SEQ ID NO 2; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                range of pathological conditions.
WPI; 2004-226740/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-2004
                                                                       condition.
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ö Gaps ö 8; Length 36; 1; Indels Protide; antibiotide; antimicrobial; interleukin-8. Score 57; DB 8; Pred. No. 0.053; 0; Mismatches Location/Qualifiers ADL70277 standard; peptide; 37 AA 89.1%; (first entry) 1 ARYKKFKKKLLKS 13 19 ALYKKFKKKLLKS 31 Peptide antibiotide PT-3. Local Similarity 92.3 es 12; Conservative

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New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                                                                                                                           Brass EP;
                                                                                                                                   /note= "Cleaved by thrombin"
                                                                                                                                                                                                            (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                           Yount NY, Edwards JE,
                                                                                                                                                                              20-AUG-2003; 2003WO-US026405
                                                                                                                                                                                             20-AUG-2002; 2002US-00225562
                                                                                                                                                                                                                                          WPI; 2004-226740/21.
                                                                                                                                                  WO2004017985-A1
                                                                                                                                                                04-MAR-2004
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The present sequence is that of Protide-3 (PT-3), a peptide antibiotide with distinct effector and activator domains. PT-3 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors in the presence of thrombin. In particular, it was designed to exert cantimicrobial activity less than that of RP-1 in the absence of thrombin, but equivalent to or exceeding that of RP-1 in the presence of thrombin. They, PT-3 exerts optimal antimicrobial activity in the context of thrombin as would be present in the setting of vascular injury or infection. PT-3 is an example of context.activity in the context of invention that have 2 or more effectors with individual distinct connection and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of Protide-4 (PT-4), a peptide antibiotide with distinct effector and activator domains. PT-4 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protide; antibiotide; antimicrobial; interleukin-8; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57; DB 8;
Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brass EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17. .18
/note= "Cleaved by MMP-9"
                       Claim 1; SEQ ID NO 3; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 4; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL70278 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.1%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2002; 2002US-00225562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ARYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ALYKKFKKKLLKS 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide antibiotide PT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yount NY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-226740/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004017985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL70278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 22
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for matrix metalloproteinase MMP-3, which is produced to dissolve the tissue in front of the growing blood vessel tip to allow for its continued tissue invasion. PT-4 was designed to be cleaved into the distinct effectors in the presence of WMP-9. In particular, PT-4 exerts antineoplastic and/or antimicrobial activity less than that of RP-1 in the absence of WMP-9, but equivalent to or exceeding that of RP-1 in the presence of WMP-9. Thus, PT-4 exerts optimal antineoplastic and/or antimicrobial activity in the context of new blood vessel formation. PT-4 is an example of context-activated proteides of the invention that have 2 or more effectors with individual distinct biological functions and one or more effectors with individual distinct biological function of one or more effectors upon of one or more effectors upon context activator the biological function of one or more effectors upon context activation. The proceides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions. 

Sequence 39 AA;

0; Gaps Score 57; DB 8; Length 39; Pred. No. 0.058; 1; Indels 0; Mismatches 89.1%; 92.3%; 1 ARYKKFKKKLLKS 13 22 ALYKKFKKKLLKS 34 12; Conservative Best Local Similarity Query Match Matches ઠે

RESULT 23 ABG69990

ABG69990 standard; peptide; 40 AA

ABG69990;

(first entry) 21-OCT-2002 Rabbit platelet microbicidal protein, PMP-2, based peptide #102

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.

Oryctolagus cuniculus Synthetic.

WO200255554-A2

18-JUL-2002

24-AUG-2001; 2001WO-US041877

25-AUG-2000; 2000US-00648816.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 2002-590659/63

ö New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

Example; Page 67; 221pp; English.

The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible erructures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as 

core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as hacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventions and segents to improve efficiency of functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular cology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short or are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic convercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of duration confidency.

Sequence 40 AA;

Gaps ; 89.1%; Score 57; DB 5; Length 40; 92.3%; Pred. No. 0.059; 1; Indels 0; Mismatches Local Similarity 92.3 Query Match Best Loca Matches

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RESULT 24 ABG69992

ABG69992 standard; peptide; 40 AA.

ABG69992;

(first entry) 21-OCT-2002 Rabbit platelet microbicidal protein, PMP-2, based peptide #104.

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.

Oryctolagus cuniculus.

Synthetic.

WO200255554-A2.

24-AUG-2001; 2001WO-US041877.

25-AUG-2000; 2000US-00648816.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Shen AJ; feaman MR,

WPI; 2002-590659/63.

New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting infections caused by organisms, multiple antibiotic resistance. 

Example; Page 67; 221pp; English.

against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from The invention relates to an antimicrobial peptide composition for use

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and retromers, extensions, combinations of the periods control and retromers, extensions, combinations of the periods control and fundion; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as individual antimicrobial against bacteria and fundi, agents in combination with other specifically against bacteria and fundi, agents in combination with other conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in functions of leukocytes, as disinfectants or preservatives for use in considered to have undesirable toxicity, immunogenicity and short been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                      included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above.
                                      derivatives. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                      truncations, extensions, combinations, fusions and their derivative possible structures are fully described in the specification. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.1%; Score 57; DB 5; Length 40; 92.3%; Pred. No. 0.059; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
and PMP-2, platelet microbiocidal protein),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57468 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US003350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ARYKKFKKKLLKS 13
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeaman MR, Shen AJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40 AA;
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The present invention describes an antimicrobial peptide (AP) for direct

Disclosure; Page 108; 166pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
             organisms such as pacteria and fungi. The Apromorises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template template template template selected from the group consisting a selected from XZBEREXE, BXZXZEB, BXZXZEB, XBEXZEBEX and its derivatives as selected from the group consisting of XBEXEBEX, REBXZEBEX, REBZXEBEX; and their derivatives selected from the group consisting of XBEXEBEX, REBXZEBEX, REBZXEBEX; where B = at least one positively charged amino acid; X = at least one aromatic amino acid, and where B, X and Z amay be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect callular disruption and rapid apoptosis of microbial cells. AMYS7463 to AAMS7557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
agents active against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabbit platelet microbicidal protein, PMP-2, based peptide #4.
                                                                                                                                                                                                                                                                                                                                                                         Score 54; DB 2; Length 13;
Pred. No. 0.064;
2; Mismatches 1; Indels
activity or for potentiating antimicrobial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG69892 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-2000; 2000US-00648816
                                                                                                                                                                                                                                                                                                                                                                                84.4%;
76.9%;
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Best Local Similarity 76.5..

Best Local 10; Conservative
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1 ARYRKFKNKILKS 13
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                                                                                                                                                                                                                                                                                                                                        Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 26
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bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and are arctromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The artimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other ornimicrobials, agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in functions of leukocytes, as disinfectants or preservatives for use in bology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian call toxicities and sective properties of free present invention considering to the present mammalian call toxicities and spectrum rectivity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian call toxicities and sectum. The present sequence is a rabbit PMP based antimicrobial peptide 

Sequence 13 AA;

Gaps ö 84.4%; Score 54; DB 5; Length 13; 76.9%; Pred. No. 0.064; rive 2; Mismatches 1; Indels 1 ARYKKFKKKLLKS 13 Local Similarity 76.5 Query Match Matches δ

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|||:||| |:||| | ARYRKFKNKILKS 13

AAY57500 standard; peptide; 18 AA. RESULT 27

Antimicrobial peptide 13C-RP-1 SEQ ID NO:38. (first entry) 25-FEB-2000 AAY57500; 

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

Synthetic

Oryctolagus cuniculus.

WO9942119-A1.

26-AUG-1999

99WO-US003350 98US-00025319 17-FEB-1999; 18-FEB-1998; (HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 1999-527417/44.

Disclosure; Page 58; 166pp; English. against bacteria and fungi

Antimicrobial peptides for potentiating antimicrobial agents active

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZENENE and its derivatives selected from XZBBZENENE, BXZXB, BXZXZB, XBBXZXBBX and BBXZBENZ; and (b)

crivity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBZEXENS and its derivatives selected from the group consisting a second peptide template XBEXZENS, XBEXZENS and BEXZENSZ; and (b) a second peptide template XBEXZENS, XBEXZENS, MEBZZENS, and consisting of XBENSENS, and their derivatives selected from the group consisting of XBENSENS, XBEXZENS, XBEZXENS, and consisting of XBENSENS, AND STREAM, AND STREAM STREAM, AND STREAM STREAM, AND STREAM S ö a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and XBBXXBBXXBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences used in the exemplification of the present invention present invention describes an antimicrobial peptide (AP) for direct Gaps Antimicrobial peptides for potentiating antimicrobial agents active Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. ö 1; Indels Score 53; DB 2; Pred. No. 0.12; 0; Mismatches Antimicrobial peptide RP-1-10F SEQ ID NO:42. (HARB-) HARBOR-UCLA RES & EDUCATION INST. Disclosure; Page 59; 166pp; English. AAY57504 standard; peptide; 18 AA. 98US-00025319. 82.8%; 99WO-US003350 against bacteria and fungi 25-FEB-2000 (first entry) Local Similarity 91.7 Les 11; Conservative 1 ARYKKFKKKLLK 12 1 ALYKKFKKKLLK 12 Oryctolagus cuniculus Yeaman MR, Shen AJ; WPI; 1999-527417/44. Sequence 18 AA; WO9942119-A1. 17-FEB-1999; 18-FEB-1998; 26-AUG-1999 Synthetic. AAY57504; Query Match Best Loc Matches RESULT 28 **AA**Y57504 셤 88888888888888 8

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide corte sequence (derived from PMP-1 and PMP-2, platelet microbiodial protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as becteria and fungi comprising a peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as becteria and fungi comprising a peptide of 13-74 containing an amino acid and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungion; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial for use in foods and cosmetics and as agents to improve efficiency of molecular foods and cosmetics and as agents to improve efficiency of molecular belongy techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short that have potent and broad are based upon natural antimicrobial peptides that have potent and broad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
                                                                                                            Length 18;
                                                                                                                                                                               2; Indels
                                                                                                            DB 2;
                                                                                                        Score 53; DB 2;
Pred. No. 0.12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG69924 standard; peptide; 18 AA.
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                                                                                                                                              Best Local Similarity 84.6%;
Matches 11; Conservative
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                                         Sequence 18 AA;
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                                                                                                        Query Match
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gainst organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acide core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as or for potentiating antimicrobial agents and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungion (2) antimicrobial peptides for potentiating antimicrobial activity of attimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance the antimicrobials.

Conventional antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabbit platelet microbicidal protein, PMP-2, based péptide #40
                                                                                                                                                                   Length 18;
                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                   Score 53; DB 5;
Pred. No. 0.12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   ABG69928 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 72; 221pp; English.
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infections caused by organisms, multiple antibiotic resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-2000; 2000US-00648816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-2002 (first entry)
                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                     1 ARYKKFKKKLLK 12
                                                                                                                                                                                                                                                                                            1 ALYKKFKKKLLK 12
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                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutant; mutein.
                                                                                                                           Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG69928;
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                              RESULT 30
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBZBXBXB, BXXZXB, XBBXZXBB, and BBXZBBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXBB, and and consisting of XBBXBBX, XBBXXBBX, BXXBXXB, BXBBXXBB, and consisting of XBBXBBX, XBBXXBBX, BXXBXXB, BXBBXXBB, and consisting of XBBZABBX, XBBXXBBX, BXXBXXB, ABBZXBBX, and consisting of XBBZABBX, XBBXXBBX, BXXBXXB, ABBZXBB, and consisting of XBBZABBX, XBBXXBB, BXXBXB, and consisting of XBBZABBX and acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7463 to AAX5757 represent sequences used in the exemplification of the present invention
foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                  82.8%; Score 53; DB 5; Length 18;
84.6%; Pred. No. 0.12;
ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide RP-5 SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 109; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY57469 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               against bacteria and fungi.
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                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALYKKFKKKFLKS 13
                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeaman MR, Shen AJ;
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                                                                                                                                                                                                                                                        Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY57469;
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 31
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ID AAYS
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Gaps

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acide core sequence (derived from PMP-1 and PMP-2, platelet microbiolial protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as artimicrobial peptides of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungions; and (2) and retromers extensions, combinations and fungion; The artimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short that have due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                               Gaps
                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                Rabbit platelet microbicidal protein, PMP-2, based peptide #5
                                                        2; Length 13;
                                                                                             1; Indels
                                                        Score 48; DB 2
Pred. No. 0.58;
                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 129; 221pp; English.
                                                                                                                                                                                                                                                                              ABG69893 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infections caused by organisms, multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-2001; 2001WO-US041877.
                                                   75.0%;
nilarity 61.5%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                1 ARYKKFKKKLLKS 13
                                                                                                                                                         1 ARYRKFRNKILRS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-590659/63.
                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200255554-A2.
                  Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                     ABG69893;
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Matches
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Gaps

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against conganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXRXB, BXZXXZB, XBBXZXBBX and BBXZBBXZ, and (b) a second peptide template XZBZXXB, XBBXZXBBX and BBXZBBXZ, and (b) a second peptide template XBBXXXBX, XBBXZXBB, and (b) a least one positing of XBBXBBX, RBBXXBXB, BXXBXXB, XBBZXXBB, and XBBZXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradelion, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                 Score 48; DB 5; Length 13; Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY57471 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                 75.0%;
61.5%;
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Best Local Similarity 61.5
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                                                                                                                                                                                                                 Sequence 13 AA
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Score 47; DB 2; Length 13; Pred. No. 0.84;

73.4%; 76.9%;

Best Local Similarity

Query Match

Sequence 13 AA;

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The invention interacts to an animalizable propertion comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,

truncations, extensions, combinations, fusions and their derivatives. The
possible structures are fully described in the specification. Also

cr included are (i) an antimicrobial peptide composition for direct activity

or for potentiating antimicrobial peptide composition for direct activity

cr for potentiating antimicrobial apente active against organisms such as

bacteria and fungi comprising a peptide of 13-74 containing an amino acid

core sequence selected from truncations of the peptides described above,

and retromers, extensions, combinations of the peptides described above,

and retromers, extensions, combinations and fusions; and (2)

antimicrobial peptides for potentiating antimicrobial activity of

antimicrobial peptides for potentiating antimicrobial activity of

cantimicrobial peptides are useful as individual antimicrobial agents

conventional antimicrobials, agents that enhance the antimicrobial activity of

conventions of leukocytes, as disinfectants or preservatives for use in

conventional antimicrobials peptides of prior art have generally

conventions of leukocytes, as disinfectants or preservatives for use in

conventional antimicrobial peptides of prior art have generally

conventions of leukocytes, as disinfectants or preservatives for use in

considered to have undesirable toxicity, immunogenicity and short

considered upon natural antimicrobial peptides that have potent and broad

spectrum activity against pathogens exhibiting multiple antibiotic

creistance. They exhibit lower inherent mammalian cell toxicities and

covercome problems of toxicity immunogenicity, and shortness of duration

creistance problems of toxicity immunogenicity, and shortness of effectiveness and ero biodegradation, retaining activity in plasma and

creistance and described active and antimicr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an antimicrobial peptide composition for use
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                                                                                                                                                                                                                                                                                                                                                            Rabbit platelet microbicidal protein, PMP-2, based peptide #7.
Indels
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7
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 130; 221pp; English.
                                                                                                                                                                                                              ABG69895 standard; peptide; 13 AA.
  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                        21-OCT-2002 (first entry)
                                                                          1 ALYKKWKNKLLKS 13
10; Conservative
                                               1 ARYKKFKKKLLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                ABG69895;
  Matches
                                                                                                                                                                    RESULT 34
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Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;

Oryctolagus cuniculus.

Synthetic

WO200255554-A2.

18-JUL-2002

mutant; mutein.

Rabbit platelet microbicidal protein, PMP-2, based peptide #6.

(first entry)

21-OCT-2002

à

ABG69894;

ABG69894 standard; peptide; 14 AA.

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ABG69894
                                                                                                              The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXXZXB, XBBXXXBXB and its derivatives selected from the group consisting of XBBXBBX, BBXXXBX, XBBXXBBX, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXBB, and XBBXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides one bused to treat bacterial and fungal infections. The peptides one leffect cellular disruption and rapid apoptosis of microbial cells. AX57463 to AAX57557 represent sequences used in the exemplification of the present invention
                                                                                        ö
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.9%; Score 46; DB 2; Length 14; 90.0%; Pred. No. 1.3; 1.1ve 1; Mismatches 0; Indels
                                           DB 5; Length 13;
                                                                                        2; Indels
                                                              0.84;
                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptide RP-6 SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 109; 166pp; English.
                                                                                                                                                                                                                                                                                                 AAY57470 standard; peptide; 14 AA.
                                        73.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                   1 ARYKKFKKKLLKS 13
                                                                                                                                                                              1 ALYKKWKNKLLKS 13
                                                              Local Similarity 76.5
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14 AA;
Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                            AAY57470;
                                           Query Match
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                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                 RESULT 35
AAY57470
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AAY57470
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AAY57470
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AAY57470
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AAY57470
DT 25-FE
DE AALIM
XW
AALIM
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AALIM
XW
AALIM
XW
AALIM
XW
AALIM
YW
AALIM
AARIM
CCC AAU
AARIM
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(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Shen AJ;

Yeaman MR,

25-AUG-2000; 2000US-00648816. 24-AUG-2001; 2001WO-US041877.

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The invention relates to an antimatorobial peptide composition for use against organisms such as bacteria and fungi composition for use gainst organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from the period are (i) an antimatorobial peptide composition. Also possible structures are fully described in the specification. Also concluded are (i) an antimatorobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers extensions, combinations of the peptides described above, and retromers extensions, combinations of the peptides described above, antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as bacteria and fungi. The combination with other antimicrobial apprides are useful as individual antimicrobial antimicrobials, agents that enhance, potentiate or restore efficiacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in clodes and cosmetics and as agents to improve efficiency of molecular belonged to have undesirable toxicity, immunogenicity and short ball-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides shibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicity and and controlled to the present machine and expected to the mammalian cell toxicities and and antimicrobial an
New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vertauce. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                      Disclosure, Page 130, 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14 AA;
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DB 5; Length 14;

71.9%; Score 46; DB 90.0%; Pred. No. 1.3;

Query Match Best Local Similarity

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Gaps

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Conservative 3 YKKFKKKLLK 12 YKKWKKKLLK 12

Local Similarity hes 9; Conserv

Best Loc Matches

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Panasik N;

Pugh C,

Firca JR, Schatz RW,

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The present sequence is an antibacterial peptide C18G, which was modified by adding a Cys-amide to the carboxy terminus. This was used to produce an immunoadapter conjugate. Making a conjugate comprises covalently.

Inking a surface-binding ligand (SBL) to a hapten via a spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the compound with immunoglobulin (Ig) under conditions that allow for non- covalent binding of the Ig to the hapten of the compound. The conjugate can be used for the diagnosis, prevention and treatment of microbial infections, e.g. the diagnosis, influenza, viremia or fungemia. They can also be used in neurology, cancer and endocrinology, where Ig targeting can provide desired therapeutic effects. The methods for producing a conjugate can use small molecule targeting ligands to efficiently direct otherwise unreactive Ig to microbial targets. This targeting allows Ig to react with microbial structures that may not normally be accessible to Ig, or are incapable of stimulating antibody production
                                                                                                                                                                                                                                                                      Antimicrobial compans. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial, metapeptide, PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide nRP-1:cRP-13 SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                               Example 39; Page 150; 227pp; English
antibodiotic; antibody; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY57508 standard; peptide; 18 AA
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                                                                                                                                         95US-00482191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.8%;
76.9%;
                                                                                                                                                                                                 Williams JA, Shekhani MS,
Stafford D;
                                                                                                                                                                      OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ARYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALYKKLLKKLLKS 13
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                                                                                                                                                                                                                                            WPI; 1997-077224/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
                                                                                                                                                                                                                                                                                                  immunoglobulin
                                                                                                              07-JUN-1996;
                                                                                                                                           07-JUN-1995;
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                                                       WO9640251-A1
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                                                                                19-DEC-1996
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                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY57508;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compsns. for treating infections sensitive to beta-lactam antibiotics -
comprise beta-lactam antibiotic and cationic oligopeptide, useful against
Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphabaledical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; cancer; endocrinology;
Gaps
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                                                                                                                                                                                                                                                          human platelet factor 4 C-13 fragment; amphipathic alpha helix.
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Pred. No. 3.5;
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 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial peptide C18G for immunoadapter synthesis
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW10351 standard; peptide; 18 AA.
                                                                                                                            AAR13927 standard; protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                     90US-00484020.
91US-00655321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.8%;
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                                                                                                                                                                                   (revised)
(first entry)
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                                                                                                                                                                                                                               Cationic oligopeptide #3
9; Conservative
                          3 YKKPKKKLLK 12
                                                     YKKWKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Darveau RP, Blake JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1991-281214/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                   25-MAR-2003
26-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                          23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                            05-SEP-1991.
                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                        AAR13927;
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                                                                                               RESULT 37
AAR13927
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Matches
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ID AAW
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DT 22-
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Gaps

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2; Length 18; Indels

Score 44; DB 2 Pred. No. 3.5; 0; Mismatches

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treating bacterial diseases.
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Matches
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                                                                                                                                                The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBXXXBX, XBBXZXBB, and their derivatives selected from the group consisting of XBBXXBBX, XBBXXXBB, BXXXBX, BXBXXXBB, and consisting of XBBXXBBXXBBX, BXXXBXB, BXBXXBB, and consisting of XBBZXBBXZBBX; and their derivatives selected from the group consisting of XBBXXBBX and their derivatives selected from the action of the peptides can be used to treat bacterial and fungal amino acids. The peptides can be used to treat bacterial and fungal neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AANS7463 to AANS7557 represent sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin; bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 2; Length 18;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial peptide C18G SEQ ID NO:2.
                                                                                                                               Disclosure; Page 60; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY68001 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firca
                                                                                                                                                                                                                                                                                                                                                             68.8%;
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           98US-00025319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-00760903
                                                                                                          against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALYKKFKKKL 10
                                                                                                                                                                                                                                                                                                                                                                                                          1 ARYKKFKKKL 10
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                                                                         4PI; 1999-527417/44
                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
           18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shekhani MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5998381-A
                                                      Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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the present an according to the compounds computed to the present and the present and the present and the sease of the present and the sease with one of more fambriane is a method of treatment for bacterial disease with one of more fambriane.

C a subject with symptoms of bacterial disease with one or more fambriane. Individual compounds comprising a mannose of a monemeric configuration, an alpha-aromatic or heteroaromatic ling attached to the mannose by a alprosidic or pseudoglycosidic linkage and a functional group which provides a site for chemical modification remote from the mannose and placopy or paramaceutically carrier; and (b) administering the fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compounds can be used for treating subjects with symptoms of and for subjects at risk from bacterial diseases. Treatment of and prevention of blood-borne and toxin mediated diseases in particular sepsis in humans and other animals can be carried out and the in vivo neutralisation of the identify bacteria according to their cell binding specificity's through conjugation to reporter substances such as dyes, luminescent or fluorescent molecules and enzymes. The compounds also inhibit the agglutination of yeast cells induced by type I pili bearing bacteria. The present sequence is used in the exemplification of the present invention
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                                                                                   present invention describes a therapeutic formulation comprising N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rabbit platelet microbicidal protein, PMP-2, based peptide #44.
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0
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Pred. No. 3.5;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
Example 39; Col 84; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-2000; 2000US-00648816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ARYKKFKKKLLKS 13
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tes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeaman MR, Shen AJ;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and resromens, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as or for potentiating antimicrobial agents active against organisms such as core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of cluckocytes against organisms such as bacteria and fungi. The artimicrobial peptides are useful as individual antimicrobial activity of antimicrobial aparents and fungi, agents in combination with other antimicrobials, against bacteria and fungi, agents in combination with other antimicrobials, against bacteria and fungi, agents in combination with other antimicrobials, against bacteria and fungi, agents of molecular for conventional antimicrobials, agents that enhance the antimicrobial considered to have undesirable to improve efficiency of molecular blology techniques. Antimicrobial peptides of prior art have generally considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of prior art have generally are based upon natural antimicrobial peptides that have potent and broad are based upon natural antimicrobial peptides that have potent and broad are based upon natural antimicrobial peptides of prior art have generally resistance mainty against pathogens exhibiting multiple antibiotic and are based upon natural antimicrobial peptides of prior art have generally resistance mainty against pathogens exhibiting multiple antibiotic and antimicrobial peptides of processed and processed and processed and proc overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide resistance. They exhibit lower inherent mammalian cell toxicities and \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Local Similarity 90.0 Sequence 18 AA; Query Match

68.8%; Score 44; DB 5; Length 18; 90.0%; Pred. No. 3.5; ive 0; Mismatches 1; Indels 1 ALYKKFKKK 10 1 ARYKKFKKKL 10 Matches g ઠે

AAW10352 standard; peptide; 19 AA. AAW10352; RESULT 42 AAW10352 

(first entry) 22-SEP-1997

Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; cancer; endocrinology; antibodiotic; antibody; antibiotic. Antibacterial peptide C19G for immunoadapter synthesis.

Synthetic.

/note= "In amide form" Location/Qualifiers Key Modified-site

WO9640251-A1 19-DEC-1996 96WO-US010227. 07-JUN-1996;

95US-00482191. 07-JUN-1995;

(OPHI-) OPHIDIAN PHARM INC.

Panasik N; Pugh C, Schatz RW, Shekhani MS, Firca JR, Williams JA, Stafford D;

WPI; 1997-077224/07.

Antimicrobial compsns. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with .uilndolgonnin

Example 39; Page 150; 227pp; English.

The present sequence is a peptide designated C19G. This was used to produce an immunoadapter conjugate. Making a conjugate comprises covalently linking a surface-binding ligand (SBL) to a hapten via a spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the compound with immunoglobulin (Ig) under conditions that allow for noncovalent binding of the Ig to the hapten of the compound. The conjugate of an be used for the diagnosis, prevention and treatment of microbial infections, e.g. sepsis, influenza, viremia or fungemia. They can also be used in neurology, cancer and endocrinology, where Ig targeting can provide desired therapeutic effects. The methods for producing a provide desired therapeutic effects. The methods for producing a conjugate can use small molecule targeting ligands to efficiently direct otherwise unreactive Ig to microbial targets. This targeting allows Ig to therwise unreactive Ig to microbial targets. This targeting allows Ig to react with microbial structures that may not normally be accessible to Ig, or are incapable of stimulating antibody production

Sequence 19 AA;

Gape ;; 0 2; Length 19; 3; Indels Score 44; DB; Pred. No. 3.6; 0; Mismatches 68.8**%**; 76.9**%**; 10; Conservative Query Match Best Local Similarity Best Loca Matches

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RESULT 43 AAY68002

AAY68002 standard; peptide; 19 AA. AAY68002; 

11-APR-2000 (first entry)

Antibacterial peptide C19G SEQ ID NO:3.

Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin; bacterial infection; antibacterial; fimbriae-binding compound; sepsis.

Synthetic.

US5998381-A

07-DEC-1999

96US-00760903 06-DEC-1996;

96US-00760903 06-DEC-1996;

(OPHI-) OPHIDIAN PHARM INC

WPI; 2000-115173/10.

Shekhani MS, Anderson B, Firca JR;

Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and treating bacterial diseases.

Example 39; Col 84; 89pp; English.

The present invention describes a therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described is a method of treatment for bacterial disease comprising: (a) providing

binding compounds comprising a mannose of an anomeric configuration, an alpha-aromatic or heteroarcomatic ring attached to the mannose by a glycosidic or pseudoglycosidic linkage and a functional group which provides a site for chemical modification remote from the mannose and a pharmaceutically carrier; and (b) administering the fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compounds can be used for treating subjects with symptoms of and for subjects at risk from bacterial diseases. Treatment of and prevention of blood-borne and toxin mediated diseases in particular sepsis in humans can dether animals can be carried out and the in vivo neutralisation of the effects of endotoxin is also possible. The compounds may also be used to identify bacteria according to their cell binding specificity's through conjugation to reporter substances such as dyes, luminescent or fluorescent molecules and enzymes. The compounds also inhibit the agglutination of yeast cells induced by type I pili bearing bacteria. The present sequence is used in the exemplification of the present invention of bacterial disease with one or more fimbriae-

Sequence 19 AA;

Gaps ö Score 44; DB 3; Length 19; Pred. No. 3.6; 0; Mismatches 3; Indels 3; Indels 68.88; 76.98; 1 ARYKKFKKKLLKS 13 1 ALYKKLLKKLLKS 13 10; Conservative Query Match Best Local Similarity Matches ઠ 셤

RESULT 44

AAY57467

AAY57467 standard; peptide; 14 AA. (first entry) 25-FEB-2000 AAY57467; 

Antimicrobial peptide RP-3 SEQ ID NO:5.

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

Synthetic.

Oryctolagus cuniculus. WO9942119-A1

26-AUG-1999

99WO-US003350 17-FEB-1999; 98US-00025319 18-FEB-1998; (HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 1999-527417/44

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure, Page 108; 166pp, English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, XBBXXXBBX and its derivatives a second peptide template XBBX and their derivatives selected from the group consisting of XBBXXBBX, BXXBXXB, XBBXXXBB, and KB XBBXXBBX, where B = at least one positively charged amino acid; X =

ô at least one non-polar hydrophobic amino acid; Z = at least one aromatia amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention 2; Length 14; 67.2%; 80.0%; Sequence 14 AA; Query Match 888888888

Gaps ö 1; Indels Score 43; DB 2 Pred. No. 4; 1; Mismatches Local Similarity 80.0 Best Loc Matches

3 YRKFKNKLLK 12 셤

YKKFKKKLLK 12

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RESULT 45 ABG69891

ABG69891 standard; peptide; 14 AA.

ABG69891;

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(first entry) 21-OCT-2002

Rabbit platelet microbicidal protein, PMP-2, based peptide #3.

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;

Oryctolagus cuniculus, mutant; mutein.

WO200255554-A2 Synthetic 

18-JUL-2002

24-AUG-2001; 2001WO-US041877.

25-AUG-2000; 2000US-00648816

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR,

WPI; 2002-590659/63.

New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting infections caused by organisms, multiple antibiotic resistance.

Disclosure; Page 129; 221pp; English.

quaint organisms such as bacteria and fundi computating a peptide of 5150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (l) an antimicrobial peptide composition for direct activity
150 core sequence selected from truncations of the peptides described above,
151 core sequence selected from truncations of the peptides described above,
152 core sequence selected from truncations and funsions; and (2)
153 and retromers, extensions, combinations and funsions; and (2)
154 containing an amino acid
155 core sequence selected from truncations and funsions; and (2)
156 and retromers, extensions, combinations and funsions; and (2)
157 containing an amino acid
158 core sequence selected from truncations and funsions; and (2)
158 core sequence selected from truncations and funsions; and (2)
158 core sequence selected from truncations and funsions; and (2)
158 core sequence selected from truncation and funsions; and (2)
158 core sequence selected from truncation and funsions; and (2)
159 core sequence selected from truncation and funsion selected from truncation with other antimicrobial segues that enhance, potentiate or restore efficacy of invention relates to an antimicrobial peptide composition for use

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conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
      8888888888888888
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Sequence 14 AA;

ö **Gaps** ö Query Match 67.2%; Score 43; DB 5; Length 14; Best Local Similarity 80.0%; Pred. No. 4; Matches 8; Conservative 1; Mismatches 1; Indels

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Search completed: May 16, 2005, 08:38:28 Job time : 54.1293 secs

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US-09-253-269A

Sequence 3, Application US/09525269A

Patent No. 6743769

GENERAL INFORMATION:
APPLICANT: Steman, Michael R.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HRS614)

CURRENT APPLICATION NUMBER: US/09/525,269A

CURRENT PILING DATE: 2000-03-13

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 39
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Best Local Similarity
Matches 13; Conserv
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-525-269A-3
US-09-525-269A-6
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US-08-760-903-2
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US-08-482-191-2
PCT-US96-10227-2
US-08-482-191-3
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Maximum Match 100%
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OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: Antimicrobiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
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| Sequence 4, Application US/09525269A
| Patent No. 6743769
| GENERAL INFORMATION:
| APPLICANT: Yeaman, Michael R.
| APPLICANT: Shem, Alexander J.
| TITLE OF INVENTION: Metapebtides
| TITLE OF INVENTION: Metapeptides
| TILE REFERENCE: 66742-025 (HR5614)
| CURRENT APPLICATION NUMBER: US/09/525,269A
| CURRENT FILING DATE: 1908-02-18
| NUMBER OF SEQ ID NOS: 39
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 4
| LENGTH: 13
US-08-480-367B-53
US-08-480-370-53
US-08-299-636-33
US-08-279-155-33
US-08-466-31-05-08-466-31
US-08-466-135-7
US-08-466-135-7
US-08-468-975-4
US-08-463-055-31
US-08-463-055-31
US-08-463-0551-31
US-08-463-0551-31
US-08-612-842-3
US-08-612-842-3
US-08-612-842-3
US-08-612-842-3
US-08-528-1348-5
US-08-528-1348-5
US-08-612-842-3
US-08-612-842-3
US-08-612-842-3
US-08-528-1348-5
US-08-582-1348-5
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RESULT 5
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                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                     1; Indels
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APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimidrobbal Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 13
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APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Der TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR PILING DATE: 1998-02-18
RIOR APPLICATION NUMBER: US 09/025,319
RIOR FILING DATE: 1998-02-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                          Score 57; DB 4;
Pred. No. 0.021;
                                                                                                                                                                                                                                                                                     0; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09525269A Patent No. 6743769 GENERAL INFORMATION:
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                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                          89.1%;
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                                                                                                                                                                                                                                                                                     12; Conservative
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                               US-09-525-269A-3
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               SEQ ID NO 3
LENGTH: 18
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                                                                                                          · FEATURE:
                                                                                                                                                                                                                                                                                     Matches
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                                                                    FEATURE:
COTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial COTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09525269A; Sequence 8, Application US/09525269A; Patent No. 6743769; Patent No. 6743769; GENERAL INFORMATION: APPLICANT: Yeaman, Michael R.; APPLICANT: Shen, Alexander J.; TITLE OF INVENITON: Antimicrobial Peptides and Derived; TITLE OF INVENITON: Metapeptides; TITLE OF INVENITON: Metapeptides; FILE REFERENCE: 6674-2025 (HR5614); CURRENT FILLING DATE: 2000-03-13; PRIOR PPLICATION NUMBER: US/09/525,269A; PRIOR PPLICATION NUMBER: 108 09/025,319; PRIOR PILLING DATE: 1998-02-18; NUMBER OF SEQ ID NOS: 39; SOFUTARE: PastSEQ for Windows Version 4.0; SEQ ID NO 8; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09525269A;
Patent No. 6743769;
GENERAL INPORMATION:
APPLICANT: Yeaman, Michael R.;
APPLICANT: Shen, Alexander J.;
TITLE OF INVENTION: Antimicrobial Peptides and Derived;
TITLE OF INVENTION: Metapeptides;
FILE REFERENCE: 66742.025(HRS614);
CURRENT FILING DATE: 2000-03-13;
PRIOR PLICATION NUMBER: US/09/525,269A;
CURRENT FILING DATE: 2000-03-13;
PRIOR PLICATION NUMBER: US/09/025,319;
NUMBER OF SEQ ID NOS: 39;
SOFTWARE: FastSEQ for Windows Version 4.0;
FAMILY OF SEQ ID NOS: 39;
FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 4,
Pred. No. 0.35;
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 61.5%;
8; Conservative
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1 ARYRKFRNKILRS 13
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Matches 10; Conservative
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Best Local Similarity
Matches 8; Conserv
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1 ARYKKFKKKLLKS 13
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APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Annes J.
APPLICANT: Darveau, Annes J.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon ; OTHER INFORMATION: microbiocidal domains from platelet microbial ; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-8
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Pred. No. 1.9;
                                                                                                          71.9%; Score 46; DB 4; Length 14; 90.0%; Pred. No. 0.75;
                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                     1; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
PILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
PILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REFERENCE/DOCKET NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08233203 Patent No. 5409898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 206/728-4800
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                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
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STATE: Washington
COUNTRY: USP
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STREET: 30
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US-08-233-203-7
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Sequence 7. Application US/08760903

SEQUENCE 7. Application US/08760903

SEQUENCE 7. Application US/08760903

SEQUENCE 7. APPLICANT: SHERMANI, MCHAMPED S. APPLICANT: SHERMANI ADDRESS, STORE S. STOR
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PATENT NO. 59818181

JAPPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILLI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITTY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104 TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICIATION NUMBER: 08/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICIATION NUMBER: OPHD-02557
TELEPONEWINICATION INFORMATION:
TELEPONEWINICATION INFORMATION:
TELEPONEWINICATION INFORMATION:
TELEPONEWINICATION INFORMATION:
TELEPONEWINICATION POS SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENDENTH 19 AND ACTION
SEURNICATION POR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Pred. No. 1.9;
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                 FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTONNEY/AGENT INPORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 0PHD-01280
TELECHONE: (415) 705-8410
TELECHONE: (415) 705-8410
TELECHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acide
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Patent No. 5998381
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Best Local Similarity 76.9%;
Matches 10; Conservative
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; MOLECULE TYPE: peptide
PCT-US96-10227-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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STRANDEDNESS: single
TOPOLOGY: unknown
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APPLICANT: SHEKTANI, MOHAWMED S.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: FIRCA, JOSEPH R
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 02-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1993
PRIOR APPLICATION NUMBER: 31,337
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
FILING DATE: 31,337
REGISTRATION NUMBER: 32,337
REGISTRATION NUMBER: 32,337
REGISTRATION NUMBER: 32,337
REGISTRATION NUMBER: 32,337
REJEPONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEGUENCE: Amino acide
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
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220 MONTGOMERY STREET, SUITE 2200
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9610227
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALYKKLLKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.8
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-08-482-191-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & STREET: 220 MONTGOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UP
ZIP: 94104
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APPLICANT: MILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: STERCA, JOSEPH R
APPLICANT: SCHATZ, NOBERH R
APPLICANT: PUGH, CHARLES
APPLICANT: POGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JRF OF SEQUENCES: 9
CORRESPONDENCE ADDRESSS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 5; Length 19; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: UNITER COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/482,191
APPLICATION NUMBER: US 08/462,191
FILING DATE: 07-UNA-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: 31,837
REGERENCE/DOCKET NUMBER: 32,837
REJECOMMINICATION INFORMATION:
FILECOMMINICATION INFORMATION:
FILECOMMINICATION INFORMATION:
                                                                                                                                                                 Sequence 3, Application PC/TUS9610227
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.8%;
76.9%;
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TELEFAX: (415) 397-838
INFORMATION FOR SEQ ID No. 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 76.9
Matches 10; Conservative
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TOPOLOGY: unknown
MOLECULE TYPE: peptide
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US-09-525-269A-5
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APPLICANT: PANASIK W.
APPLICANT: PANASIK W.
APPLICANT: PANASIK W.
APPLICANT: PANASIK W.
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.8%; Score 44; DB 4; Length 19; 76.9%; Pred. No. 2; tive 0; Mismatches 3; Indels
                                                                                                   Score 44; DB 2; Length 19;
Pred. No. 2;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 07-JUN-1995

CLASSIFICATION: 518

PRIOR APPLICATION DATA:
APPLICATION WHERE: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY ARENT INFORMATION:
NAME: CARROLL, PETER G.
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08482191
Patent No. 6579696
GENERAL INPORMATION:
APPLICANT: MILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PIRCA, ROBERT W.
                                                                                                           68.8%;
76.9%;
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                             1 ARYKKFKKKLLKS 13
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                                                                                                           Query Match
Best Local Similarity 76.9
Matches 10; Conservative
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; MOLECULE TYPE: peptide US-08-760-903-3
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STRANDEDNESS: si
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Indels

Sequence 5, Application US/09525269A Patent No. 6743769

1 ARYKKFKKKLLKS 13

Gaps

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Indels

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DB 1; Length 20;
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Pred. No. 4.7;
0; Mismatches
                                                                                                                                                                                         0; Mismatches
                                                                                                                                                  Score 42;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08233203
| Patent No. 2409898
| GENERAL INFORMATION:
| APPLICANT: Darveau, Richard P. |
| APPLICANT: Blake, James J. |
| APPLICANT: Blake, James J. |
| TITLE OF INVENTION: COMPOSITONS AND ME; |
| TITLE OF INVENTION: INFECTIONS CAUSED INTICE OF INVENTION: ANTIBIOTICS NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 000063A
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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81.8%;
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Similarity 81.8%;
9; Conservative
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TELEFAX: 206/448-4775
        20 amino acids
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Best Local Similarity 81.6
Local 9; Conservative
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                                                              : peptide
YES
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                                                                                                                                                                                                                                                                             5 YKKLLKKLLKS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YKKFKKKLLKS 13
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                                                                                                                                                                                                                                    3 YKKFKKKLLKS 13
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3005 First
CITY: Seattle
STATE: Washington
                         TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
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ZIP: 98121
                                                              MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                           US-08-233-203-11
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INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 4; Length 14;
Pred. No. 2.1;
1; Mismatches 1; Indels
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 200-03-13
FRIOR APPLICATION NUMBER: US 09/025,319
FRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bristol-Myers Squibb Company, Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98121
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAMME: POOR, BRIAN W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ON0063A
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Patent No. 5409898
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Darveau, Richard P. APPLICANT: Blake, James J. APPLICANT: Cosand, Wesley L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: ON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                            67.2%;
80.0%;
                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: COSAND, WESL
TITLE OF INVENTION: COM
TITLE OF INVENTION: INF
TITLE OF INVENTION: ANTI
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||| ||||
YRKFKNKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YKKFKKKLLK 12
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: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: 30
                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORM
US-09-525-269A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: S
STATE:
                                                                                                                                                                                                                                                                             IYPE: PRT
                                                                                                                                                                                                                                                                                                                      FEATURE:
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S AND METHODS FOR TREATING CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
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                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
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ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 75.0%;
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                  CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                              Sequence 6, Application US/08233203
Patent No. 5409998
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM ANTIBIOTICS
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APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Weeley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITI
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08233203 Patent No. 5409898
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                         STREET: 3005 First Avenue
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Best Local Similarity 69.2'
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Sequence 10, Application US/08233203
| Patent No. 5403898
| GENERAL INFORMATION: Richard P. APPLICANT: Darveau, Richard P. APPLICANT: Blake, James J. APPLICANT: Cosand, Wesley L. APPLICANT: Cosand, Wesley L. TITLE OF INVENTION: INPECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM TITLE OF INVENTION: INPECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM MUMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS: ANTIBIOTICS NUMBER OF SEQUENCES: Department STREET: 3005 First Avenue
| STREET: 3005 First Avenue | STREET: Washington | COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/08/23,203
FLING DATE: 19-FEB-1991
APPLICATION NUMBER: US/07/484,020
ATFORNEY/AGENT INPORMATION:
NAME: POOCY Brian W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REGISTRATION INFORMATION:
TELEROWMUNICATION INFORMATION:
TELEROMMUNICATION INFORMATION:
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Antimicrobiocidal peptide designed in part upon CTHER INFORMATION: microbiocidal domains from platelet microbial; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-11
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Pred. No. 7.8;
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Sequence 11, Application US/09525269A

GENERAL INFORMATION:
APPLICANT: Shem, Alexander J.
TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 60742-025(HRS614)
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTHARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 13
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Pred. No. 7
                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0063A
TELECOMMUNICATION:
TELEPHONE: 206/728-4800
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-233-203-5; Sequence 5, Application US/08233203; Patent No. 5409898; GENERAL INFORMATION:
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75.0%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                          TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 62.5
Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  linear
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Best Local Similarity
Matches 9; Conserv
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Sequence 26927, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE:
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
FRIOR PEDICATION NUMBER: US 60/074,725
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 26927
ILENGET: 73
ILENGET: 73
                                                                S AND METHODS FOR TREATING CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
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APPLICANT: Blake, APPLICANT: COSANG, Wesley L.
APPLICANT: COSANG, Wesley L.
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM STITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM STITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent "nnressee: Department "nnressee: First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
                                                                                                                                                                                                                                                                                                                  ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TYPE: Floppy disk
CMEDIUM SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
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69.2%;
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Best Local Similarity 69.2-
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 1; Length 12;
Pred. No. 15;
1; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                    8500-0135.00
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
                     NAME: Reed, Dianne E.
REGIGTRATION NUMBER: 31,292
REFERENCE/DOCKET NUMBER: 850(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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72.7%;
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          LENGTH: 12 amino acida
TYPE: AMINO ACID
STRANDEDNESS: single
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LENGTH: 13 amino acids
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Best Local Similarity 72.7
Matches 8; Conservative
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MOLECULE TYPE: protein
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: USA
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Patent No. 526221
GENEAL INFORMATION:
APPLICANT: Almquist, Ronald G.
APPLICANT: Almquist, Ronald G.
TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
TITLE OF INVENTION: BNZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: ITALL & Manella
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                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
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Pred. No. 11;
1; Mismatches 2; Indels
                                                                    DB 4; Length 73;
                                                                                                                                                                                                                                                                                                   Sequence 12. Application US/09525269A
Fatent No. 6743769
GENERAL INFORMATION
APPLICANT: Seaman, Michael R.
APPLICANT: Seam, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapoptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT APPLICATION NUMBER: US 09/025,319
PRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,540
PTI:NG DATE: 19910607
                                                                    Score 39; DB 4
Pred. No. 37;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Irell & Manella
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
                                                                 Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
; ORGANISM: Candida albicans
US-09-248-796A-26927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                          2 RYKKFKKKLLK 12
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YKRLFKKLLKS 13
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US-09-525-269A-12
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US-07-714-540-5
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APPLICANT: BELINKA Jr, BENJAMIN A.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: MODD, RICHARD
TITLE OF INVENTION: CONSTRUCTS
TITLE OF INVENTION: CONSTRUCTS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
COUNTRY: U.S.i.a
COUNTRY: U.S.i.a
COUNTRY: U.S.i.a
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOPTWADER: DANIER PC-DOS/MS-DOS
SOPTWADER: DANIER PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 13;
16;
Technetium-99m Labeled Peptides for Imaging Inflammation
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/019,864
FILING DATE: 19-FEB-1993
CLASSIPICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,367B
FILING DATE: 07-06-95
                                                                       E: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB Pred. No. 16; 1; Mismatches
                                                                                                                                                                                                                                                                                                     ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 53, Application US/08480367B Patent No. 5578288 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.8%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-06-95
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.8
Best Local Similarity 72.7
Matches 8; Conservative
TITLE OF INVENTION: Tech
TITLE OF INVENTION: Imag
WIMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                         STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Pred. No. 16;
                                                                                             2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 13;
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MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,351
FILING DATE: 28-58P-1993
CLASSIFICATION: 534
ATTORNEY/AGENT INFORMATION:
NAME: VILLACORTA Gliberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 49,038
REFERENCE/DOCKET NUMBER: 49,038
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 413-3200
TELEFRAX: (703) 413-220
TELEFRAX: (703) 413-220
TELERENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.8%; Score 37; 72.7%; Pred. No. 1
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Patent No. 5552525
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
                                                      57.8%;
72.7%;
                                     Query Match
Best Local Similarity 72./
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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YKKIIKKLLES 13
                                                                                                                                                                3 YKKIIKKLLES 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
   ; HYPOTHETICAL:
US-08-233-203-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-08-019-864-7
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                                                                                                                                                                                                                                                                              APPLICANT: BELIKKA Jr, BENJAMIN A.
APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: ALVAREZ, VERNON L.
APPLICANT: ALVAREZ, VERNON L.
APPLICANT: ALVAREZ, VERNON L.
TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
TITLE OF INVENTION: CONSTRUCTS
TITLE OF INVENTION: CONSTRUCTS
TITLE OF INVENTION: SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEUSTADT,
ADDRESSEE: NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1;
Pred. No. 16;
1; Mismatches
      Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,351
FILING DATE: 28-SEP-1993
ATTORNEY (AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-004-44
TELECOMMUNICATION INFORMATION:
TELEFRONE: (703) 413-3000
TELEFAX: (703) 413-320
                                                                                                                                                                                                                 Sequence 53, Application US/08480370
Patent No. 5609847
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33, Application US/08299636
Patent No. 5659041
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLLAK, Alfred
KIRBY, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.,
8, Conservative
                           8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide US-08-480-370-53
                                                                     3 YKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YKKFKKKLLKS 13
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                                                                                                            3 YKKIIKKLLES
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    Best Local Similarity
Matches 8; Conserv
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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US-00-487-221A-53
is Sequence 53, Application US/08487221A
is Sequence 53, Application US/08487221A
is Patent No. 559565
is GENERAL INFORMATION:
is APPLICANT: COUGHLIN, DANIEL J.
APPLICANT: ALVAREZ, VERNON L.
APPLICANT: MOOD, RICHARD
if TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
ITTLE OF INVENTION: CONSTRUCTS
NUMBER OF SEQUENCES: 56
is CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
                                                                                                                                                                                                                                                                                                                               DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & ADDRESSEE: NEUSTADT, P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,221A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/127,351
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 34,038
TELERHONE: (703) 411-3000
                                                                                                                                                                                                                                                                                                                                                    ed. No. 16;
Mismatches
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REPERENCE/DOCKET NUMBER: 2654-002A
TELECOMMUNICATION:
TELEPHONE: (703) 684-1111
TELEPAX: (703) 684-1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 amino acids
                                                                                                                                                                                                                                       TOPOLOGY: unknown; MOLECULE TYPE: peptide US-08-480-367B-53
                                                                                                                                                                                                                                                                                                                                                                                                                   3 YKKFKKKLLKS 13
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                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-487-221A-53
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57.8%; Score 37; DB 1; Length 13;

Query Match

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Gaps
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Sequence 31, Application US/08464456

Patent No. 5681541

GENERAL INFORMATION:
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: South Wacker Drive Suite 3000

STATE: Chicago
STATE: Illinois
COMPTRY: US South Wacker Drive Suite 3000

STATE: Illinois
COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
COMPUTER: IN PC Compatible
OMPUTER: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA: DS-008/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CLASSIFICATION NUMBER: US/08/464,456

FILLING DATE: DS-01MN-1995

CLASSIFICATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 39,1104-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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Pred. No. 16;
1; Mismatches 2; Indels
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                        ATTORNEY/ ACENT INFORMATION NAME: MURRAY, ROBERT B.
REGISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: P8074
TELECOMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 715 1000
TELEX: 312 715 1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                   ATTORNEY/AGENT INFORMATION: NAME: MURRAY, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 amino acids
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YKKFKKKLLKS 13.
                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-279-155-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YKKIIKKLLES 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-464-456-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 33
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APPLICANT: POLLAK, Alfred
APPLICANT: GOODBODY, Anne
TITLE OF INVONTION: PEPTIDE DERIVED RADIONUCLIDE CHELATORS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                 TITLE OF INVENTION: HYDRAZINO-TYPE RADIONUCLIDE CHELATORS
TITLE OF INVENTION: HAVING AN N3S CONFIGURATION
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 Fifteenth Street, N. W., Suite 330 - G STREET: Street Lobby CITY: Washington STATE: DC
                                                                                                                                                                                                      COMPUTER READABLE FORM:

ABDIUM TYPE: 103A

COMPUTER READABLE FORM:

MEDIUM TYPE: 1 FOADA disk

COMPUTER: 1 BM PC Compatible

OPERATING SYSTEM: PC-DOS/NM-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/299,636

FILING APPLICATION: 534

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/092,911

FILING APPLICATION NUMBER: US 08/092,911

RICHERATION NUMBER: 18-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENY Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vergion #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,155
FILING DATE: 22-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 1
Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
US-08-279-155-33
Sequence 33, Application US/08279155
Patent No. 5662885
DUNN-DUFAULT, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 57.8
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-299-636-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 YKKFKKKLLKS 13
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APPLICANT:
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Gaps
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                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCATION DATA:
APPLICATION NUMBER: US/08/468,975
FILING DATE: 06-JUN-1995
CLASSIPTICATION: 424
ATTORNEY/AGRAM: 100-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCOMMATION:
APPLICANT: POLLAK, Alfred
APPLICANT: POLLAK, Anne
TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE
TITLE OF INVENTION: CHELATORS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: NITAIDO, MARMELSTEIN, MURRAY & ORAM
ADDRESSEE: LLP
STREET: 655 Fifteenth Street, N. W., Suite 330
STREET: GSTREET: LODBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,988A
FILING DATE: 28-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/279,155
FILING DATE: 22-JUL-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURRAY, Robert B.
                                                                                                                                                                                                                                         FILING DATE: 06-UNA-09/6/100,779

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5776428nan, Kevin E
REGISTRATION NUMBER: 35,303
REGISTRANCE/DOCKET NUMBER: 92,205-M
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Application US/08703988A
Patent No. 5780006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: G Street Lobby CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.8
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                  ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YKKFKKKLLKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-703-988A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-468-975-4
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                                                                                                                        APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R
ITLE OF INVENTION: Technetium-99m Labeled Peptides for
ITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.8%; Score 37; DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Buttram, Scott
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R
TITLE OF INVENTION: Technetium-99m Labeled Peptides for NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,135
FILING DATE: 06-JUN-1995
CLASSIPICATION: 424
ATYORNEY/AGENT INFORMATION:
NAME: NO. 5720934nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Banner & Allegretti, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                          Sequence 7, Application US/08486135
Patent No. 5720934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08468975; Patent No. 5776428; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 YKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YKKIIKKLLES 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
3 YKKIIKKLLES 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
US-08-468-975-4
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Gaps
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US-08-463-052-31

Sequence 31, Application US/08463052

Patent No. 2788960

GENERAL INFORMATION:
TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Technetium-99m Labeled Polypeptides or SEQUENCES: 37

CORRESPONDENCE ADDRESS:
STREET: 10 South Wacker Drive Suite 3000

STRTE: 10 South Wacker Drive Suite 3000

STREET: 10 South Wacker Drive Suite 3000

STREET: 10 South Wacker Drive Suite 3000

STREET: 10 South Wacker Drive Suite 3000

STREET REDABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: 10 South Wacker 10 Sol 8463,052

FILING DATE: 05-UUN-1995

CLASSIFICATION NUMBER: 35,303

RESTERRING NUMBER: 35,303

REFERRING NOW STREET NUMBER: 30,1104-V

TELEFAK: 312 715 1100

TELEFAK: 312 715 1124

TELEFAK: 312 715 1124

TELEFAK: 312 715 1124

SECURING FOR SEG ID NO: 31:

SECURING FOR SEG ID NO: 31:
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Sequence 31, Application US/08480551

GENERAL INFORMATION:
APPLICANT: Dean, Richard T
ATTLE OF INVENTION: Technetium-99m Labeled Polypeptides for TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 13; Pred. No. 16; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive Suite 3000
STATE: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72...
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-052-31
    3 YKKIIKKLLES 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 YKKFKKKLLKS 13
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Pred. No. 16;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                          DB 1; Length 13;
16;
                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MCBride, William
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
TITLE OF INVENTION: Technetium-99m Labeled Peptides for ITILE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,152
FILING DATE: 06-JUN-1995 ·
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5780007nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,205-L
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
RECISTRATION NUMBER: 22,980
REFERENCE/DOCKET NUMBER: P8074-6011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acid
STRANDENRES: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08470152
Patent No. 5780007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
APPLICANT: MCBride, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 72.77
....hes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; ' MOLECULE TYPE: protein US-08-703-988A-33
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3 YKKFKKKLLKS 13

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, william
APPLICANT: Lister-James, John
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: Diatide, Inc.
STREET: 9 Delta Drive
                                                                                                                                                                                                                                            Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 2;
Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                      Score 37; DB 2;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REPERENCE/DOCKET NUMBER: DITI 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/07871282A Patent No. 5965107 GENERAL INFORMATION:
JUNE TYPE: 13 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-468-964B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                            57.8%;
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72.7%;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                Query Match
Best Local Similarity 72.7.
Best Local Similarity 72.7.
Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                             3 YKKFKKKLLKS 13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-08-612-842-33
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Pred. No. 16;
1; Mismatches 2; Indels
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APPLICANT: Dean, Richard T.

APPLICANT: Buttram, Scott

APPLICANT: McBride, William

APPLICANT: Lister-James, John

APPLICANT: Civitello, Edgar R.

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

TITLE OF INVENTION: Imaging

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USAN
ZIP: 03053
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC COMPASSION #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DUATA:
APPLICATION NUMBER: US/08/468,964B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33.194
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ST. 937-8970
TELEBEHONE: (603) 437-8970
TELEBERORE: (603) 437-8970
TELEBERORE: (603) 437-8970
                        OFTANIA STATEM PACE STATEM PAC
         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08468964B Patent No. 5922303
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STREET: 9 Delta Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 57.8
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-551-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YKKIIKKLLES 13
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US-08-468-964B-5
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STATE:
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,678A
FILING DATE: 03-JUN-1994
                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112
TELEPHONE: (603) 437-8970
TELEPHONE: (603) 437-8970
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08582134B Patent No. 6074627
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.8
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
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MOLECULE TYPE: peptide
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STRANDEDNESS: no
                                                                                               FILING DATE: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Sequence 33, Application US/08612842
Patent No. 5976495
GENERAL INFORMATION:
APPLICANT: FOLLAK, ALFRED
APPLICANT: GOODBODY, ANNE
TITLE OF INVENTION: PEPTIDE DERIVED RADIONUCLIDE CHELATORS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM
STREET: 655 15TH STREET, NW, G STREET LOBBY, SUITE
STREET: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: McEride, William
APPLICANT: McEride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                      STATE:
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/612,842
FILING DATE: 20-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERNAN, RICHARD J
REGISTRATION NUMBER: 39107
REFERENCE/DOCKET NUMBER: 39107
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08253678A
Patent No. 5997844
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 YKKFKKKLLKS 13
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                                                                                                                                                                                                                                                                                                                                   WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-612-842-33
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US-08-253-678A-5
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Gaps
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APPLICANT: Dean, Scott
APPLICANT: Buttram, Scott
APPLICANT: MeBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: TECRNETIUM-99m LABELED PEPTIDES FOR
TITLE OF INVENTION: IMAGING
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Diatide, Inc.
STREET: 9 Delta Drive
Length 13;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.30
SOCTAMEN: PAPLICATION DATA:
APPLICATION NUMBER: US/08/582,134B
FILING DATE: 14-MAY-1996
FLASSIFICATION *4.24
ATTORNEY/AGENT INFORMATION:
NAME: MCDANIER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112D1
TELEPHONE: (603) 437-8970
TELEPHONE: (603) 437-8977
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TEMPORATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
  Score 37; DB 2
Pred. No. 16;
1; Mismatches
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Sequence 9, Application US/0898526

Batent No. 6080728

GENERAL INFORMATION:
TITLE OF INVENTION:
THEAPY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STRATE: 120 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
COMPUTER: EDLAWARE
COMPUTER: EDLAWARE
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BATENCATION NUMBER: US/08/985,526
FILING DATE:
TLING DATE:
PILING DATE:
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PILING DATE:
PRICE APPLICATION NUMBER: US/08/985,526
ATTORNEY/AGENT INFORMATION:
PILING DATE:
PRICE APPLICATION NUMBER: US/08/985,526
ATTORNEY/AGENT INFORMATION:
PRICE APPLICATION NUMBER: US/08/608,845
ATTORNEY/AGENT INFORMATION:
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                                                             Score 37; DB 3; Length 13;
Pred. No. 16;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (302) 658-9141
TELEBRAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 anino acids
TYPE: amino acids
TOPOLOGY: linear
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                Query Match 57.8
Best Local Similarity 72.7
Matches 8; Conservative
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US,08-582-134B-5
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Search completed: May 16, 2005, 08:40:38 Job time : 14.8966 secs

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Sequence 9, Appli
Sequence 1, Appli
Sequence 31, Appli
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Sequence 27, Appl
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                                                                                                                                                       May 16, 2005, 08:38:44 ; Search time 48.8621 Seconds (without alignments) 88.876 Million cell updates/sec
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1: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{PUBCOMB.pep:*} \)

2: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{PUBCOMB.pep:*} \)

3: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSG6} \text{NEW PUB.pep:*} \)

4: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSG6} \text{NEW PUB.pep:*} \)

5: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSG6} \text{NEW PUB.pep:*} \)

6: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO6} \text{NEW PUB.pep:*} \)

7: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO8} \text{NEW PUB.pep:*} \)

9: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO9} \text{PUBCOMB.pep:*} \)

10: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO9} \text{PUBCOMB.pep:*} \)

11: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO9} \text{PUBCOMB.pep:*} \)

12: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO9} \text{NEW PUB.pep:*} \)

13: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO9} \text{NEW PUB.pep:*} \)

15: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSOO} \text{NEW PUB.pep:*} \)

16: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSOD} \text{PUBCOMB.pep:*} \)

17: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSOD} \text{PUBCOMB.pep:*} \)

18: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO} \text{NEW PUB.pep:*} \)

19: \( \cgn2 \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO} \text{NEW PUB.pep:*} \)

19: \( \cgn2 \frac{6}{\text{prodata}} \frac{6}{\text{prodata}} \frac{1}{\text{pubpaa}} \text{VSO} \text{NEW PUB.pep:*} \)

19: \( \cgn2 \frac{6}{\text{prodata}} \frac{6}{\text{prodata}} \text{VBOMB.pep:*} \)

19: \( \cgn2 \frac{6}{\text{prodata}} \frac{6}{\text{prodata}} \text{VBOMB.pep:*} \)

10: \( \cgn2 \frac{6}{\text{prodata}} \text{VDubpaa} \text{VSO} \text{VBO
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-424-599-182402
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US-10-382-240-1
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US-10-131-543-8
US-10-131-546-8
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US-10-131-543-14
US-10-131-546-14
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US-09-925-715-27
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 74
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Sequence 14, Appl	Sequence 14, Appl	1,7	7	4,	9	7	15,	Sequence 15, Appl	15,	15,	'n	7	m	4	11,	'n	ò	91,	91,	ij	7	49,	equence 55,	ഗ	49,	52	56,	14,	'n	Sequence 17, Appl	Sequence 17, Appl
US-10-131-346-14	US-10-415-024-14	2	US-10-752-096-2	52-	US-10-752-096-6	10-752-096	US-10-131-543-15	31-	$\preceq$	=	2	=	0-382	US-10-333-364A-4	US-10-036-869-11	US-10-462-836-3	-09	US-09-792-793A-91			US-10-333-364A-2	S.	9-820-	US-09-820-053A-56	0-109-	2	0	US-10-344-709C-14	US-10-884-355A-97	US-09-741-106-17	US-10-918-366-17
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14	15	16	17	18	19	20	21	22	23	24	25	56	. 27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 158393, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lar Robar Thomas J
APPLICANT: About Wihua
APPLICANT: Coo Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(5323)8/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 158393
LENGTH: 73
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US-10-424-599-158393
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Best Local Similarity 63.6%;
Matches 7; Conservative
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53 YKKFKNKIKRS
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US-10-424-599-158393
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; Sequence 182402, Application US/10424599 ; Publication No. US20040031072A1

RESULT 2 US-10-424-599-182402

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GENERAL INFORMATION:
APPLICANT: Mixson, James A
APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: CARRIER DNA ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:Platelet
OTHER INFORMATION: binding peptide
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STRET: 1220 Market Street, P.O. Box 2207
CITY: Wildmington
STATE: Delaware
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                    Score 37; DB
Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 57.8%; Score 37; DB Best Local Similarity 72.7%; Pred. No. 38; Matches 8; Conservative 1; Mismatches
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                 CURRENT APPLICATION NUMBER: US/09/925,715
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 27
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: McMorrow Jr., Robert G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (302) 658-9141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10036869
Publication No. US20020151516A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 13 amino acids
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                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                 h 57.8%;
Similarity 72.7%;
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Connoll
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Best Local Similarity
Matches 8; Conserv
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APPLICANT: Lar Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Shouleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 182402
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Patent No. US20020102217A1
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
TITLE OF INVENTION: agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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US-10-424-599-182402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 31, Application US/09765614B
Patent No. US20020102215A1
GENERAL INFORMATION:
APPLICANT Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: adiagnostic/therapeutic
TITLE OF INVENTION: agents
TITLE OF INVENTION: agents
CURRENT PRINCATION UNMER: US/09/765,614B
CURRENT FILING DATE: 2001-07-10
SOCITARRE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 13
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Pred. No. 38;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(45)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.8%;
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                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
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US-09-765-614B-31
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US-09-925-715-27
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Sequence 8, Application US/10131546
| Publication No. US20030103895A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: CYT, John E.
| APPLICANT: CYT, John E.
| APPLICANT: CYT, John E.
| TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
| TITLE OF INVENTION: CHECKANS
| FILE REFERENCE: 09744-018001
| CURRENT FILING DATE: 2002-04-24
| PRIOR PILING DATE: 2001-0-04-4
| PRIOR PELING DATE: 2001-10-24
| PRIOR PILING DATE: 2001-10-24
| NUMBER OF SEQ ID NOS: 29
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH: 18
            TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
TILE REFERENCE: 09744-016001
CURRENT APPLICATION NUMBER: US/10/131,543
CURRENT FILING DATE: 2000-40-24
PRIOR APPLICATION NUMBER: US 09/694,992
PRIOR APPLICATION NUMBER: US 09/694,992
PRIOR APPLICATION NUMBER: PCT/US01/50423
PRIOR PILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 18;
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Pred. No. 51;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic construct US-10-131-546-8
                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic construct
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                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.8%;
72.7%;
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Best Local Similarity 72.7
Matches 8; Conservative
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Matches 8; Conservative
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                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BIOSIGHT LTD.
TITLE OF INVENTION: PEPTIDE CONJUGATED ANTI-CANCER PRODUCTS
FILE REPERANCE: 85189-4400
CURRENT APPLICATION NUMBER: US/10/382,240
CURRENT FILING DATE: 2003-03-05
PRIOR PILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 15; Length 13;
Pred. No. 38;
1; Mismatches 2; Indels
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Publication No. US20040141922A1

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: Improvements in or relating to

TITLE OF INVENTION: adaptostic/therapeutic

TITLE OF INVENTION: adaptostic/therapeutic

TITLE OF INVENTION: agents

FILE REPERENCE: REF/Klaveness/054

CURRENT APPLICATION NUMBER: US/10/722,075

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: US/08/960,054A

PRIOR PILING DATE: 1997-10-29

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATENTING Ver. 2.1

SEQ ID NO 31

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial; OTHER INFORMATION: Sequence:Platelet; OTHER INFORMATION: binding peptide US-10-722-075-31
                                                                                                                Sequence 1, Application US/10382240 Publication No. US20030216298A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 8, Application US/10131543; Publication No. US20030072709A1; GENERAL INFORMATION:
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: homo sapiens
3 YKKIIKKLLES
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US-10-722-075-31
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US-10-131-543-8
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LENGTH: 13
                                                                      RESULT 6
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WES-10-11-546-14

Sequence 14, Application US/10131546

Bedication No. US20030103895A1

GENERAL INFORMATION:

APPLICANT: Cyr, John E.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

FILE REFERENCE: 09744-018001

CURRENT PEPLICATION NUMBER: US/10/131,546

CURRENT PEPLICATION NUMBER: US/09/695,494

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-10-24

NUMBER OF SEQ ID NOS: 29

SOFTHARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h S7.8%; Score 37; DB 14; Length 22; Similarity 72.7%; Pred. No. 62; B; Conservative 1; Mismatches 2: Indels
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Pred. No. 62;
1; Mismatches 2
                                    PRIOR FILING DATE: 2002-04-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2001-10-24
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 22
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LOCATION: 3
OTHER INFORMATION: Xaa = epsilon-Lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 3
OTHER INFORMATION: Xaa = epsilon-Lysine
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic construct FEATURE:
NAME/KSY: ACETYLATION
LOCATION: 1
FEATURE:
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 72.7%;
Matches 8; Conservative
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NAME/KEY: ACETYLATION
LOCATION: 1
FEATURE:
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Matches 8; Conserv
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; Publication No. US20040058984A1
; GENERAL INFORMATION:
; AFPLICANT: Diatide, Inc.
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HY
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HY
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HY
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HY
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HY
TITLE OF INVENTION: USING HYDROPHILIC THIOED THE SET 2003-04-24
; FRICR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/695,494
; PRIOR FILING DATE: 2000-10-24
; RRIOR FILING DATE: 2000-10-24
; RRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FABLESQ for Windows Version 4.0
; SEQ ID NO 8
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Publication No. US20030072709A1

GENERAL INFORMATION:
APPLICANT: Cyr, John E.
APPLICANT: Pearson, Daniel A.
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
FILE REPERENCE: 09744-016001
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Pred. No. 51;
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Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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FILE REFERENCE: 09744-017001
CURRENT APPLICATION NUMBER: US/10/131,346
CURRENT FILING DATE: 2002-04-24
FRIOR APPLICATION NUMBER: US 09/695,360
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
SOFTWARE: PASTEE OF Windows Version 4.0
SEQ ID NO 8
LENGTH: 18
TYPE: PRI
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic construct US-10-131-346-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic construct
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ORGANISM: Artificial Sequence
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Best Local Similarity 72.7.
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Best Local Similarity 72.7
Matches 8; Conservative
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YKKIIKKLLES 18
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US-10-131-543-14
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; NAME/KEY: VARIANT
; LOCATION: 3
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-415-024-14
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Best Local Similarity 72...
8; Conservative
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; LOCATION: (1)..(1)
; OTHER INFORMATION:
US-10-752-096-1
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SQUENCE 14, Application US/10415024

Publication No. US20040058984A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

FILE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

CURRENT APPLICATION NUMBER: US 09/694,992

PRIOR APPLICATION NUMBER: US 09/694,992

PRIOR APPLICATION NUMBER: US 09/695,494

PRIOR APPLICATION NUMBER: US 09/695,494

PRIOR APPLICATION NUMBER: US 09/695,494

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PASKEGE for Windows Version 4.0

SEQ ID NO 14

LENGTH: 22
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                                                                                                                                                 APPLICANT: CYT, JOHN E.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
FILE REPERENCE: 09744-017001
CURRENT APPLICATION NUMBER: US/10/131,346
CURRENT APPLICATION NUMBER: US/09/695,360
FRIOR APPLICATION NUMBER: US/09/695,360
FRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 22
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Pred. No. 62;
1; Mismatches 2; Indels
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                                                                                            Sequence 14, Application US/10131346
Publication No. US20030103899A1
GENERAL INFORMATION:
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72.7%;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 72...
8. Conservative
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12 YKKIIKKLLES 22
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NAME/KEY: ACETYLATION
LOCATION: 1
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LOCATION: 1
FEATURE:
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Sequence 1, Application US/10752096

Sequence 1, Application US/10752096

Publication No. US2005002861A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and TITLE OF INVENTION: Inflammation

TITLE OF INVENTION: Inflammation

TITLE OF INVENTION: Inflammation

TITLE OF INVENTION: UNMBER: US/10/752,096

CURRENT FILING DATE: 2004-01-07

PRIOR PAPLICATION NUMBER: US 60/438,316

PRIOR PAPLICATION NUMBER: EP 03 000 204.2

PRIOR PILING DATE: 2003-01-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID 0.1
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Publication No. US2005002861A1

GENERAL INFORMATION:
GENERAL SETTING TO INTERPRET INFORMATION:
TITLE OF INVENTION:
Inflammation
TITLE OF INVENTION:
INFORMATION:
GURRENT APPLICATION NUMBER: US/10/752,096
CURRENT APPLICATION NUMBER: US 60/438,316
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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64;
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Score 37; DB 15;
Pred. No. 62;
1; Mismatches 2
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Query Match 57.8%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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Sequence 7, Application US/10752096

Sequence 7, Application US/10752096

Publication No. US2005002861A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and TITLE OF INVENTION: Inflammation
TITLE OF INVENTION: Inflammation
TITLE OF INVENTION: UNMER: US/10/752,096
CURRENT FILING DATE: 2004-01-07
PRIOR PEDICATION NUMBER: US 60/438,316
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID 0.7
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Pred. No. 64;
1; Mismatches
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1; Mismatches
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OTHER INFORMATION: Complexing Agent
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OTHER INFORMATION: Complexing Agent
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Publication No. US20030072709A1
GENERAL INFORMATION:
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; OTHER INFORMATION: Penicillamine
US-10-752-096-6
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OTHER INFORMATION: Isocysteine
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Matches 8; Conservative
                              FEATURE:
NAME/KEY: ACETYLATION
LOCATION: (1)..(1)
OTHER INFORMATION:
FEATURE:
NAME/KEY: MISC FEATURE
NAME/KEY: MISC FEATURE
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OTHER INFORMATION:
FEATURE:
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US-10-131-543-15
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; Sequence 6, Application US/10752096
; Publication No. US20050002861A1
; GENERAL INFORMATION:
APPLICANT: Schering AG
; TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection an
; TITLE OF INVENTION: Inflammation
; FILE REFERENCE: SCH10663US2
; CURRENT FILING DATE: 2004-01-07
; PRIOR PLILING DATE: 2003-01-07
; PRIOR PILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 23
; TATLE OF INVENTION INVENTIO
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Sequence 4, Application US/10752096

Bublication No. US20050002861A1

GENERAL INFORMATION:

APPLICANT: Schering AG

TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection ar TITLE OF INVENTION: Inflammation

FILE REFERENCE: SCH10663US2

CURRENT APPLICATION NUMBER: US/10/752,096

CURRENT FILING DATE: 2004-01-07

PRIOR PLILING DATE: 2003-01-07

PRIOR APPLICATION NUMBER: EP 03 000 204.2

PRIOR FILING DATE: 2003-01-07

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LEWING AGENTH: 23

LEWING AGENTH: 23
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Pred. No. 64;
1; Mismatches
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Pred. No. 64;
1; Mismatches
                                 ; OTHER INFORMATION: Complexing Agent US-10-752-096-2
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                                                                                                                       57.8%;
                                                                                              Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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ORGANISM: artificial
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ORGANISM: artificial
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; OTHER INFORMATION:
US-10-752-096-4
         FEATURE:
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| FULDICALLOR NO. USAUGUSBEAGAL
| GENERAL INFORMATION: USAUGUSBEAGAL
| APPLICAMY: Diatide, Inc.
| TITLE OF INVENTION: STRBILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
| TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
| TITLE OF INVENTION: CHROMANS
| TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
| TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
| TITLE OF INVENTION: USER: USO 09/694,992
| CURRENT FILING DATE: 2000-10-24
| PRIOR PILING DATE: 2000-10-24
| PRIOR FILING DATE: 2000-10-24
| NUMBER OF SEQ ID NOS: 29
| SOFTWARE: FASTSEQ for Windows Version 4.0
| SEQ ID NO 15
| TYPE: PRI
                                                                                                                                                                               US-10-131-346-15

US-10-131-346-15

US-10-131-346-15

Publication No. US20030103899A1

GENERAL INFORMATION:

APPLICANT: Cyr, John E.

TITLE OF INVENTION:

FILE REFERENCE: 09744-017001

CURRENT APPLICATION NUMBER: US/10/131,346

CURRENT FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US/9/695,360

PRIOR APPLICATION NUMBER: PCT/US01/50423

PRIOR PILING DATE: 2000-10-24

NUMBER OF EX DID NOS: 29

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15

LEAGTH: 24

TAPE OF INVENTION OF RADIOPHARMACEUTICALION NUMBER: PCT/US01/50423

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 15

LEAGTH: 24

TAPE: DEATH OF THE OF 
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US-10-131-346-15
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NAME/KEY: ACETYLATION
LOCATION: 1
FEATURE:
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; Sequence 15, Application US/10415024
; Publication No. US20040058984A1
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Best Local Similarity 72...
Service 8, Conservative
                 3 YKKFKKKLLKS 13
                                                                                14 YKKIIKKLLES 24
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Publication No. US20030103895A1

GENERAL INFORMATION:
APPLICANT: CYT, John E.
APPLICANT: Pearson, Daniel A.
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
TITLE OF INVENTION: CHROMANS
TITLE OF INVENTION: CHROMANS
TITLE OF INVENTION: CHROMANS
TITLE OF INVENTION UNMBER: US/10/131,546
CURRENT APPLICATION NUMBER: US/10/131,546
CURRENT PILING DATE: 2002-4-24
PRIOR PILING DATE: 2002-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
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TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
FILE REFERENCE: 09744-016001
CURRENT PAPLICATION NUMBER: US/10/131,543
CURRENT PILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 09/694,992
PRIOR PILING DATE: 2000-10-24
RIOR APPLICATION NUMBER: US 09/694,992
PRIOR PILING DATE: 2001-10-24
NUMBER OF SEQ 1D NOS: 29
SOFTWARE: PSESEG for Windows Version 4.0
SEQ 1D NO 15
LENGTH: 24
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Pred. No. 67;
1; Mismatches 2; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 24
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; LOCATION: 7
; COTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-543-15
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LOCATION: 7

COTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-546-15
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ORGANISM: Artificial Sequence
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
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US-10-131-546-15
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Gaps

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; OTHER INFORMATION: SEQ ID NO. 4 is the 17-34/47-70 fragment of mutated PF-4 SEQ. ID : US-10-333-364A-4
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Sequence 3, Application US/10382240

Sequence 3, Application US/10382240

Publication No. US20030216298A1

GENERAL INFORMATION:

APPLICANT: BIOSIGHT LTD.

TITLE OF INVARINION: PEPTIDE CONJUGATED ANTI-CANCER PRODUCTS

FILE REPERENCE: 8548-4400

CURRENT APPLICATION NUMBER: US/10/382,240

CURRENT FILING DATE: 2003-03-05

PRIOR FILING DATE: 2001-09-05

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 25
                                                    Score 37; DB 16; Length 24; Pred. No. 67;
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illarity 72.7%; Pred. No. 1.1e+02;
Conservative 1; Mismatches 2
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Pred. No. 69;
1; Mismatches
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US-10-382-240-3
                                                                                          1; Mismatches
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ORGANISM: Artificial Sequence
                                                      57.8%;
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Best Local Similarity 72.7
Matches 8; Conservative
                                                    Query Match 57.8
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                    14 YKKIIKKLLES 24
; ORGANISM: Homo sapiens
US-10-718-986-2
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Best Local Similarity
Matches 8; Conserv
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| Publication No. US20050004020A1
| GENERAL INFORMATION:
| APPLICANT: FANG, Fang |
| APPLICANT: FANG, Fang |
| TITLE OF INVENTION: BROAD SPECTRUM ANTI-VIRAL THERAPEUTICS AND PROPHYLAXIS
| TITLE OF INVENTION UNMBER: US/10/718,986
| CURRENT APPLICATION NUMBER: US 60/428,535
| PRIOR PILING DATE: 2003-11-22
| PRIOR PILING DATE: 2003-04-19
| PRIOR FILING DATE: 2003-04-19
| PRIOR FILING DATE: 2003-04-19
| NUMBER OF SEQ ID NOS: 10
| SOFTWARE: PatentIn version 3.2
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Publication No. US20040086999A1
GENERAL INFORMATION NO. US20040086999A1
GENERAL INFORMATION NO. WITHOUT DES VAISSEAUX ET DU SANG
APPLICANT: INSTITUT DES VAISSEAUX ET DU SANG
TITLE OF INVENTION: MUTATED PF-4, ITS FRAGEMENTS AND MUTATED FUSION I
TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MI
TITLE OF INVENTION: AND THEIR USE FOR INHIBITING ANGIOGENESIS.
FILE REFERENCE: P-6684(128728-000172)
CURRENT APPLICATION NUMBER: US/10/333,364A
CURRENT FILING DATE: 2003-09-22
PRICE REPERIOR: PT/FR01/02341
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                                                                                                                                                     Score 37; DB 15; Length 24;
Pred. No. 67;
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                                                                                                                                                                                            2; Indels
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                                                                                              ; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-415-024-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: FR0009464
PRIOR FILING DATE: 2000-07-19
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SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 24
                                                                                                                                                     57.8%;
72.7%;
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                                                                                                                                     Query Match
Best Local Similarity 72...
8; Conservative
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   NAME/KEY: ACETYLATION
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                                                        NAME/KEY: VARIANT
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US-10-333-364A-3
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                                                                              LOCATION: 7
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                       LOCATION:
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APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION UNDER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
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72.7%; Pred. No. 1.4e+02;
tive 1; Mismatches 2
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Pred. No. 1.8e+02;
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LOCATION: (1)...(54)

OTHER INFERMATION: A modified platelet factor 4
US-10-462-836-3
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Patent No. US20020090671A1

GENERAL INFORMATION:

APPLICANT: TAM, Cherk Shing

TITLE OF INVENTION: BONE STIMULATING FACTOR

FILE REFERENCE: 709997/00123

CURRENT APPLICATION NUMBER: US/09/229,304

CURRENT FILING DATE: 1999-01-13

EARLIER APPLICATION NUMBER: US 09/048,058

EARLIER PILING DATE: 1998-03-26

EARLIER PILING DATE: 1996-09-26
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PRIOR APPLICATION NUMBER: PCT/GB98/01197
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: GB 9708265.5
PRIOR FILING DATE: 1997-04-24
NUMBER OF SEQ ID NOS: 5
SSCTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 54
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 57.8%;
Best Local Similarity 72.7%;
Matches 8; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 70
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Best Local Similarity 72...
8; Conservative
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                                                                                                                                                                                                                                       S-10-015-86y-11
Sequence 11, Application US/10036869
Sequence 11, Application US20020151516A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: THERAPY
THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/10/036,865
FILING DATE: 29-00. US20020151516A1-2001
CLASSIFICATION: <university control of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2e+02;
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Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <URNOWN>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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APPLICANT: Tolleshaug, Helge
TITLE OF INVENTION: Contrast Agents
FILE REFERENCE: REF/Klaveness/977
CURRENT APPLICATION NUMBER: US/10/462,836
CURRENT FILING DATE: 2003-06-17
PRIOR FILING DATE: 1999-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCMOLTOW Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-462-836-3
; Sequence 3, Application US/10462836
; Publication No. US20040009122A1
; GENERAL INPORMATION:
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INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Best Local Similarity 72.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A. ZIP: 19899
                                                                          32 YKKIIKKLLES 42
                                     3 YKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 YKKFKKKLLKS 13
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US-10-036-869-11
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OTHER INFORMATION: SEQ ID NO. 2 is the mutated sequence of PF-4 (Arg in position 56)
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| Sequence 2, Application US/2040086998A1
| Sequence 2, Application No. US2004008699B1
| GENERAL INFORMATION:
| APPLICANT: UNIVERSITE DE BORDEAUX 1
| APPLICANT: UNIVERSITE DE BORDEAUX 1
| TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MENA SEQUENCES
| TITLE OF INVENTION: THEIR NUE FOR INHIBITING ANGIOGENESIS.
| TITLE OF INVENTION: THEIR USE FOR INHIBITING ANGIOGENESIS.
| TITLE OF INVENTION: AND THEIR USE FOR INHIBITING ANGIOGENESIS.
| CURRENT APPLICATION NUMBER: US/10/333,364A
| CURRENT FILING DATE: 2003-09-22
| PRIOR FILING DATE: 2000-07-19
| PRIOR FILING DATE: 2000-07-19
| NUMBER OF SEQ ID NOS: 4
| SEQ ID NO 2
| LENGTH: 70
| LENGTH: 70
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                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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Pred. No. 1.8e+02;
1; Mismatches 2
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Publication No. US20030083243A1
GENERAL INFORMATION:
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELXO27
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWAREN FILING DATE: 2010-03-28
SOFTWAREN FILING DATE: 2011-03-28
SOFTWAREN FILING DATE: 2011-03-28
LENGTH: 23
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PRIOR APPLICATION NUMBER: PCT/FR01/02341
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
LENGTH: 70
                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                       57.8%;
72.7%;
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 57.8
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                      FEATURE:
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Sequence 91, Application US/20030215421A1

GENERAL INFORMATION:

APPLICANT: McDonald, John R.

APPLICANT: Coggins, Philip

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

CURRENT APPLICATION UNMBER: US/10/375,209A

CURRENT FILING DATE: 2003-02-24

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 91

LENGTH: 70
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Publication No. U020040086999A1
GENERAL INFORMATION:
JUSTOO4008699A1
GENERAL INFORMATION:
JUSTOO4008699A1
APPLICANT: UNIVERSITE DE BORDEAUX 1
APPLICANT: UNSTITUT DES VAISSEAUX ET DU SANG
JITLE OF INVENTION: MUTATED PF-4, ITS PRAGMENTS AND MUTATED FUSION PEPTIDES,
JITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MENA SEQUENCES
TITLE OF INVENTION: AND THEIR USE FOR INHIBITING ANGIOGENESIS.
JUSTIE REPREBENCE: P-6684[218728-000172]
CURRENT APPLICATION NUMBER: US/10/333,364A
CURRENT PILING DATE: 2003-09-22
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                                                                                                                                                                                                                                                                                                                     Score 37; DB 9; Length 70;
Pred. No. 1.8e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Human Chemokine polypeptide: PF-4 PUBLICATION INFORMATION:
'AUTHORS: Clark-Lewis et. al.,
JOURNAL: J. Leukoc. Biol.
                                                                                                                    OTHER INFORMATION: Human Chemokine polypeptide: PF-4
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                                                                                                                                         FUBLICATION INFORMATION:
AUTHORS: Clark-Lewis et. al.,
JOURNAL: J. Leukoc. Biol.
VOLUME: 57
                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 72.,
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  3 YKKFKKKLLKS 13
                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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Matches 8; Conserv
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PAGES: 703-711
DATE: 1995
                                                                                                                                                                                                                               ; PAGES: 703-711
; DATE: 1995
US-09-792-793A-91
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US-10-375-209A-91
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US-10-333-364A-1
      SEQ ID NO 91
LENGTH: 70
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                                                                                               FEATURE:
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RESULT 40
US-10-109-171-55
; Sequence 55, Application US/10109171
; Publication No. US20030109452A1
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USB
; FILE REFERENCE: HELXO28
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 23
                                              Sequence 56, Application US/10109171
Publication No. US20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE FILE REFERENCE: HELK028
CURRENT APPLICATION NUMBER: US/10/109,171
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Pred. No. 91;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: SYNTHETIC SEQUENCE NAME/KEY: MOD RES LOCATION: (23)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: SYNTHETIC SEQUENCE
                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        56.2%;
70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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12 FKKFAKKLAK 21
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 12 FKKFAKKLAK 21
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Pred. No. 91;
1; Mismatches 2; Indels
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                                                                                                                                                Score 36; DB 10; Length 23;
Pred. No. 91;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                               RESULT 37
US-09-820-053A-55
Sequence 55, Application US/09820053A
Publication No. US2030083243A1
GENDERLI INFORMATION:
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELKO27
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 23
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US-09-820-053A-56
; Sequence 56, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; TILE OF INVENTION:
; TILE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT APPLICATION NUMBER: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 56
; LENGTH: 23
                               FEATURE:

OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD RES
LOCATION: (23)
OTHER INFORMATION: AMIDATION
US-09-820-053A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-09-820-053A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: SYNTHETIC SEQUENCE
                                                                                                                                                     56.2%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.2%;
70.0%;
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 70.v-
                                                                                                                                    Query Match
Best Local Similarity 70.0.
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Best Local Similarity 70.0
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                      Score 36; DB 17; Length 27;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 9;
Pred. No. 70;
2; Mismatches
                                                                                                                                                                                                                                                                                                                        Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryville
STATE: CA
COUNTRY: USA
                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/741,106
FILING DATE: 12-Dec-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1994-08-05
ATTORNEY/AGENT INFORMATION:
NAME: SAVERAGE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0990.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Creasey, Abla
TITLE OF INVENTION: Chimeric Proteins
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                              Sequence 17, Application US/09741106
Publication No. US20020197667A1
GENERAL INFORMATION:
APPLICANT: Innis, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/10918366 Publication No. US20050008654A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 510-601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Innis, Michael
                    Similarity 54.5%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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Best Local Similarity 63.0
                                                                                                       2 RYKKFKKKLLK 12
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2 RFKRFRKKFKK 12
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                    Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                        RESULT 44
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Sequence 14, Application US/10344709C

Sequence 14, Application US/10344709C

Sequence 14, Application US/10344709C

Sequence 14, Application US/10344709C

Sequence 14, Application US USCOMOTIONS

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof

FILE REFERENCE: SONN:030US

CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: RCT/EP01/09529

FRIOR APPLICATION NUMBER: A 1416/2000

PRIOR APPLICATION NUMBER: A 1416/2000

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1
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US-10-344-709C-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reactive Surfaces, Ltd.
TITLE OF INVENTION: Antifungal Paints and Coatings
FILE REPERENCE: RAT-00400
FURRENT APPLICATION NUMBER: US/10/884,355A
CURRENT FILING DATE: 2004-07-02
                                                                                                                                                                                                                           Score 36; DB
Pred. No. 91;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/485,234
FINGR FILING DATE: 2004-07-02
FINGR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 199
SOPTWARE: Patentin version 3.3
SEQ ID NO 97
TURN TO 97
TURN TO 97
TURN TO 97
                                                                                                                                                       ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-10-109-171-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 97, Application US/10884355A; Publication No. US20050058689A1; GENERAL INFORMATION:
        2002-03-28
                                                                                                                                                                                                                             56.2%;
                                                                                                                          ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
CURRENT FILING DATE: 2002-(NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 56
LENGTH: 23
                                                                                                                                                                                                           Best Local Similarity 54.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RYKKFKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|:|:|| |
RFKRFRKKFKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Bovine BMAP-27
                                                                                                                                                                                                                                                                                                          3 YKKFKKKLLK 12
                                                                                                                                                                                                                                                                                                                                               12 FKKFAKKLAK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 43
US-10-884-355A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 14
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                         rype: prt
                                                                                                                                              FEATURE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton St.
CITY: Emeryvile
STRATE: CA
COUNTRY: USA
ZIATE: CA
COUNTRY: USA
ZIATE: GA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION NUMBER: US/09/918,366
FILING DATE: 16-Aug-004
FILING DATE: 16-Aug-004
FILING DATE: 05-Aug-1994
ATTORNEY/AGRYI NUMBER: US/08/286,521
FILING DATE: 05-Aug-1994
ATTORNEY/AGRYI NUMBER: 36,914
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 36,914
FILEPHOME: 510-601-2585
TELEPHOME: 510-601-2585
TELEPHOME: 510-601-2585
TELEPHOME: 510-601-2585
TELEPHOME: 510-601-2585
TELEPHOME: 12 amino acid
STRANDEDNESS: single
TOPOLOGY: 11neat
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-918-366-17
FORDENCE TARRESTER FOR THE TOPOLOGY: 11neat
NOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7-10-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.7%; Score 35; DB 17; Length 12; Best Local Similarity 63.6%; Pred. No. 70; Matches 7; Conservative 2; Mismatches 2; Indels
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3 YKKFKKKLLKS 13 ||| ||||:: YKKILKKLLEA 12

ઠે 셤 Search completed: May 16, 2005, 09:23:38 Job time : 49.8621 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 16, 2005, 08:21:21; Search time 11.2069 Seconds (without alignments) 111.611 Million cell updates/sec

US-09-648-816B-4 64 Title: Perfect score:

1 ARYKKFKKKLLKS 13 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

22893

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dp			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ΙD	Description
п	36	56.2	65	~	H64442	hypothetical prote
7	35	54.7	58	~	T12949	_
m	34	53.1	34	7	E70239	_
4	32	50.0	61	α,	C69807	hypothetical prote
ß	32	50.0	70	0	H81379	30S ribosomal prot
9	31	48.4	55		BGMS	spermatid transiti
7	31	48.4	28	7	AE2050	30S ribosomal prot
œ	31	48.4	59	7	D81363	small hydrophobic
თ	31	48.4	99	~	C81433	50S ribosomal prot
10		48.4	67	7	B72248	≍
11	31	48.4	70	7	H82673	hypothetical prote
12	31	48.4	73	7	T28252	~
13	30.5	47.7	55	~	H90520	10
14	30	46.9	46	~	T06965	ribosomal protein
15	30	46.9	49	7	E86636	50S ribosomal prot
16	30	46.9	54	~	S34541	hypothetical prote
17	30	46.9	99	~	E97818	$\overline{}$
18	30	46.9	99	~	H71666	ribosomal protein
19	30	46.9	99	7	H81897	hypothetical prote
20	29	45.3	38	7	E64551	
21	29	45.3	49	~	T07304	_
, 22	29	45.3	Ŋ	~	T42319	_
23	29	45.3	2	~	E97793	_
24	29	45.3	'n	0	F69315	ρι
25	29	•	61	~	729	hypothetical prote
56	29	•	62	~	D69384	
27	29	•	62	~		cerebellar polypep
	29	45.3	62	~	3391	cerebellar polypep
29	29	45.3	63	~	D97862	hypothetical prote

hypothetical prote hypothetical prote	40	hypothetical prote hypothetical prote hypothetical prote	hypothetical prote degenerate transpo spermatid transiti	spermatid transiti spermatid transiti	hypothetical prote conserved hypothet
G64380 C49753	534290 C64330 E87694	B70252 T07309 C97021	D89806 H97910 BGSH	BGBO BGRT	S31636 B69189
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71 20	355	4 4 0 4 6 0	0 0 0 4 0		920
45.3	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 3 3 8 8 8 8 8	43.8 83.8	64.44.4 6.6.6.6 6.6.6.0	43.8
7 7 7 8	7 7 7 7	7 8 8 7 8 8 7 8 8	7 7 8 8 8 7 8 7 8 7 8	9 9 9 9	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
30 31	ነ ጠ ጠ (	3.5 3.6 3.7	8 8 8 0	444	4 4 4 4 73

# ALIGNMENTS

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RESULT 1
H64442
hypothetical protein MJ1145 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: H6442
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, L.; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; roon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Accession: H64442
A;Accession: H64442
A;Accession: H64442
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-65 < RUL.>
A;Roser:references: UNIPROT:058545; GB:U67557; GB:L77117; NID:gl591777; PIDN:AAB99155.1; C;Genetics:

A; Map position: REV1085114-1084917

Gaps ö 56.2%; Score 36; DB 2; Length 65; 69.2%; Pred. No. 40; tive 1; Mismatches 3; Indels Local Similarity 69.2 les 9; Conservative Query Match Best Loca Matches

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1 ARYKKFKKKLLKS 13 ਨੇ g

hypothetical protein yotN - Bacillus subtilis phage SPBc2
C;Species: Bacillus subtilis phage SPBc2
C;Species: Bacillus subtilis phage SPBc2
C;Accession: T12949; H69929
R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D. submitted to the RMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage A;Reference number: Z17583

A;Accession: T12949 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-58 <LAZ>

Richard Strong S

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A; Title: Nucleotide sequence of a cDNA clone encoding mouse transition protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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(569807

hypothetical protein yfjT - Bacillus subtilis

(5,Species: Bacillus subtilis

(5,Species: Bacillus subtilis

(5,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

(5,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

(5,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

(6,Species: P.; Ogaaswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

(7, Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc

(8, Brunich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

(9, Alathors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

(1) A. Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

(1) A. Harwood, C.R.; Henaut, A.; Hulbert, M.; Levine, K.; Lapidus, A.; Lardinois,

(2) A. Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Lui, H.; Mauda, S.; Maucell

(3) M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.W.; Levine, A.; Liu, H.; Masuda, S.; Maueel y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadale, Y.; Scanton, A, Authors: Schleich, S.; Schroeter, R.; Terpetrae, F.; Seguchi, J.; Sekowska, A.; Seronon, A, Authors: Schleich, A.; Tanaka, T.; Terpetrae, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, P.; Wipat, A.; Tanaka, T.; Terpetrae, P.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Alteference number: A69580; MUID:98044033; PMID:9384377
A; Accession: H6922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein BBH39 - Lyme disease spirochete plasmid H/lp28-3
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: E70239
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
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A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:299114; GB:AL009126; NID:g2634230; PIDN:CAB13873.1; PID:e1185453;
A;Experimental source: strain 168
C;Genetics:
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A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUD:98065943; PMID:9403685
A;Accession: E70239
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-34 <KLE>
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Pred. No. 48;
2; Mismatches
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Pred. No. 53;
3; Mismatches
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60.0%;
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54.58;
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| | | | | :|:|
| YKKIKNELIK 19
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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A;Gene: yotN
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Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamamot, K.; Yasumoto, K.; Yasumoto, K.; Yasu, K.; Yoshida, K.; A; Atthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Airile: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Rocession: C69807
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:035041; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12626.1 A;Experimental source: strain 168 C;Genetics: A;Genetics:
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A; Fitle: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypk A; Reference number: A81250; MUID:20150912; PMID:10688204
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A,Experimental source: serotype O2, strain NCTC 11168
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R;Kleene, K.C.; Borzorgzadeh, A.; Flynn, J.F.; Yelick, P.C.; Hecht, N.B.
Biochim. Biophys. Acta 950, 215-220, 1988
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C;Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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R;Yelick, P.C.; Kozak, C.; Kwon, Y.K.; Seldin, M.F.; Hecht, N.B.
Genomics 11, 687-694, 1991
A;Title: The mouse transition protein 1 gene contains a B1 repetitive element and A;Reference number: A40561; MUID:92128951; PMID:1685480
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NiAlternate names: testis-specific basic protein
CiSpecies: Mus musculus (house mouse)
CiSpecies: 05-Jun-1992 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
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Similarity 62.5%;
5; Conservative
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YRKFKKQV 23
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Best Local Similarity
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A; Residues: 1-55 <YEL>
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A; Residues: 1-70 <PAR>
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C,Accession: C81433
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypany. A;Reference number: A81250; WUID:20150912; PMID:10688204
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A,Experimental source: serotype O2, strain NCTC 11168
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A;Accession: B72248
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A;Experimental source: strain MSB8
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50S ribosomal protein L31 Cj0155c [imported] - Campylobacter jejuni (strain NCTC 11168)
                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72248
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                                          Length 59;
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C;Superfamily: Escherichia coli ribosomal protein L31
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C;Superfamily: Bscherichia coli ribosomal protein L30
                                       Score 31; DB 2; I
Pred. No. 2.4e+02;
2; Mismatches 0;
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Pred. No. 2.7e+02;
1; Mismatches 1;
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                                          Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 70.0.
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Matches 6; Conservative
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48 RFKKYKK 54
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A;Molecule type: DNA
A;Residues: 1-66 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2050
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: D8153
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Ryarandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 655-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT.QBYVMO, GB:BA000019; PIDN:BAB73654.1; PID:g17131045; GSPDB:G
A,Experimental source: strain PCC 7120
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A;Experimental source: serotype O2, strain NCTC 11168
A;Reference number: JS0038; MUID:88252150; PMID:3382664
A;Accession: JS0038
A;Accession: JS0038
A;Residues: 1-55 <KLLS
A;Cross-references: EMBL:X12521; NID:954850; PIDN:CAA31039.1; PID:954851
C;Gomment: This protein replaces histones and is replaced by other transition proteins A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      emall hydrophobic protein Cj0900c [imported] - Campylobacter jejuni (strain NCTC 11168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30S ribosomal protein S21 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. Etrain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2050
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                     A;Introns: 47/1
C;Superfamily: spermatid transition protein 1
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;2-55/Product: spermatid transition protein 1 #status predicted <MAT>
F;4-0/Binding site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 2; Length 58;
Pred. No. 2.4e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: Escherichia coli ribosomal protein S21
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les 5; Conservative
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31 RKYRKSVLKS 40
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RRFKKKIQKA 26
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A; Residues: 1-58 < KUR>
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A; Residues: 1-59 < PAR>
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Best Local S:
Matches 5
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A;Gene: Cj0900c

C;Genetics:

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2 RYKKP---KKKLLK 12
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C; Keywords: cyanelle; ribosome
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                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-55 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Genetic code: SGC3
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hypothetical protein XF1492 [imported] - Xylella fastidiosa (strain 9a5c)
C; Species: Xylella fastidiosa
C; Species: Xylella fastidiosa
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C; Ccession: H82673
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A; Fitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Accession: H82673
A; Ascession: Freeliminary
A; Residues: 1-70 <SIM>A; Residues: 1-70 <
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Rishmson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H. as-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000,
A.; Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A; Authors: Machina, E.R.; Junaco, C.L.; Marques, M.V.; Martins, E.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J., de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak
A; Atthores: da Silva, A.C.R.; da Silva, R.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaineida, S.; Vettore, A.L.; Zawasak
A; Reference number: A59328
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A;Cross-references: UNIPROT:Q9YW01; EMBL:AF063866; NID:g4049647; PIDN:AAC97641.1; PID:g4
C;Genetics:
A;Nore: MSV091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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A;Reference number: Z20484; MuID:99102612; PMID:9847359 A;Accession: T28552
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75.0%; Pred. No. 2.8e+02;
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A;Molecule type: DNA
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52 YEKFGKKL 59
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nes 8; Conserv
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hes 6; Conserv
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C;Accession: H90520
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;File: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q98RD7; GB:AL445566; PID:g14089485; PIDN:CAC13245.1; GSPDB:G1
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P48130; EMBL:U30821; NID:g1016083; PIDN:AAA81308.1; PID:g101f(
A;Experimental source: strain Pringsheim LB555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg
A;Reference number: A86625; WUID:21235186; PMID:11337471
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A,Modecule type: DNA
A,Residues: 1-49 «FDO»
A,Cross-references: UNIPROT:034102, GB:AE005176, PID:g12722937; PIDN:AAK04191.1; GSPDB:GN
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C;Species: Lactococcus lactis subsp. lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribosomal protein L34 - Cyanophora paradoxa cyanelle
C;Species: cyanelle Cyanophora paradoxa
C;Species: cyanelle Cyanophora paradoxa
C;Dacession: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T68655
R;Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A. submitted to the EMBL Data Library, July 1995
A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
A;Reference number: 215840
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C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
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Pred, No. 2.9e+02;
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Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 8; Conservative 2; Mismatches 1;
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C,Superfamily: Escherichia coli ribosomal protein L34
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Best Local Similarity 58.3%;
Matches 7; Conservative
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ribosomal protein S21 - Rickettsia prowazekii
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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16 KNFKKKL 22
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Best Local Similarity
Matches 6; Conserva
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CiSpecies: Rickettsia conorii
CiDate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
CiAccession: E97818
RiOgata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; RG Science 293, 2032-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                            hypothetical protein 54 (psaC 3' region) - Buglena gracilis chloroplast
C;Species: chloroplast Euglena gracilis
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: 834541; 834908
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, Bubmitted to the BMBL Data Library, January 1993
A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentati
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A;Molecule type: DNA
A;Residues: 1-54 «HALL)>
A;Cross-references: UNIPROT:P31558; EMBL:X70810; NID:g415327; PIDN:CAA50122.1; PID:g4157
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielmar
Mucleic Acids Res. 21, 3537-3544, 1993
A;Title: Complete sequence of Euglena gracilis chloroplast DNA.
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A. Status: nucleic acid sequence not shown; translation not shown
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-54 «HAL2»
A. Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50122.1; PID:g415778
A. Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
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                                                            Length 49;
                                                                                                                2; Indels
C; Superfamily: Escherichia coli ribosomal protein L33
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C;Keywords: chloroplast
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                                                         46.9%; Score 30; DB 2;
66.7%; Pred. No. 3e+02;
tive 1; Mismatches
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Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                   Best Local Similarity 66.7
Matches 6; Conservative
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A; Residues: 1-66 < KUR>
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A, Status: preliminary
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4 KKFKKL 10

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A,Molecule type: DNA
A,Residues: 1-66 cAND>
A,Cross-references: UNIRROT:Q9ZCU6; GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15058
A,Experimental source: strain Madrid E
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A.Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81897
A;Status: preliminary
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A;Experimental source: serogroup A, strain 22491
C;Genetics:
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: E6451
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.,
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney,
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
Nature 388, 539-547, 1997
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C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: H7166
C;Accession: H7166
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71666
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: H81897
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Pred. No. 3.9e+02;
0; Mismatches 1; Indels
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C;Superfamily: Escherichia coli ribosomal protein S21
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45.3%;
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Matches 5; Conservative
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4 FDEFKKELLSN 14
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41 YGKYRRKLRK 50
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A;Molecule type: DNA
A;Residues: 1-61 <KUR>
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42319
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil
A;Reference number: Z22137; WUID:98094274; PMID:9434185
A;Accession: T42319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 49c - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Species: chloroplast Chlorella vulgaris
C;Species: chloroplast Chlorella vulgaris
C;Accession: T07304
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas
R;Title: Complete nucleotide sequence of the Chloroplast genome from the green alga Chlo
A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07304
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUD:97394467; PMID:9252185
A;Accession: E64551
A;Status: preléminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-38 <TOM>A;Residues: 1-38 <TOM>A;Cross-references: UNIPROT:025035; GB:AE000544; GB:AE000511; NID:92313337; PIDN:AAD0732
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A;Molecule type: DNA
A;Residues: 1-49 <WAKS
A;Residues: 1-49 <WAKS
C;Genetics: BMBL:AB001684; NID:g2224352; PIDN:BAA57952.1; PID:g2224468
A;Genome: chloroplast
C;Keywords: chloroplast
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hypothetical protein RC0749 [imported] - Rickettsia conorii (strain Malish 7)
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A;Molecule type: DNA
A;Residues: 1-56 «ALO»
A;Cross-references: UNIPROT:048479; EMBL:X97918; PIDN:CAA66526.1
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Pred. No. 4.9e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                               Score 29; DB 2; Length 38;
Pred. No. 3.5e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.3%; Score 29; DB 2; Length 49;
85.7%; Pred. No. 4.4e+02;
tive 0; Mismatches 1; Indels
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71.4%;
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Best Local Similarity 46,2%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                          1 ARYKKFKKKLLKS 13
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYKKIKR 56
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A;Cross-references: UNIPROT:P07734; GB:M24852; NID:g206085; PIDN:AAA41828.1; PID:g206086 R;Ziai, R.; Pan, Y.C.B.; Hulmes, J.D.; Sangameswaran, L.; Morgan, J.I. Proc. Co. Natl. Acad. Sci. U.S.A. 83, e420-e423, 1986 A;Fitle: Isolation, sequence, and developmental profile of a brain-specific polypeptide, A;Reference number: A25524; MUID:87041468; PMID:3464961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: Q92G25; GB: AE006914; PIDN: AAL03838.1; PID: 915620439; GSPDB: GA
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPROT: Q58063; GB: U67512; GB: L77117; NID: 91591352; PIDN: AAB98645.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein RC1300 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Accession: D97862
R;Ogata, H: Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Ritle: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
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A;Molecule type: DNA
A;Residues: 1-71 <BUL>
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C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C.Accession: G64380
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A;Reference number: A33915; MUID:89315855; PMID:2748608
A;Accession: A33915
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29; DB 2; I
Pred. No. 5.4e+02;
5; Mismatches 0;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.7
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48 SQFRKFQKK 56
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39 KEFKEKLEK 47
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A; Residues: 1-67 < KUR>
                                                                                                A; Molecule type: mRNA
A; Residues: 1-62 <SAN>
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                         hypothetical protein AF1076 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69384
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Asture 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woses, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69384
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C.Species Rattue norvegicus (Norway rat)
C.Species 109-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C.Accession: A33915; A25524
R.Sangameswaran, L.; Hempetead, V.; Morgan, J.I.
Proc. Natl. Acad. Sci. U.S.A. 86, 5651-5655, 1989
A.Title: Molecular cloning of a neuron-specific transcript and its regulation during nor
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S14925
cerebellar polypeptide pcp4 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S14925; S08238
R;Chen, S.L.; Orr, H.T.
Nucleic Acids Res . 18, 1304, 1990
A;Title: Sequence of a murine cDNA, pcp-4, that encodes the homolog of the rat brain-spe A;Reference number: S14925; MUID:90206810; PMID:2320430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-62 «KLB»
A;Cross-references: UNIPROT:029187; GB:AE001028; GB:AE000782; NID:g2689351; PIDN:AAB9016
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C;Genetics:
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            Length 61;
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44.4%; Pred. No. 5.4e+02;
iive 5; Mismatches 0; Indels
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Pred. No. 5.4e+02;
   45.3%; Score 29; DB 2; I larity 75.0%; Pred. No. 5.3e+02; Conservative 1; Mismatches 1;
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les 5, Conservative
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Matches 4; Conservative
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17 RKFKEVLIKA 26
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2 KKYKKGLL 9
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Best Local Similarity
Matches 6; Conserv
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C; Accession: E87694

R; Niezman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;

R; Niezman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, A.S.; Gwinn, M.L.; Haft, D.H.; Kolons

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolons

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Soi. U.S. 98, 4136-411, 2001

Proc. Natl. Acad. Soi. U.S. 98, 4136-411, 2001

A; Title: Complete Genome Sequence of Caulobacter crescentus.

A; Reference number: A87249; MUID:21173698; PMID:11259647
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                       A;Cross-references: UNIPROT:P54025; GB:U67480; GB:L77117; NID:g2826265; PIDN:AAB98230.1; C;Genetics:
A;Map position: REV232198-232130
C;Superfamily: rat ribosomal protein L41
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Fraser, C.M.; Casjens, S.; Huang, W.M.; Quackenbush, J.; Salzberg, S.; Hanson, M.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A;Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-34 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyporhetical protein CC3591 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein BBK08 - Lyme disease spirochete plasmid K/lp36
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 4.7e+02;
2; Mismatches 3; Indels
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Pred. No. 4.4e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                        Length 22
                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                Query Match.
43.8%; Score 28; DB 2; 1
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 3; Mismatches 1.
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Similarity 71.4%;
5; Conservative
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2 RWKWYKKRL 10
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KKFEKRL 25
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Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-32 <STO>
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C64330
Libosomal protein HG12 - Methanococcus jannaschii
Libosomal protein HG12 - Methanococcus jannaschii
C;Bosomal protein HG12 - Methanococcus jannaschii
C;Bosomal protein HG12 - Methanococcus jannaschii
C;Bosomal Better                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Serratia marcescens
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: C49753; S11643
R;Omori, K.; Suzuki, S.I.; Imai, Y.; Komatsubara, S.
J;Gen. Microbiol. 137, 509-517, 1991
A;Title: Analysis of the Serratia marcescens proBA operon and feedback control of prolin
A;Reference number: A49753; MUID:91237315; PMID:1851803
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C,Species: Streptococcus pyogenes
C,Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
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    Serratia marcescens (fragment)

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                                       Indels
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R, Podbielski, A.; Weber-Heynemann, September 1992
submitted to the EMBL Data Library, September 1992
A, Description: Virk gene of DF-positive group A streptococci.
A, Reference number: S34297
   Pred. No. 6.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein (proB 5' region)
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A,Molecule type: DNA
Residues: 1-21 «POD>
A,Cross-references: EMBL:X68501
Best Local Similarity 85.7
Matches (6; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                     16 KKMKKKL 22
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FKEKLIK 17
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A; Residues: 1-20 < OMO>
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White, Vugt, B.

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A;Residues: 1-50 <KUR>
A;Cross-references: UNIPROT:Q99WI4; GB:BA000018; PID:g13700309; PIDN:BAB41607.1; GSPDB:Gh
A;Experimental source: strain N315
C;Genetics:
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Bur. J. Biochem. 198, 13-20, 1991

A;Title: Wiclear translition protein 1 from ram elongating spermatids. Mass spectrometric A;Reference number: S16075; WUID:91249791; PMID:2040274

A;Accession: S16075
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C;Superfamily: spermatid transition protein 1
F;1-54/Product: spermatid transition protein 1 #status experimental <MAT>
F;1-54/Product: spermatid transition protein 1 #status experimental <MAT>
F;8,35,36,39/Binding site: phosphate (Ser) (covalent) (partial) #status experimental
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Tille: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; WUID:21429245; PMID:11544234
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C;Date: 21-Nov-1993 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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Pred. No. 7e+02;
3; Mismatches 2; Indels
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Pred. No. 6.9e+02;
1; Mismatches 5;
                                                                                                                                                                                                 DB 2;
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Pred. No. 6.5e4
4; Mismatches
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Similarity 40.0%;
4; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Matches 4; Conserv
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A;Residues: 1-53 <KUR>
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A, Molecule type: DNA
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                                                                                                                                        A;Gene: SAS012
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                                                                                               hypothetical protein 49e - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07309
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlc
A;Reference number: 215985; MUID:97303241; PMID:9159184
A;Accession: T07309
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C97021
hypothetical protein CAC0982 [imported] - Clostridium acetobutylicum
C;Species: clostridium acetobutylicum
C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97021
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, i. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q97KD7; GB:AE001437; PIDN:AAK78958.1; PID:g15023889; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K.;
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D89806
D89806
D89806
C; Species: Staphylococcus aureus
C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; State: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Rixuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
C; Shiba, T.; Hattorri, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
C; Shiba, T.; Hattorri, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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54.5%; Pred. No. 6.4e+02;
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Pred. No. 6.5e+02;
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83.3%;
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Best Local Similarity 83.3%,
5; Conservative
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les 6; Conserv
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A,Genome: chloroplast
C,Keywords: chloroplast
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A;Molecule type: DNA
A;Residues: 1-50 <KUR>
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A, Gene: CAC0982
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Matches
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B.S.; EE

us-09-648-816b-4.rpr

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C,Accession: S31636
R,Klein, J.; Ulrich, C.; Plapp, R.
submitted to the EMBL Data Library, August 1992
A,Description: Characterization and sequence analysis of a small cryptic plasmid from Lac
A; Reference number: A92171; MUID: 75095670; PMID: 1112834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.8%;
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ilarity 71.4%;
Conservative
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Matches 5; Conservative
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A;Accession: S31636
A;Status: preliminary
A;Molecule type: DNA
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Hes 5; Conser
                                            A; Accession: A92171
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A, Map position: 1
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Matches
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NyAlternate names: testis-specific basic protein

C.Species: Ratures norvegicus (Norway 12-)

C.Species: Ratures norvegicus (Norway 12-)

C.Species: Ratures norvegicus (Norway 12-)

C.Jate: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004

C.Jacession: A29095, JS0109; Ā92171; A02655; S03177

R.Heidaran, M.A.; Kistler, W.S.

Gene 54, 281-284, 1987

A,Title: Isolation of a cDNA clone for transition protein 1 (TP1), a major chromosomal p. A; Recession: A29095; MUID:88005793; PMID:2820847

A,Recession: A29095

A,Molecule type: mRNA

A,Residues: 1-55 AELS

A,Accession: A29095

A,Molecule type: MNA

A,Reference number: JS0109; MUID:89252920; PMID:2524424

A,Accession: JS0109

A,Molecule type: DNA

A,Residues: 1-55 AELS

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A; Residues: 1-55 «KIM»
A; Cross-references: UNIPROT: P17305; GB: X65041; NID: 9807; PIDN: CDA46175.1; PID: 9808
A; Note: sequence modified after extraction from NCBI backbone
R; Kremling, H.; Luerssen, H.; Adham, I.M.; Klemm, U.; Tsaousidou, S.; Engel, W.
Differentiation 40, 184-190, 1989
A; Title: Nucleotide sequences and expression of CDNA clones for boar and bull transition
A; Reference number: A37347; MUID: 89378557; PMID: 2777004
                                                                                                                                                                                                                                     spermatid transition protein 1 - bovine

NyAlternate names: testis-specific basic protein
C;Species: Bos primigenius taurus (Catatle)
C;Date: 21-Jul-1995 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Date: 21-Jul-1995 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Date: 21-Jul-1995 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
R;Kim, Y; Kreming, H; Tessmann, D; Engel, W.
DNA.Seq. 3, 123-125, 1992
A;Title: Nucleotide sequence and exon-intron structure of the bovine transition protein
A;Reference number: A56647; MUID:93091245; PMID:1457814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:X16171; NID:g805; PIDN:CAA34293.1; PID:g806
A;Note: translation of initiator Met is not shown
C;Comment: This protein replaces histones and is replaced by other transition proteins
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KeWywods DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;2-55/Product: spermatid transition protein 1 #status predicted <MMT>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted
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Pred. No. 7.1e+02;
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nes 5, Conservative
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RKYRKSSLKS 39
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A; Residues: 2-55 < KRE>
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A; Molecule type: protein
A; Residues: 2-45./s',47,D',49-55 <KIS>
R; Kistler: VS.; Noyes, C.; Heinrikson, R.L.
Biochem. Biophys. Res. Commun. 57, 341-347, 1974
A; Title: Partial structural analysis of a highly basic low molecular weight protein from A; Reference number: A901090 WUID: 7416.7115; PWID: 4829397
A; Contents: annotation; partial sequence
C; Comment: The presence of this protein in mammalian testes is correlated with the occur?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Comment: This protein replaces histones and is replaced by other transition proteins on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: spermatid transition protein 1
C;Keywords chromosomal protein; DNA binding; nucleus; phosphoprotein; spermatogenesis; t
F;2-55/Product: spermatid transition protein 1 #status experimental <MAT>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H09388
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Atlle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor, A;Reference number: A69250; MulD:98049343; PMID:9389475
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C;Species: Lactobacillus curvatus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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Pred. No. 7.1e+02;
3; Mismatches 2; Indels
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Pred. No. 7.1e+02;
1; Mismatches 1;
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RESULT 45
B69189
connerved hypothetical protein MTH67 / MTH82 - Methanobacterium thermoautotrophicum
C; Species: Methanobacterium thermoautotrophicum
C; Species: Methanobacterium thermoautotrophicum
C; Decension: B69189; B69209
C; Accession: B69189; B68209
R; Smith, D. R; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
C) Liu, D.; Spadafora, R.; Vicariare, R.; Wiard, Y.; Mierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Nao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Barteriol. 179, 7132-7155; Nao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Residues: Declininary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-60 «WTH>
A; Residues: 1-60 «WTH>
A; Residues: 1-60 «WTH>
A; Genetice: CPY1
A; Genetice: CPY2
C; Genetice: CPY2
A; Genetice: CPY2
C; Genetice: MTH67
C; Genetice: MTH87
C; C; Genetice: MTH82
                             A, Cross-references: UNIPROT: Q05642; EMBL: Z14234; NID: g43976; PIDN: CAA78601.1; PID: g4397
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                                                                                Score 28; DB 2; Length 56;
Pred. No. 7.2e+02;
3; Mismatches 3; Indels
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                                                                                Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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A;Residues: 1-56 <KLE>
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Search completed: May 16, 2005, 08:42:26 Job time : 12.2069 secs

29 YKKAKKAL 36

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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 74.9483 Seconds (without alignments) 92.887 Million cell updates/sec Run on:

US-09-648-816B-3 87 score: Perfect

1 ALYKKFKKKLLKSLKRLG 18 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

1066881 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:*geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Aay57465 Antimicro	Abg69889 Rabbit pl	Aay57501 Antimicro	Aay57499 Antimicro	<u>~</u>	Abg69925 Rabbit pl	Aay57502 Antimicro		Aay57496 Antimicro		Adl70275 Peptide a	Aay57497 Antimicro	Abg69921 Rabbit pl		Adl70278 Peptide a	Abg69990 Rabbit pl	Rabbit	Aay57504 Antimicro		Antimic	Abg69924 Rabbit pl	Aay57503 Antimicro		5 Antimic	Abg69929 Rabbit pl
ΩΙ	AAY57465	ABG69889	AAY57501	- AAY57499	ABG69923	ABG69925	AAY57502	ABG69926	AAY57496	ABG69920	ADL70275	AAY57497	ABG69921	ADL70276	ADL70278	ABG69990	ABG69992	AAY57504		AAY57500	ABG69924	AAY57503	ABG69927	AAY57505	ABG69929
* Query Match Length DB					19 5			20 5																	18 5
% Query Match I	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.4	95.4	94.3	94.3	93.1	•	88.5	88.5
Score	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87	87		83	83	82	82	81	81	77	77
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# ALIGNMENTS

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. Antimicrobial peptide RP-1 SEQ ID NO:3. AAY57465 standard; peptide; 18 AA. 25-FEB-2000 (first entry) Oryctolagus cuniculus. WO9942119-A1 Synthetic. AAY57465; RESULT 1 

26-AUG-1999.

99WO-US003350. 98US-00025319. 17-FEB-1999; 18-FEB-1998; (HARB-) HARBOR-UCLA RES & EDUCATION INST.

Shen AJ; Yeaman MR, WPI; 1999-527417/44.

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Claim 17; Page 106; 166pp; English.

activity or for potentiating antimicrobial agants active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XEBZENEXE and its derivatives selected from XEBZENEXE, BXZXZB, XEBZZEBX and BBXZBBZZ; and (b) as second peptide template XEBXX and their derivatives selected from the group consisting of XBBXBBX, BXXEXB, XBBZXBBX and BBXZBBZZ; and (b) as second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, BXBEXXB, BXBZXXBB, XBBZXXBB, ABZZKBB, ABZZKBB, ABZZKBB, ABZZBZ, and (b) at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of The present invention describes an antimicrobial peptide (AP) for direct

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The INVENTION TETATURE TO an anticontral peptide of 5-
150 amino acida containing a 7-13 amino acid core sequence (derived from
150 amino acida containing a 7-13 amino acid core sequence (derived from
150 amino acida containing a 7-13 amino acid core sequence (derived from
150 amino acida containing a 7-13 amino acid core sequence (derived from
150 cromple structures are fully described in the specification. Also
150 cromple structures are fully described in the specification. Also
151 cromple are (i) an antimicrobial peptide composition for direct activity
152 crofe sequence selected from truncations of the peptides described above,
153 core sequence selected from truncations of the peptides described above,
154 cand retromers, extensions, combinations of the peptides described above,
155 candimicrobial peptides for potentiating antimicrobial activity of
156 cantimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of
157 conventional antimicrobials, agents that enhance the antimicrobial
158 conventional antimicrobials, agents that enhance the antimicrobial
159 conventions of leukocytes, as disinfectants or preservatives for use in
158 cods and cosmetics and as agents to improve efficiency of molecular
158 cods and cosmetics and as agents to improve efficiency of molecular
159 codes and cosmetics and as agents to improve efficiency of molecular
150 considered to have undesirable toxicity, immunogenicity and short
159 chalf-lives due to biodegradation. The peptides of the present invention
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neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antimicrobial peptide composition for use
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                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                      100.0%; Score 87; DB 2; 1
100.0%; Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG69889 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALYKKFKKKLLKSLKRLG 18
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                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                   Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200255554-A2
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                                                                                                                                                                                                                                                                      Query Match
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the present invention describes an animarcobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an animo acid sequence selected from the group consisting containing an animo acid sequence selected from the group consisting as escend form XZBBZBXBXB and its derivatives a second peptide template XBBXXXBB, XBBXXBBX and their derivatives selected from the group consisting of XBBXBBX, ABBXXBBX, BBXXXBBX, BBXXXBB, and XBBXXBBXXBBXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of apoptosis of microbial cells. AAY57463 to AAAY5757 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                              ö
are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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0
                                                                                                                                                                           Length 18;
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                                                                                                                                                                       / Match 100.0%; Score 87; DB 5; L Local Similarity 100.0%; Pred. No. 1.8e-05; les 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
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                                                                                                                                                                                                                                                                                                                                                                                 AAY57501 standard; peptide; 19 AA.
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                                                                                                                                        Sequence 18 AA;
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Matches
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Length 19;

DB 2;

100.0%; Score 87;

Query Match

(first entry)

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New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                          Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                Rabbit platelet microbicidal protein, PMP-2, based peptide #35.
                                                                                                                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
  ABG69923 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                        24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                      25-AUG-2000; 2000US-00648816.
                                                                                                                                                                              Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                          (eaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-590659/63
                                                                                                                                                    mutant; mutein.
                                                                                                                                                                                                                     WO200255554-A2.
                                                       21-OCT-2002
                                                                                                                                                                                                                                                18-JUL-2002
                                                                                                                                                                                          Synthetic
                             ABG69923;
  The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXEBXB and its derivatives selected from XZBBZBXBXB, BXZXXXB, XBBXZBBXB and BBXZBBXZ; and (b) a second peptide template XBBXXBX, BXBXXBBS and BBXZBBXZ; and (b) a second peptide template XBBXXBBX, BXXBXSB, BXBBXXBB, and Consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and consisting of XBBXBBX, XBBXXBBX, BXXBXXB, ABBZXXBB, and Consisting of XBBZBBX, ABBXXBBX, BXBXXBB, and consisting of XBBZBBX and their derivatives selected from the amino acid, and where B = at least one positively charged amino acid, and where B, X and Z man and a fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX57463 to AAX5757 represent sequences
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                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial peptides for potentiating antimicrobial agents active
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               0; Indels
    Pred. No. 1.9e-05;
                                                                                                                                                                                                                     Antimicrobial peptide OC-RP-1 SEQ ID NO:37.
               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 58; 166pp; English.
                                                                                                                                     AAY57499 standard; peptide; 19 AA
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                                                           1 ALYKKFKKKLLKSLKRLG 18
                                          1 ALYKKFKKKLLKSLKRLG 18
 100.08;
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                                                                                                                                                                                          (first entry)
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Best Local Similarity 100.'
Matches 18; Conservative
               18; Conservative
                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeaman MR, Shen AJ;
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                        Synthetic.
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from FMP-1 and PMP-2, platelet microbiocidal protein), and retromers. From FMP-1 and PMP-2, platelet microbiocidal protein), and retromers. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as individual antimicrobial agents, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in the foods and cosmetics and as agents to improve efficiency of molecular belongy techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short belong are based upon natural antimicrobial peptides that have potent and broad spectrum activity against perhapses exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and expected the exhibiting multiple antibiotic resistance. They exhibit
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100.0%; Score 87; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 18; Conservative 0; Mismatches 0;
Example; Page 71-72; 221pp; English.
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Gaps

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ALYKKFKKKLLKSLKRLG 19

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RESULT 5 ABG69923

1 ALYKKFKKKLLKSLKRLG 18

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Pred. No. 1.9e-05; Mismatches 0;

100.08; Pr.

18; Conservative

Similarity

Local Best Loc Matches 18

1 ALYKKFKKKLLKSLKRLG

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2 ALYKKFKKKLLKSLKRLG 19

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25-AUG-2000; 2000US-00648816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-590659/63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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RESULT 6
ABG69925
ABG79999
ABG7999
ABG799
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RESULT
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Eventuations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial against organisms such as bacteria and fungi. The leukocytes against organisms such as individual antimicrobial agents frate mhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial agents (conventional antimicrobials, agents that enhance the antimicrobial or functions of leukocytes, as disinfectants or preservatives for use in thoology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short based upon natural antimicrobial peptides of prior art have generally convention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibicit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                             Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                 Rabbit platelet microbicidal protein, PMP-2, based peptide #37.
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                                                ABG69925 standard; peptide; 19 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAX57557 represent sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40.
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                                                                                                                                                                                               AAY57502 standard; peptide; 20 AA
1 ALYKKPKKKLLKSLKRLG 18
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Gust Local Similarity 100.v.
Best Local Similarity 100.v.
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                                                                                                                                                                                                                                                                   AAY57502;
                                                                                                                               RESULT 7
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Query Match

ABG69926

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-10 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbioidal protein), and retromers.

Eventuations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial apeptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficiacy of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and prode resistance. They exhibit lower inherent mammalian cell toxicity and short internal expense control of are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides and expense inherent mammalian cell toxicity and short invention are based upon natural antimicrobial and antimicrobial antimicrobial and antimicrobial and antimicrobial and antimicrobial antimicrobial and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
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                                                                                                                                                                                                      Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                       Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
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ABG69926 standard; peptide; 20 AA
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                                                                                                    (first entry)
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Synthetic.
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                                                                                                    21-OCT-2002
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crivity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting an amino acid sequence selected from the group consisting as elected from XZBBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXZB, XBBXXXBX and BBXZBBXZ; and (b) a second peptide template XBBXXXBX, XBBXXXBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBX, BXXBXB, BXXBXXB, and KBBZXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides also increase the antimicrobial activity of apoptosis of microbial cells. ANSTAST represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
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                                                                                                                                                                                         Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
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                                                                                    AAY57496 standard; peptide; 25
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 2 ALYKKFKKKLLKSLKRLG 19
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                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                     W09942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeaman MR,
                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                       AAY57496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                   RESULT 9
                                                                     AAY57496
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Gaps ö 100.0%; Score 87; DB 5; Length 20; 100.0%; Pred. No. 2e-05; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 18; Conservative

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ABG69920 standard; peptide; 25

RESULT 10

ABG69920

21-OCT-2002 (first entry)

ABG69920;

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1 ALYKKFKKKLLKSLKRLG 18

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ADL70275;

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid corre sequence (derived from FMP-1 and PMP-2, platelet microbicidal protein), and retromers.

Truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations and fusions; and (2) antimicrobial peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally compared to have undesirable toxicity, immunogenicity and short care based upon natural antimicrobial peptides of prior art have generally conventions are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides of prior art have generally contriberance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antimicrobial peptide composition for the prevention and treatment of setions caused by organisms, such as bacteria and fungi, exhibiting
                                                            Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit.
                   Rabbit platelet microbicidal protein, PMP-2, based peptide #32
                                                                                                                                                                                                                                                                                                                                                                                          (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 70; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                 24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                               25-AUG-2000; 2000US-00648816
                                                                                                                                                            Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 AA;
                                                                                                                                                                                                        WO200255554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeaman MR,
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                      overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
They exhibit lower inherent mammalian cell toxicities and
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                          100.0%; Score 87; DB 5; Length 25; 100.0%; Pred. No. 2.4e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 18; Conserv
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25-FEB-2000 (first entry)
                                                      AAY57497
ID AAY5
XX
AC AAY5
XX
DT 25-F
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                                                                                                        ADL70275 standard; peptide; 33 AA.
                                                 ALYKKFKKKLLKSLKRLG 18
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RESULT 11 ADL70275 ID ADL7 XX

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The present sequence is that of Prolider 1 (F1-1), a pipting an introduction with distinct effector and activator domains. PT-1 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for staphylococcus VB protease. PT-1 was designed to be cleaved into 2 distinct effectors in the presence of VB protease. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of VB protease produced by Staphylococcus aureus. Thus, PT-1 was designed to exert optimal antimicrobial activity in the context of infections due to staphylococcus activated in the context of infections due to staphylococcus ells elaborating that have 2 or was protease. PT-1 was synthesised by solid-phase synthesis It is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is that of Protide-1 (PT-1), a peptide antibiotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                         Protide, antibiotide; antimicrobial; interleukin-8; Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 87; DB 8; Length 33; 100.0%; Pred. No. 3.1e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                        15. .16
/note= "Cleaved by V8 protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brass EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1; 103pp; English.
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY57497 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                       20-AUG-2003; 2003WO-US026405
                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2002; 2002US-00225562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALYKKFKKKLLKSLKRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yount NY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-226740/21.
                                                                    Peptide antibiotide
                                                                                                                                                                                                                                                                             WO2004017985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33 AA;
                                                                                                                                                                                                                        Cleavage-site
                                 20-MAY-2004
                                                                                                                                                                                                                                                                                                                    04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      feaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                condition.
                                                                                                                                infection.
                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY57497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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and retromers, extensions, combinations and fusions; and (2)
antimicrobial peptides for potentiating antimicrobial activity of
leukocytes against organisms such as bacteria and fungi. The
antimicrobial peptides are useful as individual antimicrobial agents,
specifically against bacteria and fungi, agents in combination with other
antimicrobials, agents that enhance, potentiate or restore efficacy of
conventional antimicrobials, agents that enhance the antimicrobial
functions of leukocytes, as disinfectants or preservatives for use in
codes and comenties and as agents to improve efficiency of molecular
biology techniques. Antimicrobial peptides of prior art have generally
been considered to have undesirable toxicity, immunogenicity and short
are based upon natural antimicrobial peptides of the present invention
are based upon natural antimicrobial peptides that have potent and broad
spectrum activity against pathogens exhibiting multiple antibiotic
resistance. They exhibit lower inherent mammalian cell toxicities and
overcome problems of toxicity, immunogenicity, and shortness of duration
of effectiveness due to blodegradation, retaining activity in plasma and
serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acid core sequence (derived from PMP-1 and DMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity
                                                                                                                                                                                                                                                         New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 100.0%; Score 87; DB 5; L. Local Similarity 100.0%; Pred. No. 3.3e-05; Ne 18; Conservative 0; Mismatches 0;
                                                                                                                             (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL70276 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                              Example; Page 71; 221pp; English.
                                                                                                                                                                                                                                                                                                    multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                     25-AUG-2000; 2000US-00648816.
                                          24-AUG-2001; 2001WO-US041877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALYKKFKKKLLKSLKRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide antibiotide PT-2.
                                                                                                                                                                        Shen AJ;
                                                                                                                                                                                                                 WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35 AA;
  18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-2004
                                                                                                                                                                        Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL70276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HX S X K X B X B X B X X X X B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                        Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 87; DB 2; Length 35; 100.0%; Pred. No. 3.3e-05; ive 0; Mismatches 0; Indels
Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 126, 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG69921 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                         99WO-US003350.
                                                                                                                                                                                                                                                                                                    98US-00025319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                             Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                         Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200255554-A2
                                                                                                                                                                      WO9942119-A1
                                                                                                                                                                                                                                                       17-FEB-1999;
                                                                                                                                                                                                                                                                                                    18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-2002
                                                                                                                                                                                                                 26-AUG-1999.
                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG69921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Protide; antibiotide; antimicrobial; interleukin-8.
                                                                                                                      Location/Qualifiers
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Gaps

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RESULT 13

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Length 35; Indels 04-MAR-2004

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The present sequence is that of Protide-2 (PT-2), a peptide antibiotide with distinct effector and activator domains. PT-2 contains a C-terminal cantimicrobial peptide effector (RP-1), an N-terminal chemokinae-like peptide effector (interleukin-8 domain) and an activator site specific peptide effector (interleukin-8 domain) and an activator site specific (for C3 convertase, a complement fixing protease. PT-2 is cleaved into 2 distinct effectors in the presence of G3 convertase. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of G3 convertase. Thus, PT-2 was designed to exert coptimal activity in the complement system, which is part of the innate immune response to antigen exposure. PT-2 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more effectors with individual distinct biological functions and one or biological function of one or more effectors upon context activation. The productions are useful in the diagnosis, prophylaxis and therapy of a broad crange of pathological conditions.
                                                                                                                                                                                                                                                                        New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protide; antibiotide; antimicrobial; interleukin-8; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 87; DB 8; Length 36; 100.0%; Pred. No. 3.4e-05; tive 0; Mismatches 0; Indels
16. .17
/note= "Cleaved by C3 convertage"
                                                                                                                                                                                                             Brass EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
17. .18
/note= "Cleaved by MMP-9"
                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2; 103pp; English
                                                                                                                                                                                                             Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL70278 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALYKKFKKKLLKSLKRLG 36
                                                                                                              20-AUG-2003; 2003WO-US026405
                                                                                                                                            20-AUG-2002; 2002US-00225562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide antibiotide PT-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
Les 18; Conservative
                                                                                                                                                                                                             Yount NY,
                                                                                                                                                                                                                                          WPI; 2004-226740/21
                                               WO2004017985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004017985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 36 AA;
Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-2004
                                                                               04-MAR-2004
                                                                                                                                                                                                               Yeaman MR,
                                                                                                                                                                                                                                                                                                            condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL70278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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The present sequence is that of Protide-4 (PT-4), a peptide antibiotide with distinct effector and activator domains. PT-4 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokina-like peptide effector (interleukin-8 domain) and an activator site specific peptide effector (interleukin-8 domain) and an activator site specific for matrix metalloproteinase MMP-9, which is produced to dissolve the cissue infromt of the growing blood vessel thip to allow for its continued tissue invasion. PT-4 was designed to be cleaved into 2 distinct effectors in the presence of MMP-9. In particular, PT-4 exerts artineoplastic and/or antimicrobial activity less than that of RP-1 in the presence of MMP-9, but equivalent to or exceeding that of RP-1 in the presence of MMP-9, but equivalent to or exceeding that of RP-1 in the presence of MMP-9, the context of new blood wassel formation. PT-4 extinction and an example of context-activated protides of the invention and one or more effectors with individual distinct biological functions and one cor more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                           New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabbit platelet microbicidal protein, PMP-2, based peptide #102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 87; DB 8; Length 39; Local Similarity 100.0%; Pred. No. 3.7e-05; es 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                       Brass EP;
                                                                                                               HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 4; 103pp; English
                                                                                                                                                       Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG69990 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ALYKKFKKKLLKSLKRLG 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2001; 2001WO-US041877.
                                   20-AUG-2003; 2003WO-US026405
                                                                          20-AUG-2002; 2002US-00225562
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                                                                                                                                                       Yount NY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus
                                                                                                                                                                                            WPI; 2004-226740/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200255554-A2
                                                                                                                                                       Yeaman MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG69990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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18-JUL-2002.

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The invention relates to an antimunicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 possible structures are fully described in the specification. Also included are (1) an antimicrobial agents acity eagainst organisms such as core sequence selected from truncations of the peptides described above, core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance the antimicrobial agents that enhance the antimicrobial consetics and as agents that enhance the antimicrobial for such inventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents that enhance the antimicrobial considered to have undesirable toxicity, immunogenicity and short considered to have undesirable toxicity, immunogenicity, and short considered to have undesirable toxicity, immunogenicity, and short considered to have the benefit of the present invention considered to have undesirable toxicity, and shortness of duration considered to have undesirable toxicity, and shortness of duration of effectiveness due to biodegradation, retaining activity and short sequence problems of toxicity, immunoge
                                                                                                                                                                                                              New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                             invention relates to an antimicrobial peptide composition for use
                            (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                       Example; Page 67; 221pp; English
                                                                                                                                                                                                                                                                        multiple antibiotic resistance.
                                                                                         Yeaman MR, Shen AJ;
                                                                                                                                                  WPI; 2002-590659/63
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100.0%; Score 87; DB 5; Length 40; 100.0%; Pred. No. 3.7e-05; ive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 18; Conservative Sequence 40 AA; Query Match

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Gaps

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1 ALYKKFKKCLKSLKRLG 18 1 ALYKKFKKKLLKSLKRLG 18 g

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ABG69992 standard; peptide; 40 AA ABG69992; RESULT 17 

21-OCT-2002 (first entry)

Rabbit platelet microbicidal protein, PMP-2, based peptide #104

Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods, cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.

Oryctolagus cuniculus. Synthetic.

WO200255554-A2.

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acide core sequence (derived from 150 amino acide containing a retrobled in the specification. Also truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) acteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides are useful as individual antimicrobial agents, cantimicrobial peptides are useful as individual antimicrobial agents to entimicrobial peptides are useful as individual antimicrobial agents (2) antimicrobial peptides are useful as individual antimicrobial agents (2) antimicrobial peptides and community agents in combination with other antimicrobial antimicrobials, agents that enhance the antimicrobial peptides of procentiate or restore efficact to have undesirable toxicity, immunogenicity and short or are based upon natural antimicrobial peptides of prior art have generally become problems of toxicity immunogenicity, and shortness of covercome problems of toxicity, immunogenicity, and shortness of effectiveness due to biodegradation, retaining activity in plasma and community against pathogens exhibiting multiple antibiotic or reststence. The present mammalian cell toxicity, immunogenicity, and shortness of covercome problems of toxicity, immunogenicity, and shortness of effectiveness due to biodegradation, retaining activity in plasma and community and are based upon natural antimicrobial pept
                                                                                                                                                                                                                                                                                                                                      New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                    (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 67; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 multiple antibiotic resistance.
                                                                                                            25-AUG-2000; 2000US-00648816
                                                    24-AUG-2001; 2001WO-US041877
                                                                                                                                                                                                                                                                              WPI; 2002-590659/63.
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Gaps ö 100.0%; Score 87; DB 5; Length 40; 100.0%; Pred. No. 3.7e-05; Live. 0; Mismatches 0; Indels 1 ALYKKFKKKLLKSLKRLG 18 Local Similarity 100. Query Match Matches ò

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1 ALYKKFKKKLLKSLKRLG 18

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AAY57504 standard; peptide; 18 AA.

RESULT 18

AAY57504;

(first entry) 25-FEB-2000 Antimicrobial peptide RP-1-10F SEQ ID NO:42.

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. 

Synthetic.

Oryctolagus cuniculus.

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide corts sequence (derived from FNP-1 and PMP-2, platelet microbical protein), and retromers.

CC PMP-1 and PMP-2, platelet microbical protein), and retromers.

CC PMP-1 and PMP-2, platelet microbical protein), and retromers.

CC truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fundions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial agents, combination with other containing apprinces that enhance the antimicrobial agents of conventional antimicrobials, agents to improve efficiency of conventional antimicrobials, agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short care based upon natural antimicrobial peptides of prior art have generally biology techniques. Antimicrobial peptides of prior art have generally considered to have undesirable toxicity, immunogenicity, and short are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic creasserance. They exhibit lower inherent mammalian cell toxicity, immunogenicity, and shortness of testerore problems of toxicity, immunogenicity, and shortness of effectiveness due to biodegradation, retaining activity in plasma and companies.
                                                                                                                                                                          New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 83; DB 5; I
Pred. No. 6.6e-05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
                         (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY57500 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                             Example; Page 72; 221pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.4%;
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Best Local Similarity 94.4'
Matches 17; Conservative
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                                                                              Shen AJ;
                                                                                                                                WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000
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                                                                                 Yeaman MR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY57500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXXZXB, XBBXXZBX and BBXZBBXZ; and (b) a second peptide template XBBXX BX ABBXXBXB and and second peptide template XBBXXBXB, XBBXXBBX, BBXXBBX, BBXXBXB, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and CABAXBBXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX757463 to AAX5757 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.4%; Score 83; DB 2; Length 18; 94.4%; Pred. No. 6.6e-05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                          (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG69928 standard; peptide; 18 AA
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                                                                                                                                   99WO-US003350
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Best Local Similarity 94.4
Marches 17: Conservative
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                     NPI; 1999-527417/44.
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                           WO9942119-A1
                                                                                                                                   L7-FEB-1999;
                                                                                                                                                                                        18-FEB-1998;
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                                                                              26-AUG-1999
                                                                                                                                                                                                                                                                                                  Yeaman MR,
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RESULT 19

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Gaps

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Length 18; 1; Indels

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WPI; 2002-590659/63.
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                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                        organisms such a potential during the promptises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template SAZBARSKAB and its derivatives selected from XZBAZBARSK, BAZXXZB, KAZBAZXBAR and its derivatives as elected from XZBAZBARSK, BAZXXZBA AND BBAZZBBX; and (b) a second peptide template XBRXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, XBBXXXBBX, XBBXXXBBX, Merce B = at least one positively charged amino acid; X = at least one aromatic amino acid, and where B, X and Z amy be separated by one or more other amino acid. The peptides can be used to treat bacterial and fungal infections. The peptides last increase the antimicrobial activity of neutrophils. The peptides overall effect callular disruption and rapid apoptosis of microbial cells. ANYSY463 to AAX57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                     The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                            Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
                                                                                                                                                                                                                                                                                                                                                                                        94.3%; Score 82; DB 2; Length 18; 94.4%; Pred. No. 9.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                            (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                Disclosure; Page 58; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG69924 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALYKKFKKKLLKCLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALYKKFKKKLLKSLKRLG 18
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                     98US-00025319
99WO-US003350
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                                                                                                                         against bacteria and fungi
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Matches 17; Conservative
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                                                                 Yeaman MR, Shen AJ;
                                                                                       WPI; 1999-527417/44.
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
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17-FEB-1999;
                     18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid core sequence (derived from 150 amino acid acore sequence (derived from 150 acid actions), and retromers. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as action for potentiating antimicrobial agents active against organisms such as activities and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations and fusions; and (2) antimicrobial peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides are useful as individual antimicrobial agents. Conventional apprides are useful as individual antimicrobial agents that enhance the antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial activity of conventional antimicrobials, agents that enhance the antimicrobial for antimicrobials, agents to improve efficiency of conventional antimicrobials, agents to improve efficiency of molecular foods and cosmetics and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides of the resistance. They exhibit lower inherent mammalian cell toxicities and cosmetive and evoluted are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic cresistance. They exhibit plower inherent mammalian cell toxicity, immunogenicity, and secure are based upon actu
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New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
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                                                                                                                                                                                                     Example; Page 72; 221pp; English
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Example; Page 72; 221pp; English.

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZENEXE and BRXZENEXING SERZENEXES and BRXZENEXING SERZENEXES and BRXZENEXING SERZENEXES and ENGREDIA AND SERZENEY SERZENEY AND SERZENEY SERZENEY SERZENEY AND SERZENEY SERZENEY AND SERZENEY S
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                                                                                                                              Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
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                                                                                                                                                                                                           Disclosure; Page 59; 166pp; English.
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Best Local Similarity 94...
Best Local 17; Conservative
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                           Shen AJ;
                                                                          WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
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                     Yeaman MR,
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ABG69927
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-60 against organisms such as bacteria and fungi comprising a peptide of 5-100 amino acid a containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as or for potentiating antimicrobial agents active against organisms such as antimicrobial peptides (13-4 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as individual antimicrobial apprides are useful as individual antimicrobial agents that enhance potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial are in foods and cosmetics and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular codes and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short been considered to have undesirable toxicity, immunogenicity and short conventions are based upon natural antimicrobial peptides of prior art have generally been considered to bave undesirable toxicity, immunogenicity, and shortness of testitance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of defectiveness due to biodegradation, retaining activity in plasma and companies.
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Ouery Match 93.1%; Score 81; DB 5; Length 18; Best Local Similarity 94.4%; Pred. No. 0.00013; Matches 17; Conservative 0; Mismatches 1; Indels

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Gaps

1 ALYKKFKKKLLKSLKRLG 18 1 ARYKKFKKKLLKSLKRLG 18 ò

RESULT 24

AAY57505 standard; peptide; 18 AA. 25-FEB-2000 (first entry) AAY57505; **AAYS7505** 

Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. 99WO-US003350 Synthetic. Oryctolagus cuniculus. 17-FEB-1999; WO9942119-A1 26-AUG-1999 

(HARB-) HARBOR-UCLA RES & EDUCATION INST. 98US-00025319. feaman MR, Shen AJ; 18-FEB-1998;

WPI; 1999-527417/44

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                                                                                                                                                       organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XRDEMENEAR and its derivatives selected from XRBEMENEAR, BENZEAR, KBENZERE and its derivatives as escond peptide template XRBEX. KBENZERE and second peptide template XBEX. MEXENSE, XBENZERE, and (b) a second peptide template XBEX. ABEX. MEXENSE, XBEXZERE, and XBEXZEREX. Where B = at least one positively charged amino acid; x = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal neutrophils. The peptides overall effect callular disruption and rapid apoptosis of microbial cells. AAYS7463 to AAS75557 represent sequences used in the exemplification of the present invention
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                                                                                                                peptide (AP) for direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                The present invention describes an antimicrobial peptide (AP) for activity or for potentiating antimicrobial agents active against
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Pred. No. 0.00047;
0; Mismatches 2; Indels
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                                                                    Disclosure; Page 59; 166pp; English.
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88.9%;
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                      against bacteria and fungi.
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ABG692929
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PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, cruncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or included are (1) an antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungi. The antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The applieds are useful as individual antimicrobial agents, agents that enhance, potentiate and restore efficacy of antimicrobials, agents that enhance the antimicrobial antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of this present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic are based upon natural antimicrobial peptides that have potent and overcome problems of toxicity, immunogenicity, and shortness of effectiveness due to biodegradation, retaining activity in plasma and overcome problems of toxicity, immunogenicity, and setting activity in plasma and serum. The present sequence is a rabbit pwe based antimicrobial peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 77; DB 5; Length Lo, Pred. No. 0.00047; 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.5
Local Similarity 88.5
les 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-226740/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Matches
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The present sequence is that of Protide-3 (PT-3), a peptide antibiotide with distinct effector and activator domains. PT-3 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (RP-1), an N-terminal chemokine-like for thrombin. PT-3 was designed to be cleaved into 2 distinct effectors in the presence of thrombin. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of thrombin, but equivalent to or exceeding that of RP-1 in the presence of thrombin. Thus, PT-3 exerts optimal antimicrobial activity in the context of thrombin as would be present in the setting of vascular injury or infection. PT-3 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alpha-halical structure and is believed to act as an ionophore, making holes in bacterial call membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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100.0%; Pred. No. 0.00092;
cive 0; Mismatches 0;
                               Claim 1; SEQ ID NO 3; 103pp; English.
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91US-00655321.
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(first entry)
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Les 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-281214/38.
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26-NOV-1991
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial compens. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with
                                                                                                                                                                                                                                                                                                                                     Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; cancer; endocrinology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Panasik N;
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                                                                                                                                                                                                                                                                                                        Antibacterial peptide C18G for immunoadapter synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firca JR, Schatz RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are incapable of stimulating antibody production
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77.8%; Pred. No. 0.017;
iive 1; Mismatches 3
                              DB 2;
                                                             1; Mismatches
                              Score 66;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                          influenza, viremia, fungemia, neuro
antibodiotic, antibody, antibiotic.
                                                                                                                                                                                                             AAW10351 standard; peptide; 18 AA.
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                            75.9%;
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                                                                                           1 ALYKKFKKKLLKSLKRLG
                                                                                                               1 ALYKKLLKKLLKSAKKLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                            22-SEP-1997 (first entry)
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                                                             14; Conservative
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Best Local Similarity
                                             Local Similarity
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Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                           AAW10351;
                                Query Match
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                                                              Matches
                                                                                                                                                                             RESULT 28
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us-09-648-816b-3.rag

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Antimicrobial compsns. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with immunoglobulin.
                                                                                                                                                                                               Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; cancer; endocrinology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams JA, Shekhani MS, Firca JR, Schatz RW, Pugh C,
Stafford D;
                                                                                                                                                     Antibacterial peptide C19G for immunoadapter synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 39; Page 150; 227pp; English.
                                                                                                                                                                                                                              influenza; viremia; fungemia; neuro
antibodiotic; antibody; antibiotic.
     AAW10352 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-077224/07.
                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
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                                                                                                    22-SEP-1997
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                                                                                                                                                                                                                                                                                                         Synthetic
                                                        AAW10352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a therapeutic formulation comprising N-
(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described
is a method of treatment for bacterial disease comprising: (a) providing
cambiect with symptoms of bacterial disease with one or more fimbriae-
binding compounds comprising a mannose of an anomeric configuration, an
alpha-aromatic or heteroarcmatic ring attached to the mannose by a
clycosidic or pseudoglycosidic linkage and a functional group which
provides a site for chemical modification remote from the mannose and
pharmaceutically carrier; and (b) administering the fimbriae-binding
compounds can be used for treating subjects with symptoms of and for
subjects at risk from bacterial diseases. Treatment of and prevention of
blood-borne and toxin mediated diseases in particular sepsis in humans
can other animals can be carried out and the compounds may also be used
to identify bacteria according to their cell binding specificity's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         through conjugation to reporter substances such as dyes, luminescent or lutorescent molecules and enzymes. The compounds also inhibit the agglutination of yeast cells induced by type 1 pili bearing bacteria. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                    Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin; bacterial infection; antibacterial; fimbriae-binding compound; sepsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 3; Length 18;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                         Antibacterial peptide C18G SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson B, Firca JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 39; Col 84; 89pp; English.
                                                                                                                                                     AAY68001 standard; peptide; 18 AA
96US-00760903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.9%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -mannopyranoside or its cyst
treating bacterial diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shekhani MS,
                                                                                                                                                                                                                                                       11-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS5998381-A
                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                      AAY68001;
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Matches
                                                                                                    RESULT 29
AAY68001
AA
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/note= "In amide form"

95US-00482191.

Location/Qualifiers

(first entry

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The present sequence is a peptide designated C19G. This was used to produce an immunoadapter conjugate. Making a conjugate comprises covalently linking a surface-binding ligand (SBL) to a hapten via a spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the compound with immunoglobulin (IS) under conditions that allow for non-covalent binding of the Ig to the hapten of the compound. The conjugate can be used for the diagnosis, prevention and treatment of microbial infections, e.g. sepsis, influenca, viremia or fungemia. They can also be used in neurology, cancer and endocrinology, where Ig targeting can provide desired therapeutic effects. The methods for producing a signal
                                                                                                                                                                                                                                                                                                       conjugate can use small molecule targeting ligands to efficiently direct otherwise unreactive Ig to microbial targets. This targeting allows Ig to react with microbial structures that may not normally be accessible to Ig, or are incapable of stimulating antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.9%; Score 66; DB 2; Length 19; 77.8%; Pred. No. 0.018; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY68002 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALYKKFKKKLLKSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 77.8 tes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY68002;
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Matches
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AAY68002
ID AAY68
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AC AAY68
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Gaps ö

3; Indels

Mismatches

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cutivity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting containing an amino acid sequence selected from the group consisting selected from XZBBZBXBXB and its derivatives selected from XZBBZBXBXB BXZXZB, XBBXZXBX and BBXZBBX; and (b) a second peptide template XBBXXXB, XBBXXBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXBXXBB, BXBXXBB, and XBBZXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7463 to AAAYS757 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection; fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbit platelet microbicidal protein, PMP-2, based peptide #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 73.6%; Score 64; DB 2; Length 18; Local Similarity 76.5%; Pred. No. 0.033; Nes 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                     (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 111; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG69896 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LYKKWKNKLKRSLKRLG 18
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                                                                                                                                                    99WO-US003350
                                                                                                                                                                                                   98US-00025319
                                                                                                                                                                                                                                                                                                                                                                                                                              against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-2002 (first entry)
  Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant; mutein.
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                                                 W09942119-A1
                                                                                                                                                    17-FEB-1999;
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                                                                                                   26-AUG-1999
                                                                                                                                                                                                                                                                                                      feaman MR,
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Matches
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ID ABG6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described is a method of treatment for bacterial disease comprising: (a) providing campounds of treatment for bacterial disease comprising: (a) providing compounds of bacterial disease with one or more fimbriae-binding compounds comprising a mannose of an anomeric configuration, an alpha-aromatic or heteroaromatic ring attached to the mannose by a glycosidic or pseudoglycosidic linkage and a functional group which provides a site for chemical modification remote from the mannose and pharmaceutically carrier; and (b) administering the fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compounds can be used for treating subjects with symptoms of and for subjects at risk from bacterial diseases. Treatment of and prevention of blood-borne and toxin mediated diseases in particular sepsis in humans and other animals can be carried out and the in vivo neutralisation of the effects of endotoxin is also possible. The compounds may also be used to identify bacteria according to their cell binding specificity's through conjugation to reporter substances such as dyes, luminescent or fluorescent molecules and enzymes. The compounds also inhibit the agglutination of yeast cells induced by type 1 pili bearing bacteria. The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a therapeutic formulation comprising N-
                                                 Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin; bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.9%; Score 66; DB 3; Length 19; 77.8%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptide RP-8 SEQ ID NO:10.
Antibacterial peptide C19G SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson B, Firca JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 39; Col 84; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY57472 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                                                                                              96US-00760903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -mannopyranoside or its cyst
treating bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                             (OPHI-) OPHIDIAN PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-115173/10.
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Shekhani MS,
                                                                                                                                                                                                                                                                                                                                06-DEC-1996;
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                                                                                                                             Synthetic.
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This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphahelical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR,2003 to correct PA
                                                                                                                                                                                                                 Compsns. for treating infections sensitive to beta-lactam antibiotics -comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                     Claim 17; Page 44; 64pp; English.
                                                                                                 (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                        90US-00484020.
91US-00655321.
90US-00484020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALYKKFKKKLLKSLKRLG
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Best Local Similarity 72.2
Matches 13, Conservative
                                                                                                                                         Blake JJ,
                                                                                                                                                                                 WPI; 1991-281214/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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  23-FEB-1990;
                                                             19-FEB-1991;
                                        23-FEB-1990;
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26-NOV-1991
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                                                                                                                                           Darveau RP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                       The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acide fore sequence (derived from PMP-1 and PMP-2, platelet microbiodial protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungi. The classification peptides are useful as individual antimicrobial agents, agents useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobial peptides are useful as individual antimicrobial agents that enhance the antimicrobial agents (conventional antimicrobials, agents that enhance the antimicrobial peptides of protein and accountiation of leukocytes, as disinfectants or preservatives for use in foods and commercise and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic creatstance. They exhibit lower inherent mammalian cell toxicity, in plasma and considered to biodegradation, reteaning activity in plasma and considered to biodegradation, reteaning activity in plasma and considered to biodegradation, retaining activity in plasma and considered to biodegradation, retaining activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                              정
                                                                                                                                                            New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%; Score 64; DB 5; Length 18; 76.5%; Pred. No. 0.033; 2; Indels ive 2; Mismatches 2; Indels
                                      (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                            Disclosure; Page 130; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR13926 standard; protein; 18 AA.
                                                                                                                                                                                                        multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LYKKFKKKLLKSLKRLG 18
25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYKKWKNKLKRSLKRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 76.5
les 13; Conservative
                                                                              Shen AJ;
                                                                                                                      WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
                                                                                Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Gaps

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Score 62; DB 2; Length 18; Pred. No. 0.064; 2; Mismatches 3; Indels

5.

71.3%; 72.2%;

18

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Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is a specific example of a cationic oligopeptide suitable for un compositions with beta-lactam antibiotics. The peptide has an alpha-
                                                                                                                                                                            human platelet factor 4 C-13 fragment; amphipathic alpha helix.
                                                                    AAR13928 standard; protein; 18 AA
                                                                                                                                                                                                                                                                                                                                                            Darveau RP, Blake JJ, Cosand WL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 44; 64pp; Eńglish.
                                                                                                                                                                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB CO
         18
                                                                                                                                                                                                                                                                         90US-00484020
                                                                                                                                                                                                                                                                                                 90US-00484020
                                                                                                                                                                                                                                                                                                             91US-00655321
(revised)
(first entry)
                                                                                                                                                     Cationic oligopeptide #4.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1991-281214/38.
                                                                                                                                                                                                                                                                                                 23-FEB-1990;
                                                                                                                                                                                                                                                                                                              19-FEB-1991;
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human platelet factor 4 C-13 fragment; amphipathic alpha helix.

(first entry)

(revised)

25-MAR-2003 26-NOV-1991

AAR13926;

Cationic oligopeptide #2

WO9112815-A 05-SEP-1991

Synthetic.

Best Loc Matches

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RESULT 36

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AAR13930

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Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphahelical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13937. (Updated on 25-MAR-2003 to correct PA
                                                                                                                       numan platelet factor 4 C-13 fragment; amphipathic alpha helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human platelet factor 4 C-13 fragment; amphipathic alpha helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed. No. 0.08;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                     Blake JJ, Cosand WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13925 standard; protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 44; 64pp; English
                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO.
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91US-00655321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.3%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LYKKFKKKLLKSLKRLG
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                            Cationic oligopeptide #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cationic oligopeptide #1.
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                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 AA;
                                                                                                                                                                                                                                            23-FEB-1990;
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                                                                                                                                                                                                                                                                                          19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                     Darveau RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
26-NOV-1991
                                             25-MAR-2003
26-NOV-1991
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                                                                                                                                                        Synthetic.
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                  AAR13936;
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Best Local 8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR13925
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helical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-WAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphahalical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synexgistically. See AAR13924-R13929 and AAR13936-7. (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Compans. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                      4; Indels
                                                                                                          Score 62; DB 2;
Pred. No. 0.064;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.3%; Score 62; DB 2; 76.5%; Pred. No. 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cosand WL;
                                                                                                                                                                                                                                                                          AAR13930 standard; protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR13936 standard; protein; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 44; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                      18
                                                                                                                                                                                     ALYKKLLKKLLKKAKKLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-00655321.
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                                                                                                          71.3%;
72.2%;
                                                                                                                                                                      ALYKKFKKKLLKSLKRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Cationic oligopeptide #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Darveau RP, Blake JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-281214/38
                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 AA;
                                                                            Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-1991;
                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
26-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9112815-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                        AAR13930;
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RESULT 37 AAR13936 ID AAR13

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Matches

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Gaps

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24-AUG-2001; 2001WO-US041877.
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                                                                                                                                                                                                                                                                                                                                                                                21-OCT-2002 (first entry)
                                                                                                                                                                                                                                1 ALYKKFKKKLLKS 13
                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-590659/63.
                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200255554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                       ABG69890;
                                                                                                                                                                           Query Match
                                                                                                                                                                                                     Matches
 88888888888888
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                                                                                                                                                                                    This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alpha-helical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-WAR-2003 to correct PA
                                                                                                        Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBABXBAB and its derivatives selected from XZBABZBABAB, BXZXB, BXBXZBBAB and ibs derivatives
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial, metapeptide; PMP-2; platelet microbicidal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                              Score 61; DB 2; Length 18;
Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial peptide RP-2 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 107; 166pp; English
                                                     Cosand WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY57466 standard; peptide; 13 AA
                                                                                                                                                            Claim 17; Page 44; 64pp; English
                          (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                    1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                  91US-00655321,
                                                                                                                                                                                                                                                                                                             70.1%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US003350
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                                                                                                                                                                                                                                                                                                                                          13; Conservative
                                                    Darveau RP, Blake JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-527417/44.
                                                                               WPI; 1991-281214/38
                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                     Sequence 18 AA;
19-FEB-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-PEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY57466;
                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and XBBZXXBBXXBBXXXBBXXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid, Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptiosis of microbial cells. AAX57463 to AAX57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabbit platelet microbicidal protein, PMP-2, based peptide
                                                                                                                                                                                                                                                                                                                           DB 2; Length 13;
                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                        Score 57; DB 2;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 128; 221pp; English.
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Indels

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0.45;

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The invention relates to a novel isolated peptide which is 5-23 amino acids in length, and comprising phenylalanine, leucine, alanine or lysine residues, or contains at least 50 % of the residues. The peptides of the invention have antibacterial, fungicide, cytostatic, and vulnerary activity. The peptides are useful in treating cancer, cystic fibrosis or and, or proliferation of human fibroblasts and lymphocytes, promoting wound healing, and in enhancing the activity of a therapeutic agent. The sequences shown in ABR00759-ABR00923 represent the bioactive peptides of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated peptide for treating cancer, cystic fibrosis, wounds or acne, inhibiting growth of microbial cells, or promoting proliferation of cells, comprises phenylalanine, leucine, alanine or lysine residues.
                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; fungicide; cytostatic; vulnerary; cancer; cystic fibrosis; acne; antimicrobial; human fibroblast; human lymphocyte; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 63.2%; Score 55; DB 6; Length 23; Local Similarity 68.8%; Pred. No. 0.79; es 11; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                    Bioactive synthetic peptide Shiva 10(1-16) Ac.
  ed. No. 0.45
Mismatches
    Pred.
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                                                                                                                                                                                                                               ABR00813 standard; peptide; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 6; 133pp; English.
                                                                    18
                                                                                                               1 ALYKKLLKKLLKFAKKFG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2002; 2002WO-US009534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2001; 2001US-00820053.
28-MAR-2001; 2001US-0279505P.
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                                                                    1 ALYKKFKKKLLKSLKRLG
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                       12; Conservative
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  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               bioactive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                            ABR00813;
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                                                                                                                                                                                    RESULT 42
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              minimizionial peptides and useful as includical and includial against bacteria and fungi, agents in combinations with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventions a nimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of devertion of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphabatical structure and is believed to act as an inonphore, maxing holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprise beta-lactam antibiotic and cationic oligopeptide, useful against
Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compsns. for treating infections sensitive to beta-lactam antibiotics
as individual antimicrobial agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; DB 5; Length 13;
Pred. No. 0.24;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
  peptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13929 standard; protein; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-00484020.
91US-00655321.
                                                                                                                                                                                                                                                                                                                                                                                                                  65.5%;
92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
26-NOV-1991
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RESULT 41

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Gaps ; 0

AAY57471

64.4%; Score 56; DB 2; Length 18;

Sequence 18 AA;

Query Match

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid correspondence (derived from 150 amino acid correspondence) for sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers.

Cruncations, extensions, combinations, funions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide objective against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents to improve efficiency of molecular of foods and cosmetics and as agents to improve efficiency of molecular of foods and cosmetics and as agents to improve efficiency of molecular or foods and cosmetics and as agents to improve efficiency of molecular or bean considered to have undesirable toxicity, immunogenicity and short convertions netured antimicrobial peptides that they present invention convertion are based upon natural antimicrobial peptides that have potent and broad enter and experiment and proad are based upon natural antimicrobial schild antimicrobial peptides that have potent and some protein and proad are based upon natural antimicrobial peptides that have potent and broad entermined antimicrobial peptides that have potent and protein and protein and protein antimicrobial peptides that have potent and protein and proper protein antimicrobial peptides that the peptides that the protein and protein and protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide nRP-1:cRP-13 SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 53; DB 5;
Pred. No. 0.89;
1; Mismatches
                                                                                                                                                                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 130; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57508 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multiple antibiotic resistance.
                                                                                                                                                                            24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                    25-AUG-2000; 2000US-00648816.
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                                                                                                                                                                                                                                                                                                                                                         feaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                          WO200255554-A2
                                                                                                                     18-JUL-2002
   Synthetic.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBBB and its derivatives selected from XZBZBXBBXB. BXZXXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XZBZXXB, XBBXZXBBX and BBXZBBXZ; and (b) group consisting of XBBXBBX, and their derivatives selected from the group consisting of XBBXBBX, BXXXBXB, XBBZXXBB, and XBBZXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
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                                                                                                                  Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                       Antimicrobial peptide RP-7 SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 110; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00025319.
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(first entry)
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                                                                                                                                                                                                                                 Oryctolagus cuniculus.
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25-FEB-2000
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ABG69895;

RESULT 44
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Query Match Matches

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5; Length 13; 1; Indels

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organisms such a pacteria and fungi. The AB comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XXBZXBEXB and its derivatives selected from XZBZBEXBEXB. BXZXXZB, BXZXXBBX and BBXZBBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, XBBXXBBX, XBBXXBBX, ABBXXBBX, and their derivatives selected from the XBBZXXBBXXBBXXBBX, where B = at least one positively charged amino acid, x = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acid. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAVS7463 to AAVS7557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 60; 166pp; English.
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                                                                                                                                                                                   99WO-US003350.
                                        Synthetic.
Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                       Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                               WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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                                                                                                   WO9942119-A1
                                                                                                                                                                                   17-FEB-1999;
                                                                                                                                           26-AUG-1999
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Search completed: May 16, 2005, 08:38:28 Job time: 76.9483 secs g

1 ALYKKFKKKLLKSLK 15

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Best Local Similarity 73.3 Matches 11; Conservative

Query Match

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US-09-525-269A-3
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US-08-233-203-7
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                                                                                May 16, 2005, 08:21:21; Search time 19.2414 Seconds (without alignments) 69.833 Million cell updates/sec
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Sequence 6,
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. /cgn2_ 6/ptodata/1/iaa/5A_COMB.pep:*
    /cgn2_ 6/ptodata/1.iaa/5B_COMB.pep:*
    /cgn2_ 6/ptodata/1.iaa/6A_COMB.pep:*
    /cgn2_ 6/ptodata/1.iaa/6B_COMB.pep:*
    /cgn2_ 6/ptodata/1.iaa/PCTUS_COMB.pep:*
    /cgn2_ 6/ptodata/1.iaa/PCTUS_COMB.pep:*
    /cgn2_ 6/ptodata/1.iaa/PCTUS_COMB.pep:*
5.1.6
Compugen Ltd.
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US-08-73-203-7

US-08-60-903-2

US-08-61-191-2

US-08-61-1027-2

US-08-760-903-3

US-08-62-1027-3

US-08-23-269A-10

US-08-233-203-6

US-08-233-203-6

US-08-233-203-11

US-08-233-203-12

US-08-233-203-12

US-08-233-203-10

US-09-255-269A-9

US-07-725-331-25
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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US-07-725-331-39
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                                                                                                                                                                                                                                           513545 segs, 74649064 residues
version -
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                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       protein search, using sw model
                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                     1 ALYKKFKKKLLKSLKRLG 18
GenCore (c) 1993
                                                                                                                                     US-09-648-816B-3
87
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             Copyright
                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 74
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Match
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Perfect score:
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Maximum DB
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                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                            Searched:
                                                                                 Run on:
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Sequence 7, Application US/08233203
Sequence 7, Application US/08233203
Sequence No. 5403898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosnd, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
                                               Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09525269A
; Sequence 3, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shem, Alexander J.
; TITLE OF INVENTION: Metapebtides
; TITLE OF INVENTION: Metapebtides
; TITLE OF INVENTION: Metapebtides
; TILE REFERENCE: 66742-025 (HRS614)
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT PILING DATE: 1908-02-18
; RRIOR FILING DATE: 1908-02-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
: INRIGHT: 18
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llarity 100.0%; Pred. No. 2.9e-05;
Conservative 0; Mismatches 0;
                          US-08-955-526-11

US-08-525-269A-11

US-08-569-188-2

US-08-569-188-2

PCT-US94-07019-13

PCT-US94-07019-13

US-08-569-188-14

PCT-US94-07019-14

US-08-569-188-14

US-08-569-188-15

PCT-US94-07019-14

US-08-569-188-15

PCT-US94-07019-14

US-08-569-188-15

PCT-US94-07019-16

PCT-US94-07019-16
 PCT-US91-05047-23
PCT-US91-05047-39
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Best Local Similarity
Matches 18; Conserv
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Gaps
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APPLICANT: SHEKTANI, MCHAMMED S.
APPLICANT: STARTZ, JOSEPH R
APPLICANT: PUGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: POGH, CHARLES
APPLICANT: PAGH, CHARLES
APPLICANT: PAGH, CHARLES
APPLICANT: PAGH, CHARLES
APPLICANT: PAGH, CHARLES
APPLICANT: PREVENTION: PREVENTION AND TREATMENT OF SEPSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TOWN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
STRY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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CLASSIFICATION: 514
RAIGR APPLICATION DATA:
RAPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
RRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
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: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08482191
Patent No. 6579696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKKLLKKLLKSAKKLG 18
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TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8%;
Matches 14; Conservative
                                              TELEPHONE: (415) 705-841
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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                                                                                                                                                                                                         SS: single
unknown
                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-760-903-2
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STRANDEDNESS: si
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ZIP: 94104
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Patent No. 5998381
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: SAZE POSTOCIONE STATES OF AMERICA COUNTRY: UNITED STATES OF AMERICA CONTRY: UNITED STATES OF AMERICA ZIP: 94104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Ploppy disk COMPUTER: Ploppy disk COMPUTER: Patentin Release #1.0, Version #1.30 CURRANT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/760,903 FILING DATE: 06-DEC-1996
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTOKNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0063A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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NATORNEY/AGENI INPORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ALYKKFKKKLLKSLKRLG 18
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Best Local Similarity 77.8%;
Matches 14; Conservative
3005 First Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                   Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                               USA
                                                                            COUNTRY:
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Pred, No. 0.017;
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APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: FIRCA, JOSEPH R
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INTENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                   APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
ITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 105-207-203-8
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ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
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                                                                                                                                                                             Sequence 3, Application US/08760903
Patent No. 5998381
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Patent No. 6579696
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       1 ALYKKFKKKLLKSLKRLG 18
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                                                    1 ALYKKLLKKLLKSAKKLG 18
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Best Local Similarity 77.8%;
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                      Score 66; DB 4; Length 18;
Pred. No. 0.016;
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                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANGAST AR. NICHOLAS
APPLICANT: PANGAST AR. NICHOLAS
APPLICANT: PANGAST AR. NICHOLAS
APPLICANT: PANGAST AR. NICHOLAS
COURSEDOND:
ADDRESSES: MEDILEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: SAN PRANICISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIPTION DATA:
CLASSIPTIONIN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEFONMUNICATION NUMBER: OPHD-01280
TELEFAX: (415) 397-8338
INFORMATION FOR SEG 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9610227
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
                                                                                                                                                                                                                                                                                                                                                                                                                         SHEKHANI, MOHAMMED S.
PIRCA, JOSEPH R
                                                                                                                                                                                                                              1 ALYKKLLKKLLKSAKKLG 18
                                                                                                                                                                                                    1 ALYKKFKKKLLKSLKRLG 18
                                                                                                 Query Match 75.9%;
Best Local Similarity 77.8%;
Matches 14; Conservative
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; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-482-191-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                               RESULT 5
PCT-US96-10227-2
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APPLICANT:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB 5; Length 19; Pred. No. 0.017;
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Sequence 10, Application US/09525269A
Sequence 10, Application US/09525269A
Sequence 10, Application US/09525269A
Sequence 10, Application US/09525269A
Sequence 10, Application Sequence 10, Septicant Sequence 10, Septicant Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION: Metapeptides
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 1090-03-13
PRIOR PULING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SECTION 10
SEQ ID NO 10
SEQ ID NO 10
                                             CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 1-DEC-1993
PRIOR APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: OB-DEC-1992
APTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFOR
APPLICATION NUMBER: PCT/US96/10227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.9%;
Best Local Similarity 77.8%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
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Best Local Similarity
Matches 13; Conserva
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STRANDEDNESS: si
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APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: STAFFORD, DOUGLAS C.
TINVENTION: PREVENTION AND TREATMENT OF SEPSIS
                                                                                                              COMPUTER: PALOBY disk
COMPUTER: PLOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: PENDER: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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Pred. No. (
                                                             UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UNITED STATES OF AMERICA
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SHEKHANI, MOHAMMED S.
FIRCA, JOSEPH R
SCHATZ, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALYKKFKKKLLKSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 77.8
nes 14; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                    94104
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                                                                COUNTRY:
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Best Local S
Matches 14
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ADDRESSEE: Bristol-Myers Squibb Company, Patent
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                     3: Department
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ilarity 72.2%;
Conservative
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LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                    Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                              Seattle
                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                           ZIP: 98121
                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-233-203-11
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                                                                                                                               APPLICANT: Date. James J. APPLICANT: Blake, James J. APPLICANT: Cosand, Wealey L. APPLICANT: Cosand, Wealey L. TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING TITLE OF INVENTION: INPECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM TITLE OF INVENTION: ANTIBIOTICS NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSE: Brietal-Myers Squibb Company, Patent STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILING DATE:
PLIANG DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATE:
PILING DATE: 19-FEB-1991
APPLICATION NUMBER: US/07/655,321
PILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62;
Pred. No. (
                                                      Sequence 6, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Cosand, Wesley L.
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US-08-233-203-8
; Sequence 8, Application US/08233203
; Patent No. 5409898
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                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.3
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                        Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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APPLICANT: Darvea
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                                       US-08-233-203-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-233-203-6
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GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Blake, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Weahington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 000063A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08233203
Patent No. 5409898
COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC Compactible
OPERATING SYSTEM: PC-DOS/MS-
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Indels

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APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Blake, James J.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Weeley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.1%; Score 61; DB 1; Length 18; 72.2%; Pred. No. 0.073; ive 2; Mismatches 3; Indels
                                                                                                                                                                                               71.3%; Score 62; DB 1; Length 23; 76.5%; Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
PILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTATION NUMBER: 32,928
REFERRICE/DOCKET NUMBER: 0N0063A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08233203 Patent No. 5409898 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                         2 LYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                  7 LYKKLLKKLLKSAKKLG 23
  12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.29
Matches 13; Conservative
                                              23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 amino acids
                                                                                                                                                                                                                   Best Local Similarity 76.5
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
YES
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                              amino acid
                                                                                         linear
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                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
                                                                                     TOPOLOGY:
                                                                                                                                                        US-08-233-203-12
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                                         LENGTH:
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INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
ANTIBIOTICS
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOUTHARE: Patentin Release #1.0, Version #1.25

SOUTHARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/233,203

FILING DATE: 19-FEB-1991

APPLICATION NUMBER: US 07/484,020

FILING DATE: 19-FEB-1990

ATTORNEY/AGENT INFORMATION:

NAME: POOT, BILAIN W.

REGISTRATION NUMBER: 32,928

REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Bristol-Myers Squibb Company, Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.3%; Score 62; 76.5%; Pred. No. (
                                                           PELLING DATE: 19-FEB-1991
APPLICATION NUMBER: US/07/655,321
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08233203
Fatent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Cosand Wesley L.
TITLE OF INVENTION: COMPOSITONS AND TITLE OF INVENTION: INPECTIONS CAUS TITLE OF INVENTION: ANTIBIOTICS NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                             11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LYKKFKKKLLKSLKRLG 18
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3005 First Avenue
                                                                                                                                                                                                                                                                                  TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206/448-4775
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
US-08-233-203-11
                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
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STREET: 30
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-233-203-12
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Gaps ô

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NAME: Poor, Brian W. REGISTRATION NUMBER: 32,928
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
                                                                                                                                                                                                                        LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
US-09-525-269A-9
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LENGTH: 13
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| Sequence 10, Application US/08233203 |
| Sequence 10, Application US/08233203 |
| Patent No. 5409898 |
| GENERAL INPORMATION: |
| APPLICANT: Darveau, Richard P. |
| APPLICANT: Blake, James J. |
| APPLICANT: Cosand, Wesley L. |
| TITLE OF INVENTION: COMPOSITIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM |
| TITLE OF INVENTION: ANTIBIOTICS |
| NUMBER OF SEQUENCES: 12 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Bristol-Myers Squibb Company, Patent ADDRESSEE: Bristol-Myers Squibb Company, Patent |
| STREET: 3005 First Avenue |
| CITY: Seatile |
| STREET: Washington |
| COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 4; Length 13;
Pred. No. 0.18;
0; Mismatches 1; Indels
                                                                                                                                                                                                              APPLICANT: Yearnan, Michael R.
APPLICANT: Yearnan, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REPERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98121

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
COMPUTER: PACHING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
                                                                                                                                                Sequence 4, Application US/09525269A; Patent No. 6743769; GENERAL INFORMATION:
    1 ALYKKIIKKLESAKKLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKKFKKKLLKS 13
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Best Local Similarity 92.3
Matches 12; Conservative
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                                                                                                      RESULT 15
US-09-525-269A-4
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US-08-233-203-9

Sequence 9, Application US/08233203

Sequence 9, Application US/08233203

Sequence 9, Application US/08233203

Sequence 9, Application US/08233203

Patent No. 54091808

APPLICANT: Darveau, Richard P.

APPLICANT: Darveau, Richard P.

APPLICANT: Cosand, Wesley L.

TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING

TITLE OF INVENTION: NATIBIOTICS

TITLE OF INVENTION: ANTIBIOTICS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Antimicrobiocidal peptide designed in part upon CTHER INFORMATION: microbiocidal domains from platelet microbial; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Shen, Alexander N.
TITLE OF INVENTION: Metapeptides
TITLE REFRENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525, 269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025, 319
PRIOR PRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.4%; Score 56; Best Local Similarity 66.7%; Pred. No. (Matches 12; Conservative 1; Mismatch
REFERENCE/DOCKET NUMBER: ON0063A TELECOMMUNICATION: TELEPHONE: 206/728+800 TELEPHONE: 206/448-4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09525269A Patent No. 6743769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ALYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKKLLKKLLKFAKKFG 18
                                                                                           TELEPAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPB: PRT ORGANISM: Artificial Sequence
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Gaps

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Indels

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90.9%; Pred. No. 1.6;
                         1; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTATION NUMBER: 29,381
REFERRNCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TIBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 3126165418
TELEPAX: 3126165460
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KFKKKLLKSLKRL 17
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                         10; Conservative
                                                                    2 LYKKFKKKLLK 12
                                                                                           2 LYKKWKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                         Matches
                                                                                                                                                                             RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Sequence 8, Application US/09525269A

Patent No. 6743708

Patent No. 6743708

APPLICANT: Yeaman, Michael R.

APPLICANT: Shen, Alexander J.

TILE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REPERENCE: 66742-025 (HR5614)

CURRENT APPLICATION NUMBER: US/09/525,269A

CURRENT FILING DATE: 2000-03-13

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 39

SEQ ID NOS: 39

LENGTH: 14
                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION DATA:

FILING APPLICATION DATA:

APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 19-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.

REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: ON0063A
TELECOMMULCATION INFORMATION:

TELEPHONE: 206/728-4800
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
                                                                               STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||: ::||:|
| ALYRELLRRLLRSARRIG 18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                  Seattle
: Washington
RY: USA
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Best Local Similarity
Matches 9; Conserva
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57.5%; Score 50; DB 4; Length 14;

Query Match

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Sequence 25, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Analogues Thereof NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Milnamow Goldsmith, Sutker, Shore, STRET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: May be a C-terminal amide, and/or may OTHER INFORMATION: be acetylated at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.2%; Score 48; DB 1; Length 18; 76.9%; Pred. No. 3.7; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
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Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTONNEY, AGENT INPORMATION:
NAWE: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910117
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
REGISTATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ. 10 NO: 25:
SEQUENCE CHARACTERISTICS:
                  NUMBER: PCT/US91/05047
                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 KFKKKLLKSLKRL 17
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
PCT-US91-05047-25
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APPLICANT: Blondelle, Sylvie
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE Dressler, Goldsmith, Sutker, Shore,
STREET: 180 North Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: May be a C-terminal amide, and/or may; OTHER INFORMATION: be acetylated at N-terminus.
US-07-725-331-27
  TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Analogues Thereof NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow STREET: 180 No. 5294605th Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 St. 18; Score 48; DB 1; Length 18; Score 48; DB 1; Length 18; Conservative 1; Mismatches 4: Indela
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASETEICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UU-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Bdward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            ZIP: 60601
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEM: Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 22
PCT-US91-05047-25
Sequence 25, Application PC/TUS9105047
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: Patentin Release #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LYKKFKKKLLKSLKRL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                USA
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                                                                                                                                                                                                             COUNTRY:
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Gaps
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PCT-US91-05047-27

Sequence 27, Application PC/TUS9105047

GENERAL INFORMATION:
PAPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STRRET: 180 North Stetson
CITY: Chicago
STATE: IL
                                                                                                                          ö
May be a C-terminal amide, and/or may be acetylated at N-terminus.
                                                                                 55.2%; Score 48; DB 5; Length 18; 76.9%; Pred. No. 3.7;
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OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial CTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-5
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                      ö
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                                                                                               ; OTHER INFORMATION: May be a C-terminal amide, and/or may; OTHER INFORMATION: be acetylated at N-terminus. PCT-US91-05047-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 4; Length 13;
Pred. No. 3.7;
2; Mismatches 2; Indels
                                                                                                                                                                                                            Score 48; DB 5; Length 18;
Pred. No. 3.7;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Seaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antinicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HRS614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yeaman, Michael R.
APPLICANT: Yeaman, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 13
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09525269A, Patent No. 6743769, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09525269A, Patent No. 6743769, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.0%;
                                                                                                                                                                                                          ch 55.2%;
l Similarity 68.8%;
11; Conservative
                                                                                                                                                                                                                                                                                               2 LYKKFKKKLLKSLKRL 17
                                                                                                                                                                                                                                                                                                                     3 LLKKLKKLKKLLKKL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALYKKFKKKLLKS 13
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1 ARYRKFKNKILKS 13
  LENGTH: 18 amino acids
                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                            Query Match
Best Local Similarity
                     TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
US-09-525-269A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-525-269A-6
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                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amalogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.9%; Score 46; DB 1; Length 18; 71.4%; Pred. No. 6.7; tive 1; Mismatches 3; Indels
Score 47; DB 4; Length 14;
Pred. No. 4;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421250-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                         US-07-725-331-23
; Sequence 23, Application US/07725331
; Patent No. 5294605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 23:
  Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KKLLKKLLKKLKKL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3126165418
3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                          2 LYKKFKKKLLK 12
                                                                                                                   ||:||| ||||
2 LYRKFKNKLLK 12
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Best Local Similarity
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.9%; Score 46; DB 5; Length 18; 71.4%; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: Dressler, Milnamow STREET: 180 North Stetson
CITY: Chicago
                                            COMPUTER READBLE FORM:

MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PAPELICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION DATA:
APPLICATION NUMBER: WS 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 31250-80
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 23:
EDURNCE GIRRACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60601

ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/554,422
APLICATION NUMBER: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KKFKKKLLKSLKRL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 52.9
Best Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                              60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US91-05047-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: BOY DESCRIPTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
COMMESSPONDENCE ADDRESS:
ADDRESSEE: & Milnamow
ADDRESSEE: & Milnamow
                                               Sequence 39, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Ampliphilic Peptide Compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.9%; Score 46; DB 1; Length 18; Best Local Similarity 69.2%; Pred. No. 6.7; Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: C-terminal amide, acetylated at OTHER INFORMATION: N-terminus.
                                                                                                                                                                                                                                                                                             ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gameon, Edward P.
REGISTRATION UNDERE: 29,381
REPRENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165418
TELEPHONE: 312616540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 North Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KPKKKLLKSLKRL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US91-05047-23
                                                                                                                                                                                                                                                                                                                                                                           CITY: Chi
STATE: II
COUNTRY:
RESULT 27
US-07-725-331-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-07-725-331-39
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.7%; Score 45; DB 4; Length 13; Best Local Similarity 83.3%; Pred. No. 6.8; Aatches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-569-188-2

) Sequence 2, Application US/08569188

) Patent No. 5847047

) GENERAL INFORMATION:

APPLICANT: SHARON LIPRETTA HAYNIE

ITILE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: WILLINGTON

CITY: WILLINGTON

STATE: DELAWARE
                                                                                                                                                                                                 APPLICANT: Yeanan, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Matimicrobial Peptides and Derived
TITLE OF INVENTION: Matamicrobial Peptides
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT PPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLIANG TATES
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/082, 852
PILING DATE: JUNE 22, 1993
ATTORNEY/ACENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                               US-09-525-269A-11; Sequence 11, Application US/09525269A; Sequence 10, Application US/09525269A; GENERAL INFORMATION:
                     16 SLYKKIIKKLLESGKSL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALYKKFKKKLLK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: C-terminal amide, acetylated at CT-US91-05047-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 46; DB 5;
Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: MEMORYOR INFORMATION:
TELEPHONE: (302) 658-5413
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
                                             421250-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/08985526
Patent No. 6080728
                   REGISTRATION NUMBER: 29,381
REPERENCE/POCKET UNMBER: 4212:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 312616540
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     52.9%;
69.2%;
Gamson, Edward P
                                                                                                                                                                                  LENGTH: 18 amino acida
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 69.27
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KLKKKLLKKMKKL 14
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Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delaware U.S.A.
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US-08-985-526-11
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1 ALYKKFKKKLLKSLKRL 17

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Score 45; DB 5; Length 16;
Pred. No. 8.2;
1; Mismatches 3; Indels
                   APPLICANT:
TITLE OF INVENTION: NOVEL ANTIMICROBIAL
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH 6.0
SOFTWARE: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07019
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 aming acids
                                           NOVEL ANTIMICROBIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application PC/TUS9407019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-569-188-4; Sequence 4, Application US/08569188; Patent No. 5847047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.7%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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Best Local Similarity 71.4*
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide PCT-US94-07019-13
                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: un
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US94-07019-13
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                                                                                                                                                                                       DB 2; Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSER: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILLAINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READBLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,188
                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 525
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
ATTORNEY AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9295-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    Query Match 51.7%; Score 45; Best Local Similarity 71.4%; Pred. No. 8 Matches 10; Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application PC/TUS9407019
                                                                                                                                                                                                                                                                                                                                                                         RESULT 33
US-08-569-188-13
, Sequence 13, Application US/08569188
; Patent No. 5847047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
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71.4%;
                                                                                                                                                                                                                                                                                                2 KLLKGLKGLKKG 15
                                                                                                                                                                                                                                                                           5 KFKKKLLKSLKRLG 18
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 71.4
Matches 10; Conservative
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STRANDEDNESS: unknown
                                                                                                TOPOLOGY: unknown;
MOLECULE TYPE: peptide
US-08-569-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide US-08-569-188-13
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PCT-US94-07019-2
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APPLICANT:
TITLE OF INVENTION: NOVEL ANTIMICROBIAL
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH
OPERATING SYSTEM: MACINTOSH
OPERATION SYSTEM: MACINTOSH
OPERATION OF SEQUENCE: 08/082, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/082, 852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEC ID NO: 13:
SEQUENCE CHARRACTERISTICS:
CHARLEST STATES
INFORMATION FOR SEC ID NO: 13:
CHARLEST STATES
COMPUTED: MACINE STATES
COMPUTED: MACINTOSH
OF SEQUENCE CHARRACTERISTICS:
CHARLEST STATES
COMPUTED: MACINE STATES
COMPUTED: MACI
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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Pred. No. 8.6;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: NOVEL ANTIMICROBIAL
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07019
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 96/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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TITLE OF INVENTION: NOVEL ANTIMICROBIAL
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                            TORNEY/AGENT INFORMATION NAME: LIND ARAMETHY FLOYD
REGISTRATION UNBER: 33,692
REGISTRATION UNBER: CR-9295-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application PC/TUS9407019
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application PC/TUS9407019 GENERAL INFORMATION:
                                                                                                            REFERENCE/DOCKET NUMBER: CR-1
TELECOMUNICACION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                       FILING DATE: JUNE 22, 1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.7%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide US-08-569-188-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: unl
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS: un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERALINFORMATION:
APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
GENERAL INFORMATION:
APPLICANT: SHARON LPRETTA HAYNIE
APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVERTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                      ZURINE CONTINUED SITES OF AMERICAN ZIPS 19898
COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 525
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/082,852
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNDA AXAMETHY FLOXYD
NAME: LINDA AXAMETHY FLOXYD
REGISTRATION NUMBER: 33.692
REFERENCE/DOCKET NUMBER: CR-9295-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45;
Pred. No.
                                                                                                                                                                                                           COUNTRY: UNITED STATES OF AMERICA
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US-08-569-188-14
; Sequence 14, Application US/08569188
; Patent No. 5847047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.7%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 525
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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Gaps
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                                                                                Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08569188
Patent No. 5847047
GENERAL INFORMATION:
APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08569188
Patent No. 5647077
GENERAL INFORMATION:
APPLICANT: SHARON LPRETTA HAYNIE
TITLE OF INVENTION: NOVEL ANTIMICORBIAL COMPOSITIONS
NUMBER OF SEQUENCES: 18
CORRESPONDENCES:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MALTINGON STATES OF AMERICA CONNTRY: UNITED STATES OF AMERICA ZIP: 19898
COMPUTRY: UNITED STATES OF AMERICA ZIP: 19898
COMPUTRY: BADABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTRY: IBM FC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CLASSIFICATION: S25
PRICE DATE: UNDBER: 08/082,852
FILING DATE: JUNE 22, 1993
ATTORNEY/ARTI INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: 33,692
REFERENCE/DOCKET NUMBER: 33,692
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION OF SOCIETY OF SOCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: B. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE
                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 2;
Pred. No. 9;
                                                                                                                                      2; Mismatches
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                                                                                Score 45;
Pred. No. 9
                                                                          51.7%;
69.2%;
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Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                  Query Match
Best Local Similarity 69.27
Best Local 9; Conservative
                                                                                                                                                                                               5 KPKKKLLKSLKRL 17
                                                                                                                                                                                                                                                    2 KLRKKLLKKLKKL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: un
                       US-07-725-331-42
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                                                                                                                                                                                                                                                                                                                                        RESULT 41
US-08-569-188-6
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Fatent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: E Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: May be a C-terminal amide, may OTHER INFORMATION: be acetylated at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: US 07/554,422
FILLING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
TELEPHONE: 3126165418
TELEPHONE: 312616540
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIDIE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTIN RELEASE #1.24 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.7%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KFKKKLLKSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US94-07019-14
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: unl
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US-07-725-331-42
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Score 45; DB 5; Length 18; Pred. No. 9;
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                                                                                                                                                                                                                                                             OTHER INFORMATION: May be a C-terminal amide, may OTHER INFORMATION: be acetylated at N-terminus.
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APPLICANT:

APPLICANT:

TITLE OF INVENTION: COMPOSITIONS

ITILE OF INVENTION: COMPOSITIONS

NUMBER OF SEQUENCES: 15

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: MACINTOSH
                                                                                                                                                                                                                                                                                                                                             Score 45; DB
Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL ANTIMICROBIAL
TITLE OF INVENTION: COMPOSITIONS
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07019
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
            REFERENCE DOCKET NUMBER: 421250-80 TELECOMMUNICATION INFORMATION: TELEPAX: 3126165418
TELEPAX: 312616540
INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application PC/TUS9407019 GENERAL INFORMATION:
REGISTRATION NUMBER: 29,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: JUNE 22, 1993
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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(1 Similarity 71.4%;
10; Conservative 1
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Best Local Similarity 69.2%;
Matches 9; Conservative
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                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
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Best Local Similarity
                                                                                                                                                            TYPE: AMINO ACID STRANDEDNESS:
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GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: BLondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: E Milnamow
STREET: 180 North Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 2; Length 18;
Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPPRING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 525
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/POCKET VUMBER: CR-9295-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-ULL-1990
ATTORNEY AGENT INFORMATION:
NAME: Gamson, Edward P.
                                                             UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
: 1007 MARKET STREET WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 51.7%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                            DELAWARE
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; OPERATING SYSTEM: MACINTOSH 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:

; APPLICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07019
PRIOR APPLICATION NUMBER: 08/082,852
FILING DATE: JUNE 22, 1993
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acids
; STRANDEDNESS: unknown
; MOLECULE TYPE: peptide
; STRANDEDNESS: unknown
; MOLECULE TYPE: peptide
; PCT-US94-07019-15

Query Match
Best Local Similarity 71.4%; Pred. No. 9;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Search completed: May 16, 2005, 08:40:37 Job time : 20.2414 secs

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Sequence

Sequence 1257, 757
Sequence 68, Appl
Sequence 13, Appl
Sequence 27, Appl
Sequence 1, Appl
Sequence 1, Appli
Sequence 31, Appl
Sequence 8, Appli
Sequence 9, Appli

Appli Appli Appli Appli Appli Appli Appli

Sequence 15, Sequence 15,

Sequence Sequence

ALIGNMENTS

Sequence 15,

Appl Appl Appl

Sequence 14, Sequence 14, Sequence 14,

US-10-109-171-161 US-10-920-548A-23 US-10-920-548A-36 US-10-920-548A-36 US-10-920-548A-36 US-10-920-548A-36 US-10-920-548A-36 US-10-10-171-68 US-10-10-171-68 US-10-10-171-68 US-10-10-171-68 US-10-10-171-68 US-10-10-171-68 US-10-10-171-68 US-10-172-075-31 US-10-131-546-8 US-10-131-546-8 US-10-131-546-8 US-10-131-546-14 US-10-131-546-15 
Sequence 14,

Sequence Sequence Sequence Sequence Sequence Sequence

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49, Appl
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88.876 Million cell updates/sec
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Sequence 55,
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(gan2_6/ptodata/1/pubpaa/US07_PUBCOMB. DED: *

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                                                                                                                                                              May 16, 2005, 08:38:44; Search time 67.6552 Seconds
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-109-171-55
US-10-036-869-11
US-09-864-408A-7928
US-09-820-053A-49
US-09-820-053A-56
US-10-109-171-49
US-10-920-548A-16
US-10-920-548A-16
US-09-820-053A-9
US-09-820-053A-161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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87
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0 Maximum DB seq length: 74
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                                                                                                                                                              Run on:
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US-10-109-171-55
; Sequence 55, Application US/10109171
; Publication No. US20030109452A1
; Publication No. US20030109452A1
; Pablication No. US20030109452A1
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
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Sequence 55, Application US/09820053A; Sequence 55, Application US/09820053A; Publication No. US20030083243A1; GENERAL INFORMATION:
JITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES; CURRENT PAPLICATION NUMBER: US/09/820,053A; CURRENT FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 165; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 55; LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.2%; Score 55; DB 10
Best Local Similarity 68.8%; Pred. No. 0.58;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: SYNTHETIC SEQUENCE US-09-820-053A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LFKKFAKKLAKKL 19
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: ARTIFICIAL SEQUENCE
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161, App 9, Appli 9, Appli

Sequence

US-10-109-171-9

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

FILE REFERENCE: HELX028

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CURREAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELKO27
CURRENT APPLICATION NUMBER: US/09/820,053A
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7228
LENGTH: 56
                                                         Sequence 7928, Application US/09864408A Publication No. US20040009474A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: SYNTHETIC SEQUENCE NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LYKKFKKK-----LLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 IYKKFLKKAQDLTSLLKELKSQG 50
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Sequence 49, Application US/09820053A
Publication No. US20030083243A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 56, Application US/09820053A Publication No. US20030083243A1
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ORGANISM: ARTIFICIAL SEQUENCE
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69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: AMIDATION US-09-820-053A-49
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Best Local Similarity 69.2
Matches 9; Conservative
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-864-408A-7928
                                             JS-09-864-408A-7928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
THERAPY
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                                                                                                                                                                                                                                                      DB 14; Length 23;
                                                                                                                                                                                                                                                                                             3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE: «Unknown».
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                    Query Match 63.2%; Score 55; DB Best Local Similarity 68.8%; Pred. No. 0.55 Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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CURRENT APPLICATION NUMBER: US/10/109,171 CURRENT FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MCMORTOW Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                                                                                ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-10-109-171-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence ii, Application US/10036869
Publication No. US20020151516A1
GENERAL INFORMATION:
APPLICANT: Mixson, James A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELEFAX: (302) 658-5613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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LENGTH: 46 amino acids
            NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 SLYKKIIKKLLESGKSL 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.9%;
                                                                                                                            TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                    2 LYKKFKKKLLKSLKRL 17
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4 LFKKFAKKLAKHLKKL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-10-036-869-11
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                                                                                                                                                                     FEATURE:
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APPLICANT: Leach, Martin D.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
TITLE OF INVENTION: NO. US20040009474Alel Human Polynucleotides and Polypeptides Encoc FILE REPERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR PILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
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Pred. No. 20;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                51.7%; Score 45; DB 11; Length 56; 52.2%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELKOZD:
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTO VET. 2.1
SEQ ID NO 49
LENGTH: 23
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Sequence 16, Application US/10920548A
Publication No. US20050065072A1
GENERAL INFORMATION:
APPLICATION: CALIONIC Antimicrobial Peptides and Compositions Thereof
TITLE OF INVERTION: CALIONIC Antimicrobial Peptides and Compositions Thereof
TITLE OF INVERTION WINDER: US/10/920,548A
CURRENT APPLICATION WINDER: US/10/920,548A
CURRENT RILING DATE: 2004-08-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 16
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: E.I. DuPont de Nemours and Co., Inc.
TITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof
FILE REFERENCE: CL-2305
CURRENT APPLICATION NUMBER: US/10/920,548A
CURRENT FILING DATE: 2004-08-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 29
LENGTH: 17
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Pred. No. 21;
1; Mismatches 3; Indels
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49.4%; Score 43; DB 17;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 10; Conservative 1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic amino acid sequence US-10-920-548A-16
    Pred. No. 20;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-920-548A-29
. Sequence 29, Application US/10920548A
. Publication No. US2050065072A1
. GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 71.4%;
Matches 10; Conservative
      69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 KFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||||| ||:||
1 KCLKKLLKLLKKLG 14
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                                                                   2 LYKKFKKKLLKSL 14
                                                                                           |:||| ||| ||
11 LFKKFAKKLAKKL 23
    Best Local Similarity 69.2
Matches 9; Conservative
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; LOCATION: (2)..(17)
US-10-920-548A-29
                                                                                                                                                                       RESULT 9
US-10-920-548A-16
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US-09-820-053A-9
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Publication No. US20030109452A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
TITLE REFERENCE: HELX028
CURRENT APPLICATION WINDER: US/10/109,171
CURRENT PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 49
LENGTH: 23
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Publication No. US20030109452A1

GENERAL INFORMATION:

APPLICANT: OWNER OWNER SHORY BLOACTIVE PEPTIDES AND METHODS FOR THEIR USE

TITLE OF INVERTION SHORY BLOACTIVE PEPTIDES AND METHODS FOR THEIR USE

FILE REFERENCE: HELX028

CURRENT APPLICATION UNDER: US/10/109,171

CURRENT FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 165

SOFTWARE: PATENTIN Ver. 2.1
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OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEX: MOD_RES
                                                                                                                                                                       ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-09-820-053A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-10-109-171-56
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOOTWARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 23
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 69.2%;
Matches 9; Conservative
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ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 69.2
Matches 9; Conservative
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LENGTH: 23
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81.8%;
                         TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 64.7%;
Matches 11; Conservative
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Best Local Similarity 64.7%;
Matches 11; Conservative
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                                                                                                          ; OTHER INFORMATION: AMIDATION
US-10-109-171-9
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Best Local Similarity
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      LENGTH: 23
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Publication No. US20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE FILE REPERENCE: HELX028
CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
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49.4%; Score 43; DB 10; Length 23;
Best Local Similarity 64.7%; Pred. No. 28;
Matches 11; Conservative 1; Mismatches 5; Indels
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                  APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELXOZ:
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
LENGTH: 23
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US-09-820-053A-161
Sequence 161, Application US/09820053A
Publication No. US20030083243A1
GENERAL INFORMATION:
TILLE OF INVERTION: SHORT BIOACTIVE PEPTIDES
TILLE OF INVERTION: SHORT BIOACTIVE PEPTIDES
CURRENT APPLICATION WHMBER: US/09/820,053A
CURRENT APPLICATION NUMBER: 2011-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                   OTHER INFORMATION: SYNTHETIC SEQUENCE NAME/KEY: MOD_RES
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ORGANISM: ARTIFICIAL SEQUENCE
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ORGANISM: ARTIFICIAL SEQUENCE
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Matches 11; Conserv
GENERAL INFORMATION:
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US-10-109-171-9
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LENGTH: 23
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Sequence 6, Application US/10920548A

Sequence 6, Application US/10920548A

Publication No. US20050065072A1

GENERAL INFORMATION:

APPLICANT: E.I. DuPont de Nemours and Co., Inc.

TITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof

FILE REFERENCE: CL-2305

CURRENT APPLICATION NUMBER: US/10/920,548A

CURRENT FILING DATE: 2004-08-18

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Version 3.2

SEQ ID NO 6

LENGTH: 16
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Sequence 161, Application US/10109171

Sequence 161, Application US/10109171

Publication No. US20030109452A1

GENERAL INFORMATION:

APPLICANT: Owen, Donald R.

TITLE OF INVENTION:

TITLE REFERENCE: HELK02B

CURRENT APPLICATION WUMBER: US/10/109,171

CURRENT PILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 165

SEQ ID NO 161

SEQ ID NO 161

LENGTH: 23
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                                                                                                                                                             Score 43; DB 14; Length 23; Pred. No. 28; 1; Mismatches 5; Indels
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28;
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Pred. No.
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PEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD RES
LOCATION: (23)
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US-09-820-053A-68
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US-10-920-548A-36
i Sequence 36, Application US/10920548A
i Publication No. US20550065072A1
i GENERAL INFORMATION:
APPLICANT: E.I. DuPont de Nemours and Co., Inc.
ITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof
ITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof
CURRENT APPLICATION NUMBER: US/10/920,548A
CURRENT FILING DATE: 2004-08-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
LENGTH: 16
                                                                                                                RESULT 16
US-10-540A-23
US-10-920-548A-23
Squence 23, Application US/10920548A
Squence 23, Application No. US20050065072AI
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cationic Antimicrobial Peptides and Compositions Thereof
FILE REFERENCE: CL-2305
CURRENT APPLICATION UNDBER: US/10/920,548A
CURRENT FILING DATE: 2004-08-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 16
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Pred. No. 27;
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 1; Indels
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1; Mismatches
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; Publication No. US20030113798A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: artificial sequence
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Matches 9; Conservative
9; Conservative
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KKLLKLKKIG 13
                                                     8 KKLLKSLKRLG 18
                                 KKLLKSLKRLG 18
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US-10-920-548A-36
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US-10-225-567A-1257
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 Matches
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1220-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PARENTIN VERSION 3.1
SEQ ID NO 1257
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Sequence 68, Application US/10109171

Sequence 68, Application US/10109171

Sequence 68, Application US/10109171

GENERAL INFORMATION:

APPLICANT: Owen, Donald R.

TITLE OP INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE

TITLE OF INVENTION: US/10/109,171

CURRENT APPLICATION UNMBER: US/10/109,171

CURRENT PILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 165

SEQ ID NO 68

LENGTH: 20
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29;
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APPLICANT: Owen, Donald R.; TILLE OF INVENTION: SHORT BIOACTIVE PEPTIDES; TILE REPRENCE: HELK027; CURRENT APPLICATION NUMBER: US/09/820,053A; CURRENT FILING DATE: 2001-03-28; NUMBER OF SEQ ID NOS: 165; SOFTWARE: Patentin Ver: 2.1; SEQ ID NO 68; LENGTH: 20
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Pred. No. 29;
6; Mismatches
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Pred. No.
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Best Local Similarity 46.7%;
Matches 7; Conservative
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Best Local Similarity 60.0%;
Matches 9; Conservative
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US-09-820-053A-68
                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-1257
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Sequence 1, Application US/10382240 Publication No. US20030216298A1 GENERAL INFORMATION:
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Publication No. US20020151516A1
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47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Wilmington STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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Best Local Similarity 75.0
Matches 9; Conservative
                                       9; Conservative
                                                                               2 LYKKFKKKLLKS 13
                                                                                                                   2 LYKKIIKKLLES 13
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Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                     JS-10-036-869-9
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Fatent No. US2002017A1

Fatent No. US2002017A1

Fatent No. US2002017A1

Fatent No. US2002017A1

FAPPLICANT Nycomed Imaging AS

FILE REFERENCE: REF Klaveness/206

FILE REFERENCE: REF Klaveness/206

CURRENT APPLICATION UMBER: US/09/925,715

CURRENT FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIN Ver. 2.1

LENGTH: 13
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US-09-925-715-27
                                                                                                                                                                              48.3%; Score 42; DB 14; Length 20; ilarity 60.0%; Pred. No. 34; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31. Application US/09765614B
Patent No. US20020102215A1
GENEBAL INNORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: adapts in or relating to
TITLE OF INVENTION: adagnostic/therapeutic
TITLE OF INVENTION: adagnostic/therapeutic
GURRENT APPLICATION NUMBER: US/09/765,614B
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 31
SEQ ID NO 31
LENGTH: 13
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Pred. No. 30;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:Platelet OTHER INFORMATION: binding peptide US-09-765-6148-31
                                                        OTHER INFORMATION: SYNTHETIC SEQUENCE NAME/KEY: MOD_RES
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
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75.0%;
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ORGANISM: Artificial Sequence
                                                                                                ; LOCATION: (20); COTHER INFORMATION: AMIDATION US-10-109-171-68
                                                                                                                                                                                                                                                                2 LYKKFKKKLLKSLKR 16
                                                                                                                                                                                                                                                                                                  4 LFKKALKKLKKALKK 18
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Best Local Similarity 75.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: CURROWN.>
PRIOR APPLICATION DATA:
CLASSIFICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13;
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TITLE OF INVENTION: PREPTIDE CONJUGATED ANTI-CANCER PRODUCTS FILE REFERENCE: 85189-4400
CURRENT APPLICATION NUMBER: US/10/382,240
CURRENT FILING DATE: 2003-03-05
Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.1%; Score 41; DB 13; 75.0%; Pred. No. 30; cive 1; Mismatches 2,
Score 41; DB 9;
Pred. No. 30;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/IL01/00839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: McMorrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
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TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: CYT, John E.
APPLICANT: CYT, John E.
APPLICANT: CYT, John E.
APPLICANT: Pearson, Daniel A.
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
FILE REFERENCE: 09744-01601
CURRENT APPLICATION NUMBER: US/10/131,543
CURRENT APPLICATION NUMBER: US/09/694,992
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FASELSEQ for Windows Version 4.0
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Pred. No. 30;
1; Mismatches 2; Indels
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Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: agents
TITLE OF INVENTION: agents
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/10/722,075
CURRENT PILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: US/08/960,054A
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 31
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial OTHER INFORMATION: Sequence:Platelet OTHER INFORMATION: binding peptide US-10-722-075-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 30;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/10722075; Publication No. US20040141922A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 26
US-10-131-543-8
; Sequence 8, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
                                                                                                                                                                              47.1%;
75.0%;
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ORGANISM: Artificial Sequence
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75.08;
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
                                                                                                                                                             Query Match
Best Local Similarity 75.u.
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                   TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                            RESULT 25
US-10-722-075-31
                                                                                                                                         US-10-382-240-1
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LENGTH: 18
                                                              SEQ ID NO 1
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Sequence 8, Application US/10131546

Sequence 8, Application US/10131546

Publication No. US20030103895A1

GENERAL INFORMATION:

APPLICANT: Cyr, John E.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING BATE: 2002-04-24

PRIOR PELICATION NUMBER: US 09/695, 494

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-10-24

NUMBER OF SEQ ID NOS: 29

SOFUTARE: RESESEQ for Windows Version 4.0

LENGTH: 18
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Sequence 8, Application US/10131346
Sequence 8, Application US/10131346
Publication No. US20030103899A1
GENERAL INFORMATION:
THIS OF INVENTION: STABLIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS
TITLE OF INVENTION NUMBER: US/10/131,346
CURRENT FILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 18
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47.1%; Score 41; DB 14; Length 18;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 2; Indels
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Best Local Similarity 75.0%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 2
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Synthetic construct US-10-131-546-8
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Sequence 14, Application US/10131543
; Sequence 14, Application US/10131543
; Publication No. US20030072709A1
; GENERAL INFORMATION:
; APPLICANT: Cyr, John B.
; APPLICANT: Pearson, Daniel A.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
; FILE REFERENCE: 09744-016001
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/694,992.
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LEATTH: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE: Design of Model Amphipathic Peptides Having TITLE: Potent Antimicrobial Activities JOHRNAL: Blochemistry VOLUME: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGES: 12688-12694
; DATE: 1992
; RELEVANT RESIDUES IN SEQ ID NO: 10: FROM 1 TO 18
US-10-414-342-10
                                     PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB .
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Pred. No.
                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-FEB-1997
ATTORNEY AGENT INFORMATION:
NAME: RUnnels, John H.
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: 9619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (504) 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic construct
                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Blondelle, Sylvie E.
AUTHORS: Houghten, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (504) 346-8049
INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Best Local Similarity 69.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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LOCATION: 3
                                                                                                                                          FILING DATE
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TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: CHROMANS
FILE REFERENCE: 09744-015W01
CURRENT APPLICATION NUMBER: US/10/415,024
CURRENT APPLICATION NUMBER: US 09/694,992
PRIOR FILING DATE: 2000-10-24
PRIOR PLING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR PLING DATE: 2000-10-24
                                                                                                                                                                                       Gaps
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| Publication No. US2004005908BA1 | GENERAL INFORMATION: | GENERAL INFORMATION: | APPLICANT: Yokum, Thomas S. | APPLICANT: Buright, Frederick M. | APPLICANT: Bright, Frederick M. | APPLICANT: Bright, Frederick M. | APPLICANT: Bright, Frederick M. | APPLICANT: Harmer, Robert P. | TITLE OF INVENTION: Short Amphipathic Peptides with TITLE OF INVENTION: Activity | DORESPECTION | DOR
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                                                                                                        Score 41; DB 14; Length 18; Pred. No. 42;
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                                                                                                                                                                                   2; Indels
                                                                                                                                                                               1; Mismatches
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; OTHER INFORMATION: Synthetic construct US-10-131-346-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10415024; Publication No. US20040058984A1; GENERAL INFORMATION:
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ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
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P. O. Box 2471
                                                                                                            47.1%;
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ORGANISM: Artificial Sequence
                                                                              Query Match
Best Local Similarity 75.0
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Best Local Similarity 75.0
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US-10-414-342-10
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US-10-752-096-1
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CURRENT APPLICATION NUMBER: US/10/131,546
CURRENT FILING DATE: 2002-04-24
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Forbitcation No. US20030103899A1

GENERAL INFORMATION:

APPLICANT: CYT, John E.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS

FILE REFERENCE: 09744-017001

CURRENT APPLICATION NUMBER: US 09/695,360

PRIOR APPLICATION NUMBER: DCT/US01/50423

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2001-10-24

NUMBER OF SEQ ID NOS: 29

SOFFWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14
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                                                                                Score 41; DB 14; Length 22;
Pred. No. 51;
1; Mismatches 2; Indels
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PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SENGTH: 22
; OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-543-14
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US-10-131-546-14
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                                                                                                                                                                                                                                                                                                                   US-10-131-546-14; Sequence 14, Application US/10131546; Publication No. US20030103895A1; GENERAL INFORMATION:
                                                                                  Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 9; Conservative
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US-10-131-346-14
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WES-10-415-024-14

Sequence 14, Application US/10415024

Sequence 14, Application US/10415024

BUDIcation No. US20040058984A1

GENERAL INFORMATION:

APPLICANT: Diatide, Inc.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: CHROWANS

TITLE OF INVENTION: CHROWANS

TITLE OF INVENTION: CHROWANS

FILE REFERENCE: 09744-015WOL

CURRENT APPLICATION NUMBER: US 09/694,992

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 09/695,360

PRIOR FILING DATE: 2000-10-24

SEQ ID NOS: 29

SEQ ID NOS: 29

LENGTH: 22
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Pred. No. 51;
1; Mismatches 2;
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                                                                                                                                                                                                                          , OTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-346-14
                                                                  OTHER INFORMATION: Synthetic construct
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 75.0%;
Matches 9; Conservative
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                                                                                     FEATURE:
NAME/KEY: ACETYLATION
LOCATION: 1
FEATURE:
NAME/KEY: VARIANT
LOCATION: 3
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Sequence 6, Application US/10752096

Publication No. US20050002861A1

GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and TITLE OF INVENTION: Inflammation

FILE REFERENCE: SCH10663US2

CURRENT PILING DATE: 2004-01-07

PRIOR APPLICATION NUMBER: US 60/438,316

PRIOR APPLICATION NUMBER: US 60/438,316

PRIOR APPLICATION NUMBER: EP 03 000 204.2

PRIOR APPLICATION NUMBER: EP 03 000 204.2

PRIOR PILING DATE: 2003-01-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

LENGTH: 23
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            FILE REPERENCE: SCH10663US2
CURRENT APPLICATION NUMBER: US/10/752,096
CURRENT FILING DATE: 2004-01-07
PRIOR APPLICATION NUMBER: US 60/438,316
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
NUMBER: EQ 1D NOS: 7
SEQ 1D NO 4
SEQ 1D NO 4:
LENGTH: 23
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Pred. No.
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                                                                                                                                                                                                                                                                                                              ORGANISM: artificial FEATURE: OTHER INFORMATION: Complexing Agent FEATURE:
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LOCATION: (6). (6)
OTHER INFORMATION: Penicillamine
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75.08;
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Best Local Similarity 75.0
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)..(1); OTHER INFORMATION: US-10-752-096-4
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US-10-752-096-6
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TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection an TITLE OF INVENTION: Inflammation FILE REFERENCE: SCHIOGGSUSZ CURRENT SCHIOGGSUSZ CURRENT APPLICATION NUMBER: US/10/752,096 CURRENT FILING DATE: 2004-01-07 PRIOR APPLICATION NUMBER: US 60/438,316 PRIOR PILING DATE: 2003-01-07 PRIOR APPLICATION NUMBER: EP 03 000 204.2 PRIOR PILING DATE: 2003-01-07 SOFTWARE: PEP 03 000 204.2 PRIOR FILING DATE: 2003-01-07 SOFTWARE: Patentin version 3.1 SEQ ID NO 1

LENGTH: 23
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TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection an TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection an TITLE OF INVENTION: Inflammation
FILE REPERENCE: SCH10663US2
CURRENT APPLICATION NUMBER: US/10/752,096
CURRENT APPLICATION NUMBER: US 60/438,316
PRIOR APPLICATION NUMBER: US 60/438,316
PRIOR FILING DATE: 2003-01-07
PRIOR PLING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
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APPLICANT: Schering AG
TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection an
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                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Complexing Agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2, Application US/10752096; Publication No. US20050002861A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 23
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Best Local Similarity 75.0
Matches 9; Conservative
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Matches 9; Conservative
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OTHER INFORMATION:
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US-10-752-096-2
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Sequence 15. Application US/10131546

Fublication No. US2003103895A1

GENERAL INFORMATION:

APPLICANT: Cyr, John E.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY

TITLE OF INVENTION UNMERR: US 09/695,494

PRIOR PAPLICATION NUMBER: US 09/695,494

PRIOR APPLICATION NUMBER: PCT/US01/50423

PRIOR PILING DATE: 2001-10-24

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PSSESEQ for Windows Version 4.0

SEQ ID NO 15

LEAGTH: 24
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Publication No. US20030103899A1
GENERAL INPORMATION:
APPLICAMT: CYT, JOHN E.
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILC 6-HYDROXY CHROMANS
FILE REFERENCE: 09744-017001
CURRENT APPLICATION NUMBER: US/10/131,346
CURRENT FILING DATE: 2002-04-24
CURRENT FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
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75.0%; Pred. No. 56;
tive 1; Mismatches 2
                                                                                                                                                                                              1; Mismatches
                                                                                                                                               Score 41;
Pred. No.
FEATURE:
NAME/KEY: VARIANT
LOCATION: 7
OTHER INFORMATION: Xaa = epsilon-Lysine
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                                                                                                                                               47.18;
75.0%;
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Best Local Similarity 75.0
Matches 9; Conservative
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NAME/KEY: ACETYLATION
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Best Local Similarity
Matches 9; Conserv
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                                       Sequence 7, Application US/10752096
Publication No. US2005002861A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Enhanced Scintigraphic Imaging Agents for Imaging of Infection and TITLE OF INVENTION: Inflammation
FILE REFERENCE: SCH10663U32
CURRENT APPLICATION NUMBER: US/10/752,096
CURRENT APPLICATION NUMBER: US 004-01-07
FRICK PILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Version 3.1
SEQ ID NO 7
LENGTH: 23
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US-10-131-543-15

Sequence 15, Application US/10131543

Publication No. US20030072709A1

GENERAL INFORMATION:

APPLICANT: Pearson, Daniel A.

TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: USING HYDROPHILIC THIOFTHERS

TITLE OF INVENTION: USING HYDROPHILIC THIOFTHERS

FILE REPRENCE: 09744-016601

CURRENT FILING DATE: 2002-04-24

CURRENT FILING DATE: 2000-10-24

PRIOR PRILING DATE: 2000-10-24

NUMBER OF SEQ ID NOS: 29

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 15

LENGTH: 24
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Pred. No. 54;
1; Mismatches 2; Indels
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OTHER INFORMATION: Synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE
LOCATION: (6). (6)
OTHER INFORMATION: ISOCYSTEINE
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Best Local Similarity 75.0%;
Matches 9; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: artificial
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Search completed: May 16, 2005, 09:23:37
Job time : 67.6552 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | GENERAL INCLURING THE COMPOSITIONS | JOHNSHAM INCLURING APPLICANT: Distide, Inc. | TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS | TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS | TITLE OF INVENTION: CHROMANS | TITLE OF INVENTION: CHROMANS | FILE REPERENCE: 09744-015WOl | CURRENT APPLICATION NUMBER: US/10/415,024 | CURRENT FILING DATE: 2003-04-24 | PRIOR APPLICATION NUMBER: US 09/694,992 | PRIOR PR
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Pred. No. 56;
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Pred. No. 56;
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
LOCATION: 7
COTHER INFORMATION: Xaa = epsilon-Lysine
US-10-131-346-15
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US-10-415-024-15
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US-10-415-024-15
Sequence 15, Application US/10415024
Publication No. US20040058984A1
GENERAL INFORMATION:
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                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0°
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Best Local Similarity 75.0
Matches 9; Conservative
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RESULT 44 US-10-333-364A-3 ; Sequence 3, Application US/10333364A

13 LYKKIIKKLLES 24

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; OTHER INFORMATION: SEQ ID NO. 3 is the 47-70 fragment of mutated PF-4 SEQ ID. NO. US-10-333-364A-3
APPLICANT: UNIVERSITE DE BORDEAUX 1
APPLICANT: UNIVERSITE DE SALSSEAUX ET DU SANG
APPLICANT: INSTITUT DES VALSSEAUX ET DU SANG
TITLE OF INVENTION: MUTATED PP-4, ITS FRAGMENTS AND MUTATED FUSION PEPTIDES,
TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MRNA SEQUENCES
TITLE OF INVENTION: THEIR ANALOGUES, CORRESPONDING DNA, CDNA AND MRNA SEQUENCES
TITLE OF INVENTION: AND THEIR USE FOR INHIBITING ANGIOGENESIS.
CURRENT APPLICATION NUMBER: US/10/333,364A
CURRENT FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2000-07-19
NUMBER: PACHAIN VERSION 3.1
SOFTWARE: PACHAIN VERSION 3.1
SOFTWARE: PACHAIN VERSION 3.1
SEQUENCES
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TITLE OF INVENTION: BROAD SPECTRUM ANTI-VIRAL THERAPEUTICS AND PROPHYLAXIS
FILE REPRENCE: NB-00101.P.1-US
CURRENT PLILING DATE: 2003-11-21
PRIOR PELLING DATE: 2003-11-22
PRIOR FILING DATE: 2002-11-22
PRIOR FILING DATE: 2003-14-19
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHTON NCYBER: US
LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.1%; Score 41; DB Best Local Similarity 75.0%; Pred. No. 56; Matches 9; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10718986
Publication No. US20050004020A1
GENERAL INFORMATION:
APPLICANT: YU, Mang
APPLICANT: FANG, Fang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.18;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LYKKFKKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LYKKIIKKLLES 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-718-986-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-718-986-2
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GenCore version 5.1.6
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- protein search, using sw model OM protein

ü Ö Run

May 16, 2005, 08:21:21; Search time 15.5172 Seconds (without alignments) 111.611 Million cell updates/sec

US-09-648-816B-3 87 Perfect score:

1 ALYKKFKKKLLKSLKRLG 18 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

22893 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 74 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	spermatid transiti	hypothetical prote		pro		ribosomal protein	u	spermatid transiti	spermatid transiti	spermatid transiti	esculentin-la - ed	antimicrobial pept	hypothetical prote	. ribosomal protein	30S ribosomal prot	conserved hypothet	hypothetical prote	hypothetical prote	spermatid transiti	hypothetical prote	30S ribosomal prot	ribosomal protein	v	ribosomal protein	ribosomal protein	ribosomal protein	Mx protein - pig (	hypothetical prote	spermatid transiti
SUMMARIES	01	BGMS	C72262	E82329	B72248	S38425	T49214	T07304	BGSH	BGBO	BGRT	G53578	S33731	D59103	A70375	H81379	D70241	E70239	870245	BGPG	D69384	E97818	H71666	T10809	JC4278	JQ1617	JC4685	820679	F84007	всни
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	Query Match Length	55	69	31	67	25	25	49	54	55	55	46	46	62	67	70	32	34	54	22	62	99	99	73	25	25	52	36	41	52
d	Query Match	44.8	44.8	42.5	42.0	41.4	41.4	41.4	41.4	41.4	41.4	40.2	40.2	40.2	40.2	40.2	39.1	39.1	39.1	39.1	39.1	39.1	39.1	39.1	37.9	37.9	37.9	37.9	37.9	37.9
	Score	39	39	37	36.5	36	36	36	36	36	36	35	35		35		34	34	34	34	34	34	34	34	33	33	33	33	. 33	33
	Result No.	7	7	٣	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		29

	hypothetical prote hypothetical prote hypothetical prote	ribosomal protein ribosomal protein hypothetical prote		hypothetical prote hypothetical prote hypothetical prote	
AB2125 G71830	H64442 D84156 H81897	H70131 T38719 T07315	G90010 T29619 H98094	E95230 S31636 T12949	E97179 B84092
000	000	0 0 0	000	000	0 0
64	9 65	69 4 6 6	53	5.5 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0	63
37.9	37.9 37.9	37.9 36.8 36.8	36.8 36.8	36.8 36.8 36.8	36.8 36.8
333	m m m	3 3 3	222	3 5 5 3 7 8 3 8 8	32
30	ы с с И с 4.	36 37	8 8 8 8 0 0	4 4 4 4 2 8	44 5

## ALIGNMENTS

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spermatid transition protein 1 - mouse
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NyAlternate names: testis-specific basic protein
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A40561; JS0038
R;Yelick, P.C.; Kozak, C.; Kwon, Y.K.; Seldin, M.F.; Hecht, N.B.
A;Yelick, P.C.; Kozak, C.; Kwon, I J. 687-694, 1991
A;Title: The mouse transition protein 1 gene contains a B1 repetitive element and is loc

A, Accession: A40561 A, Molecule type: DNA A, Residues: 1-55 < YEL>

A,Cross-references: UNIPROT:P10856; GB:S80846; NID:g244180; PIDN:AAB21244.1; PID:g244181
R;Kleene, K.C.; Borzorgaadeh, A.; Flynn, J.F.; Yelick, P.C.; Hecht, N.B.
Biochim. Bjophys. Acta 950, 215-220, 1988
A;Hitle: Nucleotide sequence of a cDNA clone encoding mouse transition protein 1.
A;Reference number: JS0038; MUID:88252150; PMID:3382664

A, Accession: JS0038
A, Molecule type: mRNA
A, Residues: 1-55 «KLB»
A, Foresidues: 1-55 «KLB»
A, Foresidues: 1-55 «KLB»
A, Forestreferences: EMBD: X12521; MID: 954850; PIDN: CAA31039.1; PID: 954851
C, Comment: This protein replaces histones and is replaced by other transition proteins or C, Genetics:
A, Map position: 1
A, Introns: 47/1
C, Superfamily: spermatid transition protein 1
C, Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
C, Keywords: DNA binding; nucleus; phosphorotein 1 #status predicted «MAT»
F, 40/Binding site: phosphate (Ser) (covalent) #status predicted

Gaps

ö Score 39; DB 1; Length 55; Pred. No. 53; 4; Mismatches 2; Indels Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative

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16 :|::| :|| ||| 31 RKYRKSVLKSRKR 43 4 KKFKKKLLKSLKR ઠ 셤

RESULT 2

hypothetical protein - Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C,Accession: C72262 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

Nature 199, 121-129, 1999 A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequ

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|::|| :||: 54 YERFKNELEKKAKRI 68

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3 YKKFKKKLLKSLKRL 17

Query Match
Best Local Similarity 46.74
Local 7, Conservative

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A;Cross-references: UNIPROT:P62122; EMBL:X75423; NID:g407800; PIDN:CAA53175.1; PID:g40780
C;Superfamily: rat ribosomal protein L41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T99214
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.; N. submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25014
A;Accession: T49214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein 49c - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07304
R;Waakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakasł
Proc. Natl. Acad. Sci. U.S.A. 94, S967-S972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P62120; EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.200
A;Experimental source: cultivar Columbia; BAC clone F27K19
                                       ä
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                                                                                                                                                                                                                                                                                                    ribosomal protein GL41 - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein GL41-like - Arabidopsis thaliana
NiAlternate names: protein F27K19.200
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cibate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                       Gaps
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                                       11;
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                                       Indels
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            Pred. No. 1.5e+02;
2; Mismatches 2;
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41.4%; Score 36; DB 2;
Best Local Similarity 58.3%; Pred. No. 71;
Matches 7; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
3
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Turley, R.B.; Ferguson, D.L.; Meredith, W.R. submitted to the EMBL Data Library, October 1993 A;Reference number: S38425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                 ----LKRLG 18
                                                                                                                                                        3 KKLKIKLVKSPIGYSWDQKDTVKRLG 28
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         | Similarity 42.3%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S KFKKKLLKSLKR 16
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4 KWKKKRMRRLKR 15
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4 KWKKKRMRRLKR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Status: preliminary
A Molecule type: DNA
A Residues: 1-25 <BEN>
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-25 < TUR>
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            Best Local
Matches 1
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A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72262
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-69 cARN>
A;Cross-references: UNIPROT:Q9X1A6; GB:AE001791; GB:AE000512; NID:G4981929; PIDN:AAD3645
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B72248
Libosomal protein L30 - Thermotoga maritima (strain MSB8)
C;Bocies: Thermotoga maritima
C;Species: Tl-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72248
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Rosidues: 1-67 -ARN>
A;Cross-references: UNIPROT:Q9XLJ1; GB:AE001798; GB:AE000512; NID:g4982033; PIDN:AAD3654
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9KUX1; GB:AE004126; GB:AE003852; NID:g9654802; PIDN:AAF9356
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein VC0387 (imported] - Vibrio cholerae (strain N16961 serogroup O1) C.Species: Vibrio cholerae C.Becies: Vibrio cholerae C.Becies: Vibrio cholerae C.Bete: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C.Accession: B82329 R.Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. A.Ruture 406, 477-483, 2000 A.Fitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A,Reference number: A82035; MUID:20406833; PMID:10952301 A,Status: preliminary A,Status: preliminary A,Residues: 1-31 < HEI>
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.5%; Score 37; DB 2; Length 31; 46.7%; Pred. No. 62; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                       2; Length 69;
                                                                                                                                                                                                                                                                                                                                                                4; Indels
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                                                                                                                                                                                                                                                                                                       44.8%; Score 39; DB 46.7%; Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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: || :| | |:||: 11 FYKFSQKTLASVKRI 25

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C,Genetics: A,Gene: TM1482

Query Match

3 YKKFKKKLLKSLKRL 17

Query Match
Best Local Similarity 46.7
Matches 7; Conservative

A,Gene: VC0387 A,Map position: 1

C;Genetics:

g ઠ

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A;Cross-references: GB:X16171; NID:g805; PIDN:CAA34293.1; PID:g806
A;Note: translation of initiator Met is not shown
C;Comment: This protein replaces histones and is replaced by other transition proteins on C;Genetics:
A;Gene: TNP1
A;Introns: 47/1
C;Superfamily: spermatid transition protein 1
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;2-55/Product: spermatid transition protein 1 #status predicted <MAT>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatid transition protein 1 - rat
NyAlternate names: testis-specific basic protein
C;Species: Rattus norvegicus (Norway rat)
C;Dapeis 24-Apr-1884 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A29095; JS0109; A2171; A02655; S03177
R;Heidaran, M.A.; Kistler, W.S.
Gene 54, 281-284, 1987
A;Title: Isolation of a cDNA clone for transition protein 1 (TP1), a major chromosomal pray. Reference number: A29095; MUID:88005793; PMID:2820847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: mRNA
A,Rosdidues: 1-55 AHEI>
A)Cross-references: UNIPROT:PD2317; GB:M17096; NID:g207414; PIDN:AAA42260.1; PID:g207415
R,Heidaran, M.A.; Kozak, C.A.; Kistler, W.S.
Gene 75, 39-46, 1989
A,Fitle: Nucleotide sequence of the Stp-1 gene coding for rat spermatid nuclear transitic
A,Reference number: JS0109; MUID:89252920; PMID:2524424
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R;Kistler, W.S.; Noyes, C.; Hsu, R.; Heinrikson, R.L.
S. Biol. Chem. 250, 1847-1853, 1975
A;Title: The amino acid sequence of a testis-specific basic protein that is associated way. A;Reference number: A92171; MUID:75095670; PMID:1112834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: protein.
A.Residues: 2-45, '8', 47', 'D', 49-55 «XIS»
A.Residues: 2-45, '8', 47', 'D', 49-55 «XIS»
B.Kitieler, W.S.; Noyes. Commun. 57, 341-347, 1974
B.A.Fitle: Partial structural analysis of a highly basic low molecular weight protein from A.Reference number: A90190; WUID:74167135; PMID:4829397
A.Contents: annotation; partial sequence
C.Comment: The presence of this protein in mammalian testes is correlated with the occurr
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Keywords: chromosomal protein; DNA binding; nucleus; phosphoprotein; spermatogenesis;
F;2-55/Product: spermatid transition protein 1 #status experimental <MAT>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted
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Pred. No. 1.5e+02;
3; Mismatches 3; Indels
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Pred. No. 1.5e+02;
3; Mismatches 3; Indels
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53.8%;
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Best Local Similarity 53.0.
Best Local 7; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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A;Molecule type: DNA
A;Residues: 1-55 <HBI2>
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R;Chizat, F.; Martinage, A.; Briand, G.; Kouach, M.; van Dorsselaer, A.; Loir, M.; Sauti Bur. J. Biochem. 198, 13-20, 1991
R;Title: Vuclear transition protein 1 from ram elongating spermatids. Mass spectrometric A;Reference number: S16075; MUID:91249791; PMID:2040274
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 2.Jul-1995 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: A56647; B37347
R;Kim, Y.; Kremling, H.; Tessmann, D.; Engel, W.
A;Kim, Y.; Kremling, H.; Tessmann, D.; Engel, W.
A;Title: Nucleotide sequence and exon-intron structure of the bovine transition protein
A;Reference number: A56647; MUID:93091245; PMID:1457814
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A;Orces-references: UNIPROT: P22613
A;Note 27-G19 was also seen in about 20% of the molecules
C;Comment: This protein replaces histones and is replaced by other transition proteins
C;Superfamily: spermatid transition protein 1
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
P:1-54/Product: spermatid transition protein 1 #status experimental cMAT>
P:8,35,36,39/Binding site: phosphate (Ser) (covalent) (partial) #status experimental
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                                                   A;Accession; T07304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-49 < WAKA
A;Residues: 1-49 < WAKA
A;Cross-references: EMBL:AB001684; NID:g2224352; PIDN:BAA57952.1; PID:g2224468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spermatid transition protein 1 - sheep
NiAlternate names: testis-specific basic protein; TP1; transition protein T
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 21-Nov-1993 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
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Pred. No. 1.3e+02;
0; Mismatches 5; Indels
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                  A; Reference number: Z15985; MUID: 97303241; PMID: 9159184
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Matches 7; Conservative
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A,Genome: chloroplast
C,Keywords: chloroplast
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A; Residues: 2-55 < KRE>
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us-09-648-816b-3.rpr

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ribosomal protein S21 - Aquifex aeolicus
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ilarity 50.0%;
Conservative
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Best Local Similarity 35.7<sup>3</sup>
Matches 5; Conservative
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16 YRKFKKQVDRNL 27
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53 RKKILKALKK 62
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Best Local Similarity
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                                                                                  A; Genome: plasmid
C; Genetics:
A; Gene: pXO1-100
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Santimicrobial peptide esculentin - edible frog

C,Species: Rana esculenta (edible frog)

C,Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C,Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C,Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

R,Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.

FEBS Lett. 324, 159-161, 1993

A,Title: Novel antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion of the European frog Rana escular antimicrobial peptides from skin secretion a
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C;Species: Bacillus anthracis
C;Species: Bacillus anthracis
C;Species: Data: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: D59103
R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
J. Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori
A;Reference number: A59091; MUID:99445483; PMID:10515943
A;Accession: D59103
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-62 < OKI>
                                                                                                                                                                                                                                                                                                                       Rana esculenta. Molecular clonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: UNIPROT: P40843
S. Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology C; Keywords: antibacterial; disulfide bond; skin F; 40-46/Disulfide bonds: #status experimental
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                                                                     esculentin-la - edible frog
C;Species: Rana esculenta (edible frog)
C;Species: Rana esculenta (edible frog)
C;Dacession: G53578
R;Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
J. Balol. Chem. 269, 11956-11961, 1994
A;Title: Antimicrobial peptides from skin secretions of Rana esculenta. Mole A;Reference number: A53578; MUID:94216303; PMID:8163497
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Pred. No. 1.7e+02;
2; Mismatches 6; Indels
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A;Residues: 1-46 cSIM-
A;Cross-references: UNIPROT: P32414
A;Experimental source: skin
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KKIKNLLISGLKNVG 23
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Best Local Similarity 46.74
Best Local 7, Conservative
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Matches 7; Conservative
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C,Accession: A70375
R,Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
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A,Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30S ribosomal protein S21 Cj0370 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81379
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-669, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <PAR>
A;Cross-references: UNIPROT: Q9FID2; GB:AL139075; GB:AL111168; NID:96967817; PIDN:CAB74206
A;Experimental source: serotype O2, strain NCTC 11168
A;Cross-references: UNIPROT:Q9X369; GB:AF065404; NID:g4894216; PIDN:AAD32404.1; PID:g489
A;Experimental source: strain Sterne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-67 < AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                         Score 35; DB 2; Length 62;
Pred. No. 2.3e+02;
7; Mismatches 2; Indels
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C;Superfamily: Escherichia coli ribosomal protein S21
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40.2%; Score 35; DB 2; I
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 4; Mismatches 0;
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Pred. No. 2.6e+02;
5; Mismatches 1;
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Gapa

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A; Molecule type: DNA
A; Residues: 1-54 < SCH>
A; Cross-references: UNIPROT: Q44505; EMBL: Z46887; NID: G599643; PIDN: CAA86987.1; PID: G1181:
A; Experimental source: ATCC 29413
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: testis-specific basic protein
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S21670; A37347
R;Keime, S.; Heitland, K.; Kumm, S.; Schloesser, M.; Hroch, N.; Holtz, W.; Engel, W.
Biol. Chem. Hoppe-Seyler 373, 261-270, 1992
A;Title: Characterization of four genes encoding basic proteins of the porcine spermatid A;Reference number: S21670; MUID:92329006; PMID:1627265
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A; Residues: 1-55 <KEI>
A; Residues: 1-55 <KEI>
A; Cross-references: UNIPROT: P17306; EMBL: M80679; NID:g164700
B; Kremling, H.; Luersen, H.; Adham, I.M.; Klemm, U.; Tsaousidou, S.; Engel, W.
Differentiation 40, 184-190, 1989
A; Title: Nucleotide sequences and expression of cDNA clones for boar and bull transition
A; Reference number: A37347; MUID: 89378557; PMID: 2777004
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: GB:X16170; NID:g2139; PIDN:CAA34292.1; PID:g2140
A;Cross-references: GB:X16170; NID:g2139; PIDN:CAA34292.1; PID:g2140
A;Note: translation of initiator Met is not shown
C;Comment: This protein replaces histones and is replaced by other transition proteins on
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Kreywords: DNA binding; nucleus; phosphoprotein; spermatogenesis; testis
F;2-55/Product: spermatid transition protein 1 #status predicted <MAT>
F;40/Binding site: phosphate (Ser) (covalent) #status predicted
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egions as part of the nif1/2 gene clusters.

A;Reference number: 870242; MUID:96296457; PMID:8709854

A;Accession: 870245

A;Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 2.8e+02;
1; Mismatches 3; Indels
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53.8%; Pred. No. 2.9e+02;
ive 3; Mismatches 3; Indels
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Matches 7; Conservative
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C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: E70239
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Bowman, C.; Garland, S.; Hujai, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hanson, M.; Vugt, S. A;Authors Smith, H.O.; Venter, J.C.
A;Authors Smith, H.O.; Venter, J.C.
A;Authors Genquence of a Lyme disease spirochaete, Borrelia burgdorferi.
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C;Species: Anabaena variabilis
C;Species: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S70245
R;Schrautemeier, B.: Neveling, U.; Schmitz, S.
Mol. Microbiol. 18, 357-369, 1995
A;Title: Distinct and differently regulated Mo-dependent nitrogen-fixing systems evolved
                                                                                                                                                                                          Conserved hypothetical protein BBI13 - Lyme disease spirochete plasmid I/lp28-4 C.Species: Borrelia burgdorferi (Lyme disease spirochete)
C.Species: Borrelia burgdorferi (Lyme disease spirochete)
C.Species: Dornelia burgdorferi (Lyme disease spirochete)
C.Species: Dornelia burgdorferi (Lyme disease spirochete)
C.Species: Dornelia Barguence_revision 13-Feb-1998 #text_change 09-Jul-2004
C.Accession: D70241
R.Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A.Authors: Smith, H.O.; Venter, J.C.
A.Authors: Smith, H.O.; Venter, J.C.
A.Authors: Smith, H.O.; WulD:98065943; PMID:9403685
A.Accession: D70241
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Experimental source: strain B31
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:050867; GB:AE000789; NID:92690079; PIDN:AAC66183.1; PID:9269
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YKKIKNELIK 19
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Best Local Similarity
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Richeldstra, A. Nilsen, G.; van Kammen, A.; Bisseling, T.; Martinez-Abarca, F. Ribedistra, R.; Nilsen, G.; van Kammen, A.; Bisseling, T.; Martinez-Abarca, F. submitted to the EMBL Data Library, November 1996
A;Description: Nod factor induced expression of leghemoglobin to study the mechanism of A;Reference number: Z17164
A;Reference number: Z17164
A;Reference number: Z17164
A;Retarning: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-73 < HBI>
A;Residues: 1-73 < HBI>
A;Residues: 1-73 < HBI>
C;Genetics: Gub_species nigra; tissue_type root
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C;Superfamily: rat ribosomal protein L41
C;Keywords: ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tibosomal protein L41.e. - human
NyAlternate names: HG12 protein; ribosomal protein YL41
NyAlternate names: HG12 protein; ribosomal protein YL41
C;Species: HOmo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JOG617, JUS559; Sales
C;Accession: JOG617, JUS559; Sales
R;Klaudiny, J: von der Kammer, H ; Scheit, K.H.
Biochem. Biophys. Res. Commun. 187, 901-906, 1992
A;Ritle: Characterization by cDNA cloning of the mRNA of a highly basic human protein hor A;Reference number: JQ1617; MUID:92412140; PMID:1326959
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A;Residues: 1-25 «KLA»
A;Cross-references: UNIPROT:P28751; EMBL:Z12962; NID:g36135; PIDN:CAA78306.1; PID:g36136
R;Lee, J.H.; Kim, J.M.; Kim, M.S.; Lee, Y.T.; Marshak, D.R.; Bae, Y.S.
Biochem. Biophys. Res. Commun. 238, 462-467, 1997
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                                                                                              C,Species: Vicia sativa (spring vetch, tare)
C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C,Accession: T10809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal protein L41, cytosolic [similarity] - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
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R;Chan, Y.L.; Olvera, J.; Wool, I.G.
Biochem, Biophys. Res. Commun. 214, 810-818, 1995
A;Title: The primary structures of rat ribosomal proteins L4 and A;Reference number: JC4277; MUID:96024571; PMID:7575549
A;Accession: JC4278
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Pred. No. 3.8e+02;
3; Mismatches 1
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                                                                     leghemoglobin 1 - spring vetch (fragment)
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50.0%;
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Best Local Similarity 50.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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32 FKKAMLKTIK 41
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A; Residues: 1-25 < CHA>
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A,Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69384
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62 <KLEs
A;Residues: 1-62 <KLEs
A;Cross-references: UNIPROT:029187; GB:AE001028; GB:AE000782; NID:92689351; PIDN:AAB9016
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A;Experimental source: strain Madrid E
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C;Species: Rickettsia prowazekii
C;Species: Nackettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: H71566
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 ribosomal protein S21 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Dates 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97818
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2092-2098, 2001
A;Tile: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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Pred. No. 3.4e+02;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                   Score 34; DB 2; Length 62;
Pred. No. 3.2e+02;
5; Mismatches 3; Indels
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A;Gene: rpsU
C;Superfamily: Escherichia coli ribosomal protein S21
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Best Local Similarity 42.9%;
Matches 6; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
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A;Residues: 1-66 <AND>
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A; Residues: 1-66 < KUR>
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A; Status: preliminary
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A;Gene: rpsU; RP615
C;Superfamily: Esche
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[imported] - Bacillus halodurans (strain C-125)
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53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.9%;
Best Local Similarity 57.1%;
Matches 8; Conservative
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15 LLKELLKKNLKNLK 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|::| ||| ||
RKYRKGNLKSRKR
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A,Map position: 2q35-2q36
C,Superfamily: spermatid t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA; Residues: 1-55 < LUE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
Residues: 1-55 <LUE1>
                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-41 <STO>
                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: A37106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: S01241
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                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: BH2862
                                 hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
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820679

Mx protein - pig (fragment)

C;Species: Sus acrofa domestica (domestic pig)

C;Accession: $20679

C;Accession: $20679

R;Mueller, M.; Brem, G.; Winnacker, E.L.

submitted to the EMBL Data Library, August 1990

A;Description: Porcine MX - System.

A;Reference number: $20679

A;Residues: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <MUE>

A;Residues: 1-36 <MUE>

A;Cross-references: UNIPROT: Q29072; EMBL: X54328; NID: G2017; PIDN: CAA38225.1; PID: g136425

C;Superfamily: dynamin-related protein VPS1
A; Title: The highly basic ribosomal protein L41 interacts with the beta subunit of prote A; Reference number: JC5659; MJD:97446005; PMID:9299532
A; Accession: JC5659
A; Molecule type: mRNA
A; Residues: 1-25 < LEE>
A; Crose-references: EMBL: Z12962; NID:936135; PIDN:CAA78306.1; PID:936136
C; Comment: This protein stimulates phosphorylation of the beta chain of DNA topoisomeras C; Superfamily: rat ribosomal protein L41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT:P28751; GB:U22229; NID:9950108; PIDN:AAB01667.1; PID:9950109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tibosomal protein L41 - cat
C;Species: Pelis silvestris catus (domestic cat)
C;Species: Pelis silvestris catus (domestic cat)
C;Species: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Datcession: JC4685
R;Starkey, C.R.; Menon, R.P.; Prabhu, S.; Levy, L.S.
Biochem. Biophys. Res. Commun. 220, 648-652, 1996
A;Title: Primary sequence and evolutionary conservation of ribosomal protein genes fareference number: JC4685; MuID:96183078; PMID:8607819
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                                                                                                                                                                                                          Score 33; DB 2; Length 25;
Pred. No. 2e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 2; Length 25;
Pred. No. 2e+02;
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A;Gene: rpL41
C;Superfamily: rat ribosomal protein L41
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LYSQYEEKLRPCIDLIDSLRALG 28
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                                                                                                                                                                                                          37.9%;
50.0%;
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                                                                                                                                                                                                                                  Best Local Similarity 50.0
Matches 6; Conservative
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KWRKKRMRRLKR 15
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KWRKKRMRRLKR 15
                                                                                                                                                                                                                                                                                                       5 KFKKKLLKSLKR 16
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-25 <STA>
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C;Accession: F84007
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirar Nucleic Acids Res. 28, 4117-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-raferences: UNIPROT:Q9K8Z0; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB0658
A,Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NyAternate names: testis-specific basic protein
NyAternate names: testis-specific basic protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A37106; S01241
R;Luerssen, H.; Mattei, M.G.; Schroeter, M.; Grzeschik, K.H.; Adham, I.M.; Engel, W.
A;Title: Nucleotide sequence of the gene for human transition protein 1 and its chromoson
A;Reference number: A37106; MUID:91065651; PMID:2249851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: EMBL:X07948; NID:g37237; PIDN:CAA30774.1; PID:g37238; Comment: This protein replaces histones and is replaced by other transition proteins on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:P09430, GB:MS9924, NID:g339778, PIDN:AAA61202.1, PID:g339779; Experimental source: leukocyte
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein asl2553 [imported] - Nostoc sp. (strain PCC 7120)
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ucleic Acids Res. 16, 7723, 1988
'JTtle: The nucleotide sequence of human transition protein 1 cDNA, Reference number: S01241; MUID:88319961; PMID:3412903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 2; Length 41;
Pred. No. 3.18+02;
2; Mismatches 4; Indels
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Pred. No. 4e+02;
3; Mismatches 3; Indels
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37.9%;
53.8%;
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                                                                                                                                                             Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                             1 ALYKKFKKKLLKSLK 15
                                                                                                                                                                                                                                                                                                              34 ARIKKRKEKNLKSIR 48
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Best Local Similarity 46.2
Matches 6; Conservative
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A;Residues: 1-65 <STO>
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A;Residues: 1-66 <PAR>
                    A;Residues: 1-65 <BUL>
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H70131
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. etrain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2125
By A;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2125
A;Status: preliminary
A;Residues: 1-60 < KUR>
                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q8YU08; GB:BA000019; PIDN:BAB74252.1; PID:g17131645; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
G71830
G71830
C;926cies: Helicobacter pylori
C;Species: Helicobacter pylori
A;Variety: etrain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nattitle: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: G71830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9ZJR0; GB:AE001548; GB:AE001439; NID:g4155845; PIDN:AAD0682 A;Experimental source: strain J99 C;Genetics: A;Genetics:
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H64442
H64442
Cypothetical protein MJ1145 - Methanococcus jannaschii
cypothetical protein MJ1145 - Methanococcus jannaschii
cypothetical protein MJ1145 - Methanococcus jannaschii
cypate: 13-8ep-1996 #sequence_revision 13-8ep-1996 #text_change 09-Ju1-2004
Cypate: 13-8ep-1996 #sequence_revision 13-8ep-1996 #text_change 09-Ju1-2004
CyAccession: H64442
R;Bulc, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.J.; White, O.; Oston, W.D.; Roberts, K.G.; Marrick, J.M.; Glodek, A.; FROIN, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Soience 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klank, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Aftle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: H64442
A;Accession: H64442
A;Accession: H64442
A;Accession: H64442
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Pred. No. 4.7e+02;
5; Mismatches 3; Indels
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Pred. No. 4.4e+02;
5; Mismatches 3; Indels
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42.9%;
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18 EKYEETLLKSAKHI 31
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Matches 6; Conservative
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Best Local Similarity 42.9
Matches 6; Conservative
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:09K5N6; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB0777
A;Experimental source: strain C-125
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A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9JUI5; GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84546
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: NMA1294
A;Cross-references: UNIPROT:Q58545; GB:U67557; GB:L77117; NID:g1591777; PIDN:AAB99155.1;
C;Genetics:
A;Map position: REV1085114-1084917
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Cifrecies: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aypothetical protein BH4052 [imported] - Bacillus halodurans (strain C-125)
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Pred. No. 4.8e+02;
4; Mismatches 3; Indels
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Pred. No. 4.7e+02;
3; Mismatches 3; Indels
                                                                                                                                              Length 65;
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                                                                                                                                              Score 33; DB 2; I
Pred. No. 4.7e+02;
                                                                                                                                                                                                                    3; Mismatches
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C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07315
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Titls: Complete nucleotide sequence of the chloroplast genome from the green alga Chlos A;Reference number: Z1S985; MUID:97303241; PMD:9159184
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A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
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A;Experimental source: strain N315
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C;Genetics:
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G90010
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Cibate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
Cibacesion: T29619
R;Wamsley, P.; Bradshaw, H.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid R10A10.
A;Reference number: Z20653
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Pred. No. 5.3e+02;
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A;Molecule type: DNA
A;Residues: 1-46 <WAK>
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53.8%;
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 53.0.
Best Tocal 7; Conservative
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                4 KWRKKRVRRLKR 15
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C; Keywords: chloroplast
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A; Residues: 1-51 < KUR>
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ribosomal protein S21 (rpsU) - Lyme disease spirochete (Species: Borrelia burgdorferi (Lyme disease spirochete) (Species: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004 (Spacession: H7013) (Species) (Speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: UNIPROT:051271, GB:AE001136; GB:AE000783; NID:g2688152; PIDN:AAC6663
A,Experimental source: strain B31
C;Superfamily: Escherichia coli ribosomal protein S21
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-69 «KLE»
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C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38719; T38711, T3811, B.G.; Rajandream, M.A.; Walsh, S.V.
Bubmitted to the EMBL Data Library, February 1996
A;Accession: T38719
A;Accession: T38719
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 5e+02;
4; Mismatches 4; Indels
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KKFKKKLLKSLKRL 17
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A; Residues: 1-25 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-25 <BOT>
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Residues: 1-25 <GEN>
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A;Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13873.1; PID:e1185453;
A;Experimental source: strain 168
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C; Species: Streptococcus pneumoniae
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C; Accession: E95230
R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, anson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Rieference number: A95000; MUID:21357209; PMID:11463916
A; Accession: E95230
A; Astatus preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q8CY95; GB:AE007317; PIDN:AAL00589.1; PID:g15459470; GSPDB:G
C;Genetics:
A;Gene: spr1786
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A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1971
A;Molecule type: DNA
A;Residues: 1-53 <WAM>
A;Residues: 1-53 <WAM>
A;Cross-references: UNIPROT:P91403; EMBL:U80449; PIDN:AAB37825.1; GSPDB:GN00019; CESP:R1
A;Experimental source: strain Bristol N2; clone R10A10
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein spr1786 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 09-Jul-2004
C;Accession: H98094
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Is, R.; Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, Bremoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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                                                                                                                                                                                                                                                 Length 53;
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                                                                                                                                                                                                                                         36.8%; Score 32; DB 2; Le
llarity 63.6%; Pred. No. 5.5e+02;
Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.8%; Score 32; DB 2; I ilarity 37.5%; Pred. No. 5.5e+02; Conservative 6; Mismatches 4;
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Pred. No. 5.6e+02;
6; Mismatches 4;
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LYTYFQEKKRENLKKI 34
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illarity 37.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                     5 KFKKKLLKSLK 15
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Best Local Similarity
Matches 6; Conserva
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es 6; Conserv
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Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-53 <KUR>
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A: Residues: 1-54 < KUR:
                                                                                                                                       A; Gene: CESP:R10A10.1
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A; Introns: 51/1
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C;Accession: S31636
R;Klein, J.; Ulrich, C.; Plapp, R.
submitted to the RML Data Library, August 1992
A;Description: Characterization and sequence analysis of a small cryptic plasmid from Lac
A;Reference number: S31636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein yotN - Bacillus subtilis phage SPBC2
C;Species: Bacillus subtilis phage SPBC2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12949; H6924; H6924; A; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophace
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A; Molecule type: DNA
A; Residues: 1.58 c.LAZ>
A; Cross-references: UNIRROT:064196; EMBL:AF020713; NID:93025478; PID:93025663; PIDN:AACI:
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chool
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, F.; Sckfouch, D.; Sckiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Vamane, K.; Vasumoto, K.; Yata, K.; Yoshida, K.
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: UNIPROT: Q05642; EMBL: Z14234; NID: 943976; PIDN: CAA78601.1; PID: 943977
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                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Lactobacillus curvatus
C;Species: Lactobacillus curvatus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
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50.0%; Pred. No. 5.8e+02;
tive 3; Mismatches 3;
2 LYKKFKKKLLKSLKRL 17
                                                       20 LYTYFQEKKRENLKKI 35
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Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-56 <KLE>
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Length 58;

Score 32; DB 2; Pred. No. 6e+02;

36.8%; 35.7%;

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3; Indels

6; Mismatches

5; Conservative

Matches

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hypothetical protein CAC2267 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97179
R;Nolling, J; Breton, G; Omelchenko, M.V; Markarova, K.S.; Zeng, Q; Gibson, R.; Lee, Daly, M.J; Bennett, G.N.; Koonin, B.V; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'Species: Bacillus halodurans
C'Date: Ol-Dec-2000 #sequence_revision Ol-Dec-2000 #text_change 09-Jul-2004
C;Accession: B84092
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Puji, F.; Hira
Nucleic Acids Res 28, 4317-431, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            À,Cross-references: UNIPROT:Q97GU8; GB:AB001437; PIDN:AAK80224.1; PID:g15025271; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:09K735; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB072
A;Bxperimental source: strain C-125
C;Genetics:
A;Gene: BH5538
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B84092
hypothetical protein BH3538 [imported] - Bacillus halodurans (strain C-125)
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.8%; Score 32; DB 2; Length 58;
52.2%; Pred. No. 6e+02;
tive 1; Mismatches 4; Indels
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18 MWVRSKKEVIEKLARVG 34
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7 YEELKKKTIKVVQK 20
                                                      3 YKKFKKKLLKSLKR 16
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Best Local Similarity 29.4<sup>1</sup>
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 52.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: E97179
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-58 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: B84092
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Search completed: May 16, 2005, 08:42:25 Job time : 17.5172 secs

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Mon May 16 13:48:01 2005
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 14.9655 Seconds (without alignments) 69.833 Million cell updates/sec Run on:

US-09-648-816B-8 Title: Perfect score:

1 KLYKKWKKKLLKLK 14 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 segs, 74649064 residues Searched:

301394 Toťal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/cgn2_6/ptodata/1/iaa/SA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/RGCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* 4.6.6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de				
Result No.	Score	Query Match	Length DB	DB	ΩI	Description
-	74	0.001	14	4	TIS-09-525-269A-8	Semence 8 Appli
	2.5	75 7	14	٠ 4	5	ď
ım	2 2	74.3	13	4	US-09-525-269A-9	, 0
4	51	689	18	4	US-09-525-269A-10	10,
S	20	67.6	18	4	-09	
9	46	62.2	13	4	US-09-525-269A-4	4
7	46	62.2	18	٣	US-09-450-315A-1	ı,
80	46	62.2	18	4	US-09-447-966-1	H
O	46	62.2	20	m	US-09-000-692-1	1, 1
10	45	60.8	20	П	US-08-233-203-11	1,
11	45	60.8	23	Н	US-08-233-203-12	12,
12	42	56.8	18	Н	US-07-725-331-27	27,
. 13	42	56.8	18	ч	US-07-725-331-29	29,
14	42	56.8	18	Ŋ	PCT-US91-05047-27	27
15	42	56.8	18	S	PCT-US91-05047-29	Sequence 29, Appl
16	41	55.4	18	4	US-09-493-211-6	ý
17	41	55.4	9	4	US-09-248-796A-23525	23
18	40	54.1	17	Н	US-07-725-331-54	54,
19	40	54.1	17	Ŋ	PCT~US91-05047-54	54,
20	40	54.1	18	-	US-07-725-331-30	30,
21	40	54.1	18	-	US-08-233-203-7	7,
22	40	54.1	18	-	US-08-233-203-8	æ
23	40	54.1	18	-	US-08-233-203-10	2,
24	40	54.1	18	~	US-08-760-903-2	7
25	40	54.1	18	4	US-08-482-191-2	7
56	40	54.1	18	ß	PCT-US91-05047-30	30,
27	40	54.1	18	ß	PCT-US96-10227-2	7

Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 30, Appli Sequence 7, Appli Sequence 8, Appli Sequence 8, Appli Sequence 43, Appli Sequence 53389, A Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 99, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli
US-08-760-903-3 US-08-482-191-3 US-09-493-211-1 PCT-US96-1027-3 US-09-525-269A-11 US-08-290-853-30 US-08-505-318-7 US-08-182-175A-8 PCT-US92-06412-8 US-07-725-331-43 PCT-US91-05047-43 US-09-270-767-40173 US-09-270-767-40173 US-09-270-767-40173 US-09-270-767-99 US-08-434-120-99 US-08-465-325-98 US-09-434-737-98
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04444666666666666666666666666666666666
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

## ALIGNMENTS

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Gaps
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            Sequence 8. Application US/09525269A

Batent No. 6743769

GENERAL INFORMATION:
APPLICANT: Standar J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HRS614)
CURRENT FILING DATE: 200-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PREUSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
US-09-525-269A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-525-269A-8
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ö 100.0%; Score 74; DB 4; Length 14; 100.0%; Pred. No. 0.002; tive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 14; Conservative

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1 KLYKKWKKKLLKLK 14

KLYKKWKKKLLKLK 14 충_. 음

RESULT 2
US-09-525-269A-5
i Sequence 5. Application US/09525269A
j Patent NO. 6743769
j GENERAL INFORMATION:
j APPLICANT: Yeaman, Michael R.
j TITLE OF INVENTION: Antimicrobial Peptides and Derived
j TITLE OF INVENTION: Antimicrobial Peptides
j TITLE OF INVENTION: Antimicrobial Peptides
j TITLE OF INVENTION: Antimicrobial
j CURRENT APPLICATION NUMBER: US/09/525,269A
j CURRENT FILING DATE: 2000-03-13
prior Application NUMBER: US 09/025,319
j PRIOR FILING DATE: 1998-02-18
j NUMBER OF SEQ ID NOS: 39

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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 9; Conserv
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US-09-525-269A-4
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US-09-525-269A-3
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                                          FEATURE:
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                                                                                                   OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon CTHER INFORMATION: microbiocidal domains from platelet microbial COTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
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Pred. No. 0.45;
0; Mismatches 1; Indels
                                                                                                                                                                                                                         Score 56; DB 4; Length 14;
Pred. No. 0.36;
                                                                                                                                                                                                                                                                    1; Indels
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US-09-525-269A-10

| Sequence 10, Application US/09525269A
| Patent No. 6743769
| GENERAL INFORMATION:
| APPLICANT: Yeaman, Michael R.
| APPLICANT: Shen, Alexander J.
| TITLE OF INVENTION: Metapeptides
| TITLE OF INVENTION: Metapeptides
| FILE REFERENCE: 66742-025 (RR5614)
| CURRENT APPLICATION NUMBER: US/09/525,269A
| CURRENT FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-02-18
| NUMBER OF SEQ ID NOS: 39
| SEQ ID NO 10
| LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Steman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antinicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REPERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT APPLICATION NUMBER: US 09/025,319
PRIOR PILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for WindowsqVersion 4.0
SEQ ID NO 9
LENGTH: 13
'TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09525269A Patent No. 6743769 GENERAL INFORMATION:
                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                         75.78;
78.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.3%;
90.9%;
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1 KLYRKFKNKLLKLK 14
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                                                                                                                                                                                                                                                                    11; Conservative
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Best Local Similarity
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Best Local Similarity
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US-09-525-269A-9
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OTHER INFORWATION: Antimicrobiocidal peptide designed in part upon OTHER INFORWATION: microbiocidal domains from platelet microbial TOTHER INFORWATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OCHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-3
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Pred. No. 2.5;
1; Mismatches 0; Indels
                                                                                           68.9%; Score 51; DB 4; Length 18; 90.0%; Pred. No. 1.9; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived;
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastEEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09525269A Patent No. 6743769
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 10; Conservative
                                                                                                                                  9; Conservative
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NUMBER OF SEQ ID NOS:
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ORGANISM: Unknown
                                                                                                                                                                                                        US-09-447-966-1
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US-09-000-692-1
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APPLICANT: Slattum, Paul M
APPLICANT: Slattum, Paul M
APPLICANT: Slattum, Paul M
APPLICANT: Budker, Vladimir G
APPLICANT: Budker, Vladimir G
APPLICANT: Budker, Vladimir G
APPLICANT: Rozema, David B
TITLE OF INVENTION: INTRAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID
FILE REPERENCE: Mirus 013.03
CURRENT APPLICATION NUMBER: 05/0121730
PRIOR APPLICATION NUMBER: 60/121730
PRIOR PILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hagstrom, James E
APPLICANT: Budker, Vladimir G
APPLICANT: Budker, Vladimir G
APPLICANT: Bozema. David B
TITLE OF INVENTION: INTRAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID
FILE REPERENCE: Mirus 013.03
CURRENT APPLICATION NUMBER: US/09/450,315A
CURRENT FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/121730
PRIOR APPLICATION NUMBER: 60/146564
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: synthesized OTHER INFORMATION: amphipathic peptide with alternating hydrophilic OTHER INFORMATION: and hydrophobic residues.
OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
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Pred. No. 8.1;
                                                                                                               Score 46; DB 4; Length 13;
Pred. No. 6.2;
                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09450315A Patent No. 6379966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09447966
Patent No. 6627616
                                                                                                               62.2%;
90.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WOLFF, JON A
APPLICANT: Monahan, Sean D
APPLICANT: Slattum, Paul M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLYKKWKKKLLKLK 14
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Monahan, Sean D
Slattum, Paul M
                                                                                                                                                      9; Conservative
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                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
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APPLICANT: WOLFF,
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                                                      ; US-09-525-269A-4
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COMPÓSITONS AND METHODS FOR TREATING
INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
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Sequence 1, Application US/09000692

SERNEAL INFORMATION:

APPLICANT: HAGSTROM, JAMES B

APPLICANT: BUDKER, VLADIMIR G

APPLICANT: SLATTUM, PAUL M

APPLICANT: SLATTUM, PAUL M

APPLICANT: HANSON, LISA J

TITLE OF INVENTION: FROM A TEMPLATE DRUG

FILE REFERENCE: TPCIP000692

CURRENT APPLICATION NUMBER: US/09/000,692

CURRENT PAILING DATE: 1997-12-30

EARLIER FILING DATE: 1997-01-03

SOFTWARE: PAUCHIN Ver. 2.0

SEQ ID NO:

1 SOFTWARE: PAUCHIN Ver. 2.0
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; OTHER INFORMATION: Description of Unknown Organism:AMPHIPATHIC
US-09-000-692-1
                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: 18-mer OTHER INFORMATION: positive charge
                                                                                                                                                                                                                                         Query Match 62.2%; Score 46; DB 4; Length 18; Best Local Similarity 71.4%; Pred. No. 8.1; Matches 10; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 3; Length 20;
Pred. No. 8.8;
0; Mismatches 4; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08233203
Fatent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND
TITLE OF INVENTION: INFECTIONS CAUS.
TITLE OF INVENTION: ANTIBIOTICS
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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71.4%;
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Best Local Similarity 71.4
Matches 10; Conservative
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GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 1; Length 23;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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CLASSIFICATION: 514
CLASSIFICATION: 514
PROR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFRAN: 3126165418
TELEFRAN: 3126165409
TELEFRAN: 1126165460
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                     FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTOCNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 0N0063A
TELEPHONE: 206/728-4800
TELEPHONE: 206/728-4800
TELEPHONE: 206/448-4775
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
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Patent No. 5409898
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Cosend, Wesley L.
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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Pred. No. 12;
0; Mismatches 2; Indels
                                                                                                                                                        MEDIUM TYPE: FIDOPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,203

FILING DATE: 19-FEB-1991

APPLICATION NUMBER: US/07/655,321

FILING DATE: 19-FEB-1991

APPLICATION NUMBER: US/07/655,321

FILING DATE: 19-FEB-1991

ATTORNEY AGENT INFORMATION:

NAME: POOT, Brian W.

REFERENCE/DOCKET NUMBER: 32,928

REFERENCE/DOCKET NUMBER: 32,928

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 11:

SEQUIPMENCE CHARACTERISTICS:

LEMENT. 206/448-4775

INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY: WEALTH TEACH TO THE TEACH TO THE TEACH TO THE TEACH THE TE
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Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
CITY: Seattle
STATE: Washington
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GY: linear
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US-08-233-203-12
                                                                 COUNTRY:
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COUNTRY:
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 May be a C-terminal amide, and/or may be acetylated at N-terminus.
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: EMIlnamow
ADDRESSEE: EMIlnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1; Length 18;
Pred. No. 26;
0; Mismatches 3; Indels
                                                                          Length 18;
                                                                                                             3; Indels
                                                                        Score 42; DB 1;
Pred. No. 26;
                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-ULL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 9,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                            Sequence 29, Application US/07725331
Patent No. 5294605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                      56.8%;
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                                                                                                                                                 1 KLYKKWKKKLLKL 13
                                                                      Query Match 56.8
Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                2 KLLKKLKKKLKKL 14
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Best Local Similarity 76.9
Matches 10; Conservative
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MOLECULE TYPE: peptide
OTHER INFORMATION:
COTHER INFORMATION:
US-07-725-331-27
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US-07-725-331-29
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Gaps
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                                      APPLICANT: Houghten, Richard
APPLICANT: Houghten, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Houghten, Richard
APPLICANT: Houghten, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSE: Dressler, Goldsmith, Sutker, Shore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 5; Length 18;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                           ADDRESSEE: Dressler, Goldsmith, Sutker, Shore
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                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
Sequence 27, Application PC/TUS9105047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application PC/TUS9105047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                               ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.8%;
76.9%;
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180 North Stetson
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLYKKWKKKLLKL 13
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US91-05047-27
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                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                           60601
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR RELING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
   STREET: 180 No. 5294605th Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 54, Application US/07725331
Patent No. 5294605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.4%;
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 KOFKKWLKLNLKIK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLYKKWKKKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-248-796A-23525
   JS-09-248-796A-23525
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TITLE OF INVENTION:
TOOPER OF THE REPERBLE OF OF THE REPERBRUE OF THE TEPERBRUE.
TOTRENT APPLICATION NUMBER: US/09/493,211
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER: PCT/NL97/00449
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE:
PARENTE:
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Pred. No. 34;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 5; Length 18;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                OPEKATING STEEM: PUCLUOS/NB-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION ST4
PRIOR APPLICATION NUMBER: US 07/554,422
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: GAMEON, Edward P.
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-493-211-6
                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTER.STICS: LENGTH: 18 amino acids TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.8%;
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Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KLKKKWKAAKKFLK 15
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Best Local Similarity 76.2
Best Local 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
CTHER INFORMATION:
PCT-US91-05047-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6
LENGTH: 18
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STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-233-203-7
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PCT-US91-05047-54
| Sequence 54, Application PC/TUS9105047
| GENERAL INFORMATION:
| APPLICANT: Houghten, Richard APPLICANT: Blondelle, Sylvie
| TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Annologues Thereof NUMBER OF SEQUENCES: 68
| CORRESPONDENCE ADDRESS: ADDRESSEE: E Milhamow | ADDRESSEE: E Milhamow |
| ADDRESSEE: E Milhamow |
| ADDRESSEE: Milhamow |
| ADDRESSEE: A MILHAMOW |
| A MI
                                                                                                                                                                                                                             Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.1%; Score 40; DB 5; Length 17; 71.4%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                        4; Indels
                                                                       OTHER INFORMATION: C-terminal amide, acetylated OTHER INFORMATION: at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: C-terminal amide, acetylated OTHER INFORMATION: at N-terminus.
                                                                                                                                                                                                                         DB 1;
44;
                                                                                                                                                                                                                                                                                                        0; Mismatches
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ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9207/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAMME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELEPHONE: 3126165460
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids

"THE ANTON ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                         Score 40;
Pred. No.
                                                                                                                                                                                                                     Query Match 54.1%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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: 180 North Stetson
Chicago
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MOLECULE TYPE: peptide
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Andes J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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Sequence 30, Application US/07725331

Patent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
ADDRESSEE: E Milnamow
STREET: 180 No. 5294605th Stetson
CITT: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 May be a C-terminal amide, and/or may be acetylated at N-terminus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: GAMBON: Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08233203
Patent No. 5409898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLYKKWKKKLLKLK 14
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OTHER INFORMATION:
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Best Local Similarity
Matches 10; Conserv
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0; Mismatches
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Pred. No.
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-PEB-1991
APPLICATION NUMBER: US 07/484,020
                                        US 07/484,020
            FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,
FILING DATE: 23-FEB-1990
ATTORNEY AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 32,928
REFERENCATION TOWNER: 0N006
TELECOMMUNICATION INFORMATION:
TELEPAX: 206/728-4800
TELEPAX: 206/448-4775
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATTON:
ADME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFRENCE/POCKET NUMBER: ONFO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3005 First Avenue
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Best Local Similarity 81.6
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: YES
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APPLICATION NUMBER:
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CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-233-203-10
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Sequence 8, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
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                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION DATE:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOC. BILAIM W
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENTIN Release #1.0, Version #1.25
SOFTWARE: PatentIN Ralease #1.0, Version #1.25
SOFTWARE: APPLICATION DATA:
FILING DATE:
FLING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bristol-Myers Squibb Company, Patent
Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 46;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.1%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 206/448 4775
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: YES
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                     Washington
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Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
XX: linear
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                                          USA
                                                           98121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-233-203-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: 8
STATE:
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Sequence 10, Application US/08233203

Batent No. 5409898
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Mesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
                                                              Gaps
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DB 1; Length 18;
                                                              2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
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PCT-US91-05047-30

Sequence 30, Application PC/TUS9105047

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 4; Length 18;
Pred. No. 46;
                                                                           APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                     COUNTRY: UNITED SIRIES OF ACCOMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-UM-1995
CLASSIFICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
RIOR APPLICATION NUMBER: US 08/164,067
FILING DATE: 17-DEC-1993
RIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 08-DEC-1993
RIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 1-DEC-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELERPAX: (415) 795-8410
TELERPAX: (415) 797-8338
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TUBNGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow STREET: 180 North Stetson CITY: Chicago
                                                                                                                                                            ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTCOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
               SCHATZ, ROBERT W.
PUGH, CHARLES
PANASIK JR., NICHOLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.1%;
81.8%;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08760903
Fatent No. 599381
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SHEKANI, MOHAWMED S.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL, LLP
STREET: 220 MONTCOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2; Length 18; Pred. No. 46;
                                                                                                                        54.1%; Score 40; DB 1; Length 18; 81.8%; Pred. No. 46;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 25
1S-08-482-191-2
1S-08-482-191-2
1 Patent No. 6579696
1 GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
1 APPLICANT: SHEKHANI, MOHAMMED S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 54.1
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                            Best Local Similarity 81.8 Matches 9; Conservative
                 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
                                                                                                                                                                                                             2 LYKKWKKKLLK 12
                                                                                                                                                                                                                                          2 LYKKLLKKLLK 12
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amino acid
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                                                                ; HYPOTHETICAL
US-08-233-203-10
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US-08-760-903-2
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                                                                                                                          Query Match
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08760903
Patent No. 5998381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: S
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown;
MOLECULE TYPE: peptide
PCT-US96-10227-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYKKWKKKLLK 12
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unknown
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
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GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: STRCA, JOSEPH R
APPLICANT: SCHARTZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May be a C-terminal amide, a be acetylated at N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION UNDERS:

FILING DATE:

CLASSIPICATION:

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

AND NUMBER:

ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                  NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 42:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & (
                                                                                                                                                                                                                                                                                                                                                                                                                     3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION:
) OTHER INFORMATION:
PCT-US91-05047-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -US96-10227-2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STEACHAIL, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
CORRESSED MEDRESS: ADDRESS: ADDRESSE: ADDRESSE: ADDRESSER: ADDRESSER: STREET: SUITE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903 FILING DATE: 06-DEC-1996 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA, REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
PILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECHONE: (415) 397-8410
TELECHONE: (415) 397-8438
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Pred. No. 4
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-493-211-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9610227 GENERAL INFORMATION:
                                                                            Sequence 1, Application US/09493211
Patent No. 6624140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLYKKWK--KKLLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial
                                                          US-09-493-211-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 31
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                                 Score 40; DB 2; Length 19;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 4; Length 19;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHNI, WOHAMMED S.
APPLICANT: SCHATZ, JOSEPH R
APPLICANT: SCHATZ, MOBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PRAGSIK JR., NICHOLAS
APPLICANT: PRAFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: PSTANDE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PELDEDY disk
COMPUTER: PELDEDY MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: DC-DOS/MS-DOS
TLING DATE: 07-JUN-1995
CLLASSIFICATION: 514
PRILOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 09HD-01280
TELERPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                         Sequence 3, Application US/08482191
Patent No. 6579696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-8338
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 81.0
Local Similarity 81.0
Local Similarity 1.0
                  Query Match
Best Local Similarity 81.0
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                                                                                                                      2 LYKKWKKKLLK 12
                                                                                                                                                         2 LYKKILKKILK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYKKWKKKLLK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: SAN FRANCISCO
US-08-760-903-3
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Academisch Ziekhuis Bij De Universiteit
TITLE OF INVENTION: No. 6624140el synthetic peptides with antimicrobial and endotoxi
TITLE OF INVENTION:
PILLE REFERENCE: Q57666
CURRENT APPLICATION NUMBER: US/09/493,211
CURRENT PILING DATE: 2000-01-28
PRIOR RELING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 19
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APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFRORD, DOUGLAS C.
APPLICANT: STAFRORD S.
APPLICANT: STAFRORD C.
APPLICANT: STAFRORD C.
APPLICANT: STAFRORD C.
APPLICANT: STAFRORD C.
APPLICANT: MOHAMMED C.
APPLIC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200
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10 South Wacker Drive, Suite 3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
RATTORNEY/AGENT INFORMATION:
NAME: No. 6107459nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 92,37 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000 TELER, 910-221-5317 INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLYKKWKKKLLK 12
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                                                                                                       ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
STREET: 1v CITY: Chicago CTATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-290-853-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Pred. No. 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASPLIANCE NO. S9813-30
Sequence 30, Application US/08290853
Sequence 30, Application US/08290853
Sequence 30, S98519
SERVERAL INFORMATION:
APPLICANT: Dean, Richard T
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 37
COMPASSONDEDICE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-525-269A-11

| Sequence 11, Application US/09525269A |
| Patent No. 6743769 |
| Patent No. 6743769 |
| GENERAL INFORMATION: |
| APPLICANT: Yeaman, Michael R. |
| APPLICANT: Shen, Alexander J. |
| TITLE OF INVENTION: Antimicrobial Peptides and Derived TITLE OF INVENTION: Metapeptides FILE REFERENCE: 6742-025 (HR5614) |
| CURRENT APPLICATION NUMBER: US/09/525,269A |
| CURRENT FILING DATE: 1090-03-13 |
| PRIOR FILING DATE: 1998-02-18 |
| NUMBER OF SEQ ID NOS: 39 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 11 |
| LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
           FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 0PHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                        LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown; MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LYKKWKKKLLK 12
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                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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Gaps
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TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Diagnostic Imaging
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
                                                                                                 OPEKATING SISIEM: F. LOSSING-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/505,318
FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
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                                                                                                                                                 Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 30;
                                                                                                                                                                                      Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUNESSE: E.I. du Pont de Nemours and Company STREET: 1007 Market Street CITY: Wilmington STATE: Delaware COUNTRY: USA
                                                                                                                                             52.0%; Score 38.5; DB 1;
illarity 58.8%; Pred. No. 1.1e+02;
Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%; Score 38.5; DB 5; 58.8%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 AUGUST 1991
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOWNUNICATION INFORMATION:
must FPHING NAMBER: 30,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                   NAME/KEY: Protein
CCATION: 1..30
CTHER INFORMATION: /label= name
CTHER INFORMATION: /note= "CSP 1"
US-08-182-175A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= name
/note= "CSP 1"
                                                                                                                                                                                                                                                                                                                                                       PCT-US92-06412-8; Sequence 8, Application PC/TUS9206412; GENERAL INFORMATION:
                                                                                                                                                                                                                               1 KLYKKW---KKKLLKLK 14
                                                                                                                                                                                                                                                      1 KLYKKW---KKKLLKLK 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 1..30
; OTHER INFORMATION:
; OTHER INFORMATION:
PCT-US92-06412-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID STRANDEDNESS: un
                                                                                                                                                                Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19898
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                   RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.1. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                      /label= Tc-99m-chelator
/note= "A bis-amino, bis-thiol Tc-99m chelator
[BAT] is covalently attached to the N-terminal
amino group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 3; Length 18;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
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MEDIUM TYPE: Floppy Disk

COMPUTER: Macintosh back

COMPUTER: Macintosh System, 6.0

SOFTWARE: Microsoft Word, 4.0

CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/182,175A

FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 9 August 1991

ATTORNEY/AGENT INFORMATION:

NAME: Linda Axamethy Floyd

REGISTRATION NUMBER: 33,692

REFERENCE/POCKET NUMBER: BB-1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
  90,1104-FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08182175A Patent No. 5559223
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                 52.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (302) 892-4929
(302) 892-7949
                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                         LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 30 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.0 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 835420
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLYKKWKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 KLYKKIIKKLLE 17
                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                   LOCATION: 1..2
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 35
US-08-182-175A-8
                                                                                                                                                                                                                                                                                                                                                                        US-08-505-318-7
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Sequence 40173, Application US/09270767

Sequence 40173, Application US/09270767

EARERAL INFORMATION:
APPLICANT: Homburst et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40173
LENGTH: 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%; Score 38; DB 5; Length 18; 69.2%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           May be a C-terminal amide, r
be acetylated at N-terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-40173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                          SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 907/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                      COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLYKKWKKKLLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KLHKKLLKKLKKL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.4
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 3126165418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYKKWKKKLLK 12
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39 MYRKWKKTNFK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                         3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION:
) OTHER INFORMATION:
PCT-US91-05047-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 39
US-09-270-767-40173
                      60601
  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                               Sequence 43, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.4%; Score 38; DB 1; Length 18; 69.2%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , CIHER INFORMATION: May be a C-terminal amide, may j OTHER INFORMATION: be acetylated at N-terminus. US-07-725-331-43
                                                                                                                                                                                                                                   ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnanow STREET: 180 No. 5294605th Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60601
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: STATEM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 3126165460
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: & Milnamow
STREET: 180 North Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLYKKWKKKLLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 amino acide
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2 KLHKKLLKKLKKL 14
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Best Local Similarity 69.2
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
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RESULT 37
US-07-725-331-43
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1 KLYKKWKKKLLKLK 14
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                                                                                                                                                                     Query Match 50.0
Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-434-120-99
                                    MOLECULE TYPE: peptide
                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Roseland
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                    linear
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Best Local Similarity
Matches 9; Conserv
STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07068
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US-08-434-120-99
                                                                                                                                  US-08-193-521-5
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                                                               APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55389
LENGTH: 52
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                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 4; Length 52;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Kari, U. Prasad
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Therefor
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi & Stewart STREFT: 6 Becker Farm Road CITY: Roseland STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DN4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/193,521
FILING DATE:
CLASSIPFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/870,960
                                Sequence 55389, Application US/09270767
Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                            51.4%;
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Matches 6, Conserv
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                  US-09-270-767-55389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 41
US-08-193-521-5
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TITLE OF INVENTION: Biologically Active Peptides With Reduced
Toxicity in Animals and a Method for Preparing Same
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Sequence 7, Application US/09434345
Patent No. 651676
GENERAL INFORMATION:
APPLICANT: Boulika Teni
APPLICANT: Boulika Teni
TITLE OF INVENTION: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO
TITLE OF INVENTION: LIPOSOMES
TITLE OF INVENTION: LIPOSOMES
FILE REFERENCE: TB 2001.00
CURRENT APPLICATION NUMBER: US/09/434,345
CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                NUMBER OF SEQUENCES: 156
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
                                                                                                                                                                                                                                                                                     MEDIUM LIFE: FLOPPY ALEA
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,737
FILING DATE: 15-0u1-1998
CLASSIFICATION WIMBER: 08/465,330
FILING DATE: 05-UN-1995
APPLICATION NUMBER: 08/184,462
FILING DATE: 05-UN-1995
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-UN-92
ATTORNEY/AGENT INFORMATION:
MANAGE DELICATION NUMBER: 07/891,201
FILING DATE: 01-UN-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 16;
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: An amphiphilic fusogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 05387.0021-06000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-400
TELEFRY: (202) 408-4400
                                                                                                                                     STREET: 1300 I Street, N.W. Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 37; DB 3; 64.3%; Pred. No. 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) MOLECULE TYPE: peptide
) SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-115-737-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
                                                                                                                                                                                                                     ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 98: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLYKKWKKKLLKLK 14
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                                                                                                                                                             CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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les 9; Conserve
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Matches
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                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Magainin Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: 5110 Campus Drive
APPLICANT: 5110 Campus Drive
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS: ADDRESSE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: O5-JUN-1995
CLASSIFTCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 I. Street, N.W. Suite 700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%; Score 37;
64.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
ZIP: PEADABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC COMPATINE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98, Application US/09115737
Patent No. 6348445
GENERAL INFORMATION:
APPLICANT: U. Prasad Kari
Taffy J. Williams
Michael McLane
                                                                                                                                     RESULT 43
US-08-465-325-98
'Sequence 98, Application US/08465325
'Patent No. 568663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,984
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                            KLYKKWKKKLLKLK 14
                                                                      KLLKKLKKLLKKLR 15
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Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fordis, Jean B
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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US-09-115-737-98
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Query Match 50.0%; Score 37; DB 4; Length 16; Best Local Similarity 75.0%; Pred. No. 99; Matches 9; Conservative 0; Mismatches 3; Indels
                                                                                                                          1 KLYKKWKKKLLK 12
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US-09-434-345-7
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Search completed: May 16, 2005, 08:40:40 Job time : 14.9655 secs

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May 16, 2005, 08:38:44; Search time 52.6207 Seconds (without alignments) 88.876 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB_pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB_pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1432185 segs, 334051727 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                    US-09-648-816B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 74
                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Sequence 6, Appli Sequence 47529, A	9	49	22,	26,	49,	55,	26,	1583	Sequence 1082, Ap		Sequence 236809,	Sequence 48620, A	Sequence 246569,	Sequence 64, Appl	Sequence 37456, A	Seguence 219597,	Š,		62	Sequence 7, Appli	7	'n	Sequence 4, Appli	12,	7, Ap	Sequence 4, Appli	a	Sequence 4, Appli	Sequence 223572,	Sequence 48512, A
US-10-609-515-6 US-09-864-761-47529	US-10-609-515-1	US-09-820-053A-49	US-09-820-053A-55	US-09-820-053A-56	US-10-109-171-49	US-10-109-171-55	US-10-109-171-56	15 US-10-424-599-158309	US-10-472-928-1082	US-09-864-761-44624	US-10-424-599-236809	US-09-864-761-48620	US-10-424-599-246569	US-09-854-204-64	US-09-864-761-37456	US-10-424-599-219597	US-09-854-204-65	US-09-876-904A-15	US-09-876-904A-629	US-10-350-470-7	US-10-609-515-7	US-10-609-515-2	US-10-609-515-4	US-10-017-672-12	US-09-853-897-7	US-09-865-553-4	US-10-106-698-5301	US-10-467-513-4	US-10-424-599-223572	US-10-767-701-48512
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35	19	23	23	23	23	23	23	26	26	73	35	37	63	16	63	71	12	16	16	16	18	19	19	25	59	40	40	40	43	4
55.4 55.4	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	54.1	52.7	52.7	52.7	51.4	51.4	51.4	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	20.0
414	40	40	40	40	40	40	40	40	. 40	40	39	39	39	38	38	38	37	37	37	37	37	37	37	37	37	37	37	37	37	37
14	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	. 40	41	42	43	44	45

## Sequence 125, Application US/09820053A Publication No. US20030083243A1 GENERAL INFORMATION: APPLICANT: Owen, Donald R. TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES FILE REPERBRENCE: HELKOZ7 CURRENT APPLICATION UNMER: US/09/820,053A CURRENT FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 165 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 125 LENGTH: 16 US-09-820-053A-125

ALIGNMENTS

ORGANISM: ARTIFICIAL SEQUENCE TYPE: PRT

70.3%; Score 52; DB 10; Length 16; 76.9%; Pred. No. 2.4; cive 1; Mismatches 2; Indels OTHER INFORMATION: SYNTHETIC SEQUENCE US-09-820-053A-125 Best Local Similarity 76.9 Matches 10; Conservative Query Match

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Gaps

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US-10-109-171-125 셤

Sequence 125, Application US/10109171
; Publication No. US20030109452A1
; GBNERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE

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CTHER INFORMATION: AMIDATION US-10-109-171-124
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SOFTWARE: PatentIn Ver. 2.0
LOCATION: (17)
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LENGTH: 18
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US-10-109-171-124
Sequence 124, Application US/10109171
Publication No. US20030109452A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
TITLE OF INVERTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
CURRENT APPLICATION WUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 124
LENGTH: 17
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Pred. No. 2.4;
1; Mismatches 2; Indels
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US-09-820-053A-124
; Sequence 124, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 201-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.3%; Score 52; DB: 76.9%; Pred. No. 2.5; tive 1; Mismatches
              CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 125
LENGTH: 16
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OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD_RES
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LOCATION: (17)
                                                                                                                                                                                                  ) OTHER INFORMATION: SYNTHETIC SEQUENCE US-10-109-171-125
                                                                                                                                                          ORGANISM: ARTIFICIAL SEQUENCE
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ORGANISM: ARTIFICIAL SEQUENCE
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Best Local Similarity 76.9%;
Matches 10; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
FILE REFERENCE: HELX028
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LENGTH: 17
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APPLICANT: Slattum, Paul M
APPLICANT: Slattum, Paul M
APPLICANT: Hagelrom, James B
APPLICANT: Hagelrom, James B
APPLICANT: Budker, Vladimir G
APPLICANT: Rozema, David B
TITLE OF INVENTION: INTERAVACULAR DELIVERY OF NON-VIRAL NUCLEIC ACID
FILE REFERENCE: Mins. 013.03.
CURRENT APPLICATION NUMBER: US/09/447,966
CURRENT PILING DATE: 1999-11-23
PRIOR PLILING DATE: 1999-02-66
PRIOR PLILING DATE: 1999-07-30
PRIOR PLILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PATENTIN Ver. 2.0
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| Publication No. US20010019723A1
| GENERAL INFORMATION:
| APPLICANT: WOLFF, JON A
| APPLICANT: Monahan, Sean D
| APPLICANT: Budker, Vladimir G
| APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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. OTHER INFORMATION: Description of Artificial Sequence: 18-mer; OTHER INFORMATION: positive charge
US-09-447-966-1
    DB 14; Length 17;
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Pred. No. 16;
0; Mismatches 4; Indels
Score 52; DB 1
Pred. No. 2.5;
1; Mismatches
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Patent No. USZ0010004636A1
GENERAL INFORMATION:
APPLICANT: WOLFF, JON A
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ORGANISM: Artificial Sequence
    70.3%;
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Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                               1 KLWKKWAKKWLKL 13
    Query Match 70.3
Best Local Similarity 76.9
Matches 10; Conservative
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Sequence 1, Application US/10600098 Publication No. US20030216347A1 GENERAL INFORMATION:
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APPLICANT: Mirus Corporation APPLICANT: Wolff, Jon
LENGTH: 18
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
PEATURE:
                                                                                                                                       62.2%;
nilarity 71.4%;
Conservative
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SOFTWARE: Patentin version 3.1
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ilarity 71.4%;
Conservative
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                                                                                                                                                                                                                          1 KLYKKWKKKLLKLK 14
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                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserva
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nes 10; Conserv
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ORGANISM: Artificial
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LENGTH: 18
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Matches
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APPLICANT: Hagstrom, James B
APPLICANT: Hagstrom, James B
APPLICANT: Hagstrom, James B
APPLICANT: Slattum, Paul B
APPLICANT: Slattum, Paul B
APPLICANT: Budker, Vladimir G
TITLE OF INVENTION: Intrascular Delivery of Non-Viral Nucleic Acid
FILE REFERENCE: Mirus.013.04.03
FILE REFERENCE: Mirus.013.04.03
CURRENT FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                            FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: synthesized
CTHER INFORMATION: amphipathic peptide with alternating hydrophilic
CTHER INFORMATION: and hydrophobic residues.
US-09-450-115A-1
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APPLICANT: MONHAM, SEAN
APPLICANT: MONHAM, SEAN
APPLICANT: WALFF, JON
APPLICANT: SLATTUM, PAUL
APPLICANT: SLATTUM, PAUL
APPLICANT: BUDKER, VIADIMIR
APPLICANT: SOZEMA, DAVID
TITLE OF INVENTION: POLYNUCLEOTIDE COMPLEX DELIVERY
CURRENT APPLICATION NUMBER: US/10/085,378
CURRENT APPLICATION NUMBER: US/10/085,378
CURRENT FILING DATE: 2002-02-7
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: synthetic amphipathic sequence
                                                                                                                                                                                                     Score 46; DB 9;
Pred. No. 16;
0; Mismatches
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Pred. No. 16;
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Publication No. US20030166280A1
GENERAL INFORMATION:
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                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                     Query Match 62.2%;
Best Local Similarity 71.4%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                       1 KLYKKWKKKLLKLK 14
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Matches 10; Conservative
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ORGANISM: Artificial
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US-10-085-378-2
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LENGTH: 18
SEQ ID NO 1
LENGTH: 18
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APPLICANT: "CALL James
APPLICANT: Hagetron, James
APPLICANT: Slattum, Paul
APPLICANT: Slattum, Paul
APPLICANT: Slattum, Paul
APPLICANT: Budker, Vladimir
TITLE OF INVENTION: Intravascular Delivery of No. US20030216347A1-Viral Nucleic Acid
TITLE OF INVENTION: Intravascular Delivery of No. US20030216347A1-Viral Nucleic Acid
TITLE OF INVENTION: 12003.03.06.20
CURRENT PILING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 18
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APPLICANT: Hagstrom, James
APPLICANT: Monahan, Sean
APPLICANT: Salttum, Paul
APPLICANT: Budker, David
APPLICANT: Budker, Vladimir
TITLE OF INVENTION: Intravascular Delivery of No. US20040019007A1-Viral Nucleic Acid
FILE REPERENCE: Mirus 013.03.1
CURRENT APPLICATION UNMBER: US/10/600,290
CURRENT FILING DATE: 2003-06-20
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                                                                                  Length 18;
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                                                                                Score 46; DB 14;
Pred. No. 16;
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Pred. No. 16;
0; Mismatches 4
                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-600-098-1
; OTHER INFORMATION: CATIONIC PEPTIDE US-10-085-378-2
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Gaps

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Length 18;

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; OTHER INFORMATION: synthetic amphipathic peptide US-10-609-938-2
                                                                                       Score 46; DB 16;
Pred. No. 16;
0; Mismatches 4
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71.4%;
                                                                                       ch 62.2%;
11 Similarity 71.4%;
10; Conservative
                                                                                                                                                                    1 KLYKKWKKKLLKLK 14
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ORGANISM: Glycine max
                                                                                         Query Match
Best Local Similarity
Matches 10; Conserva
ORGANISM: Artificial FEATURE:
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ORGANISM: Artificial
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Best Local Similarity
Matches 7; Conserv
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TITLE OF INVENTION: Intravascular Delivery of Non-Viral Nucleic Acid
FILE REFERENCE: Mirus.013.03.4
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Pred. No. 16;
0; Mismatches 4; Indels
                                                                                                              4; Indels
                                                                     Score 46; DB 15;
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: amphipathic synthetic peptide US-10-628-734-2
                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Monahan, Sean
APPLICANT: Hagstrom, James
APPLICANT: Rozema, David
APPLICANT: Bucker, Vladimir
APPLICANT: Slattum, Paul
TITLE OF INVENTION: KLLKKLIKLWKKLLKKLK
FILB REFERRNCE: Mirus. 013.07
CURRENT APPLICATION NUMBER: US/10/628,734
CURRENT FILING DATE: 2003-07-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/609,938
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: US 09/917154
PRIOR FILING DATE: 2001-06-27
               ; OTHER INFORMATION: synthetic peptide US-10-600-290-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10609938 Publication No. US20040106567A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             Sequence 2, Application US/10628734 Publication No. US20040072785A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.2%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                     Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
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APPLICANT: Mirus Corporation
APPLICANT: Hagstrom, James E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolff, Jon A
Monahan, Sean D
Rozema, David B
Budker, Vladimir
Slattum, Paul M
                                                                                                                                                                            S KLLKLWKKLLKKLK 18
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mirus Corporation APPLICANT: Wolff, Jon
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                                                                                                                                                 1 KLYKKWKKKLLKLK 14
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SEQ ID NO 2
'LENGTH: 18
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LENGTH: 18
FEATURE:
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US-10-609-515-6

Sequence 6, Application US/10609515

Sequence 6, Application US/10609515

Publication No. US20040049011A1

GENERAL INFORMATION:

APPLICANT: Academisch Ziekhuis Bij De Universiteit

APPLICANT: Academisch Ziekhuis Bij De Universiteit

APPLICANTON: Droperties for management of the sepsis syndrome

TITLE OF INVENTION: Droperties for management of the sepsis syndrome

FILE REFREENCE: 057666

CURRENT PAPLICATION NUMBER: US/10/609,515

CURRENT FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 1997-07-31

PRIOR FILING DATE: 1997-07-31

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 6
Sequence 165455, Application US/10424599
Publication No. US20040011072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: About Vihua
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 165455
LENGTH: 61
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US-10-424-599-165455
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Pred. No. 1.5e+02;
3; Mismatches 1
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US-10-609-515-6
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APPLICANT: Academisch Ziekhuis Bij De Universiteit
TITLE OF INVENTION: DESCO040049011A1el synthetic peptides with antimicrobial and er
TITLE OF INVENTION: Droperties for management of the sepsis syndrome
FILE REPERENCE: 05766
CURRENT APPLICATION NUMBER: US/10/609,515
CURRENT APPLICATION NUMBER: US/09/493,211
PRIOR APPLICATION NUMBER: US/09/493,211
PRIOR FILING DATE: 2000-01-28
PRIOR PILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATCHILING NOS: 9
SOFTWARE: PATCHILING VARSION 3.0
SEQ ID NO 1
LENGTH: 19
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Pred. No. 1.2e+02;
2; Mismatches 2
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Sequence 49, Application US/09820053A

Publication No. US20030082243A1

GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELKO27;
CURRENT APPLICATION NUMBER: US/09/820,053A

CURRENT PILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 165

SEQ ID NO 49

LENGTH: 23
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-609-515-1
                                                                                                                                                                 Sequence 1, Application US/10609515
Publication No. US20040049011A1
GENERAL INFORMATION:
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60.0%;
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Similarity 66.7%;
8; Conservative
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Best Local Similarity 60.0°
Matches 9; Conservative
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6 KLIKKWRKK 14
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ORGANISM: Artificial
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Best Local Similarity
Matches 8; Conserv
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US-09-820-053A-55
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
        Gaps
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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
US-09-864-761-47529
     2; Indels
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     Mismatches
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-
                                                                                                                                                                                                                                                  Sequence 47529, Application US/09864761
Patent No. US20020048763A1
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                                                         1 KLYKKWK--KKLLK 12
                                                                                                          KLKKKWKAAKKFLK 15
     10; Conservative
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ORGANISM: Homo sapiens
     Matches
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; Sequence 55, Application US/09820053A

1 KLYKKWKKK 9

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TYPE: PRT ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                  54.1%;
66.7%;
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                         ; LOCATION: (23); COTHER INFORMATION: AMIDATION US-10-109-171-49
                                                                                              Query Match
Best Local Similarity 66.7
Matches 8, Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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KLFKKFAKKLAK 21
       NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                       RESULT 21
US-10-109-171-55
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US-10-109-171-49
US-10-109-171-49
Sequence 49, Application US/10109171
Publication No. US20030109452A1
GENERAL INFORMATION:
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
FILE REPERENCE: HELXO28
CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                             Length 23;
                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                           Score 40; DB 10;
Pred. No. 1.2e+02;
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US-09-820-053A-56
Sequence 56, Application US/09820053A
Publication No. US20030083243A1
GENERAL INFOWATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REPERENCE: HELKOZI
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 56
GENERAL INFORMATION:
APPLICATION NO. US20030083243A1
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELXO27
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                               ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-09-820-053A-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-09-820-053A-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: SYNTHETIC SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                  ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                           54.1%;
66.7%;
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10 KLFKKFAKKLAK 21
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LENGTH: 23
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Publication No. US20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
FILE REFERENCE: HELKOSTON NUMBER: US/10/109,171
CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 23
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                                               Gaps
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TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
PILE REFERENCE: HELX028
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Length 23;
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Score 40; DB 14; Length 23
Pred. No. 1.2e+02;
2; Mismatches 2; Indels
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66.7%; Pred. No. 1.2e+02;
iive 2; Mismatches 2
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CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 23
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.1
GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILLING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-09-04
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2000-06-30
PRIOR PILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-09-31
PRIOR PILLING DATE: 2000-09-31
PRIOR PILLING DATE: 2000-09-31
PRIOR PILLING DATE: 
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Pred. No. 3.3e+02;
3; Mismatches 2;
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illarity 61.5%;
Conservative
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APPLICANT: Kovalic David K
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Honeshi, David K.
APPLICANT: Chen, Wenesheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                               APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: A POUR MAINT STATE OF THE S
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| Sequence 1082, Application US/10472928
| Sequence 1082, Application US/10472928
| Publication No. US2005002081341
| Publication No. US2005002081341
| GENERAL INFORMATION:
| APPLICANT: CHIRON SPA
| APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
| TILLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
| TILLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
| CURRENT APPLICATION NUMBER: US/10/472,928
| PRIOR APPLICATION NUMBER: 2003-09-26
| PRIOR PELLOR DATE: 2001-03-27
| NUMBER OF SEQ ID NOS: 4979
| SEQ ID NO 1082
| LENGTH: 56
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4; Indels
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US-10-424-599-158309
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Pred. No. 2.6e+02;
                                         Sequence 158309, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 IWKQWKKKSRRLWGLLKL 37
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Best Local Similarity 50.0%;
Matches 7; Conservative
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LENGTH: 56
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Gaps

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Sequence 246569, Application US/10424599
Sequence 246569, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Coard Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 246569
LENGTH: 63
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OTHER INFORMATION: EXPERSED IN BONE MARROW, SIGNAL = 1.6
OTHER INFORMATION: EST HUMAN HIT: AU118020.1, EVALUE 4.00e-15
OTHER INFORMATION: SWISSPROT HIT: Q9Y5N6, EVALUE 3.00e-16
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US-10-424-599-246569
                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 48620
LENGTH: 37
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Pred. No. 3.9e+02;
3; Mismatches 3
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| Patent No. US20020098236A1
| GENERAL INFORMATION: US20020098236A1
| GENERAL INFORMATION: Peter Martin
| APPLICANT: Fischer, Peter Martin
| APPLICANT: Zhelev, Nikolai
| TILE OF INFORTION: Transport Vectors
| TILE REFERENCE: CCI-010
| CURRENT FILING DATE: 2001-05-11
| PRIOR APPLICATION NUMBER: 09/438,460
| PRIOR PILING DATE: 1999-11-12
| PRIOR PLLING DATE: 1999-11-13
| PRIOR PLLING DATE: 1998-11-13
| PRIOR PILING DATE: 1998-11-13
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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5 IYKLWTKRFLRL 16
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21 YEEWKRKILE 30
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ORGANISM: Homo sapiens
FEATURE:
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US-10-424-599-246569
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APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 236809
LENGTH: 35
TYPE. no. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
IITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL, FOR IITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-06-26
PRIOR PLING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/23, 366
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48620, Application US/09864761 Batent No. US20020048763A1 GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cn 52.7%;
l Similarity 71.4%;
10; Conservative (
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ORGANISM: Glycine max
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Matches 10; Conserv
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US-09-864-761-48620
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Excalic David K
APPLICANT: Scoulce David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 219597
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N FETAL LIVER, SIGNAL = 1.1

N BYA74, SIGNAL = 1.5

N BRAIN, SIGNAL = 1.9

N BONE WARROW, SIGNAL = 1.6

N LUNG, SIGNAL = 1.6

N HELA, SIGNAL = 1.9
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OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.7
COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
US-09-864-761-37456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 9; Length 63;
Pred. No. 5.3e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             PLACENTA, SIGNAL = 1.3
   PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APLICATION NUMBER: US 09/774,203
PRIOR APLICATION NUMBER: US 09/774,203
PRIOR APLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 3456
LENGTH: 63
TYPE: PAT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
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US-10-424-599-219597
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Pred, No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 219597, Application US/10424599 Publication No. US20040031072A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.4%;
50.0%;
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Best Local Similarity 72.7
Matches 8; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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62 IWSKWKKRLI 71
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ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37456, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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Pred. No. 1.7e+02;
0; Mismatches 4; Indels
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILMG DATE: 2001-05-23
PRIOR PAPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLILING DATE: 2000-06-26
PRIOR PLILING DATE: 2000-06-36
PRIOR PLILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: GB 9902525.0
PRIOR FILING DATE: 1999-02-04
PRIOR PILING DATE: 1999-02-04
PRIOR PILING DATE: 1999-02-04
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-06-22
PRIOR PILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%;
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Best Local Similarity
Matches 8; Conserv
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US-09-876-904A-629
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Fublication No. US20030072794A1

GENERAL INFORMATION:
TITLE OF INVENTION: ENCRPSULATION OF PLASMID DNA (LIPOGENES TW) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSGENIC PEPTIDE
TITLE OF INVENTION: CONJUGARE INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
FURBENT PAPLICATION NUMBER: US/09/876,904A
CURRENT PAPLICATION NUMBER: US 60/210,925
FRIOR FILING DATE: 2001-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patentin Ver. 2.1
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.. OTHER INFORMATION: Description of Artificial Sequence: Synthetic amphiphilis
.. OTHER INFORMATION: fusogenic peptide
US-09-876-904A-15
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Pred. No. 2.3e+02;
0; Mismatches 3; Indels
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Pred. No. 1.8e+02;
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                                 CURRENT PETLING DATE: 2010-05-11
PRIOR APPLICATION NUMBER: US/09/854,204
CURRENT FILING DATE: 2001-05-11
PRIOR PLILING DATE: 1999-11-12
PRIOR PLLING DATE: 1999-11-13
PRIOR PLLING DATE: 1999-11-13
PRIOR PLLING DATE: 1999-11-13
PRIOR PLLING DATE: 1999-11-13
PRIOR PELLOATION NUMBER: GB 9825001.2
PRIOR PELLING DATE: 1999-11-13
PRIOR PLLING DATE: 1999-10-10
PRIOR PLLING DATE: 1999-02-04
PRIOR PLLING DATE: 1999-06-20
PRIOR PLLING DATE: 1999-06-20
PRIOR PLLING DATE: 1999-06-21
PRIOR PLLING DATE: 1999-06-22
PRIOR PLLING DATE: 1999-10-11
PRIOR PLLING DATE: 1999-10-11
PRIOR PLLING DATE: 1999-10-11
PRIOR PLLING DATE: 1999-11-11
PRIOR PLLING DATE: 1999-11-11
OF INVENTION: Transport Vectors
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77.8%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 9; Conserv
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US-09-876-904A-15
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LENGTH: 16
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RESULT 34

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Sequence 7, Application US/10609515
Publication No. US20040049011A1
GENERAL INFORMATION:
APPLICANT: Academisch Ziekhuis Bij De Universiteit
TITLE OF INVENTION: No. US20040049011A1el synthetic peptides with antimicrobial and er
TITLE OF INVENTION: properties for management of the sepsis syndrome
FILE REFERENCE: Q5766
CURRENT APPLICATION NUMBER: US/10/609,515
Sequence 629, Application US/09876904A

Publication No. US20030072794A1

GENERAL INFORMATION:

APPLICANT: BOULIKAS, TENI

TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSGENIC PEPTIDE

TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

FILE REFERENCE: TB-2002.00

CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2000-06-09

FRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 629
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TITLE OF INVENTION: THERAPY FOR HUMAN CANCERS USING
TITLE OF INVENTION: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO
TITLE OF INVENTION: LIPPSOMES
FILE REPERENCE: TB 2001.00
CURRENT APPLICATION NUMBER: US/10/350,470
CURRENT FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 10
SOPTWARE: FASTEEQ for Windows Version 4.0
SEQ ID NO?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 14;
Pred. No. 2.3e+02;
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 9; Conservative
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Sequence 7, Application US/09853897

Sequence 7, Application US/09853897

Publication No. US20020146701A1

GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: HEREOF USING FUSION PROTEINS
FILE REFERENCE: 3759-0122P

CURRENT APPLICATION NUMBER: US/09/853,897

CURRENT FILING DATE: 2001-05-14

PRIOR APPLICATION NUMBER: US 60/203,712

PRIOR APPLICATION NUMBER: US 60/203,712

PRIOR PERIOR DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SEQ ID NO 7

LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lai, Hung-sen
APPLICANT: Lai, Hung-sen
APPLICANT: Songyang, Zhou
APPLICANT: Songyang, Zhou
APPLICANT: Saries, Michael B.
APPLICANT: Cantley, Lewis C.
TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
FILE REPERENCE: C01123/70001 (JRV)
CURRENT APPLICATION NUMBER: US/0/017,672
CURRENT FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 25
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Pred. No. 2.6e+02;
2; Mismatches 3;
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Pred. No. 3.3e+02;
1; Mismatches 0;
                                                                                                                                             , OTHER INFORMATION: Synthetic peptide US-10-609-515-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/10017672
Publication No. US20030148377A1
GENERAL INFORMATION:
APPLICANT: NISHİKAWA, KİYOLAKA
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85.7%;
  NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 19
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                            TYPE: PRT
ORGANISM: Artificial
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US-09-853-897-7
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APPLICANT: Academisch Ziekhuis Bij De Universiteit
TITLE OF INVENTION: No. US20040049011Alel synthetic peptides with antimicrobial and
TITLE OF INVENTION: properties for management of the sepsis syndrome
FILE REFERENCE: 057666
CURRENT APPLICATION NUMBER: US/10/609,515
CURRENT APPLICATION NUMBER: US/09/493,211
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR PRILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
LEWARE: Patentin version 3.0
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TITLE OF INVENTION: No. US20040049011Alel synthetic peptides with anti
TITLE OF INVENTION:
TITLE OF INVENTION:
PLUS REPERENCE: Q57-66
CURRENT APPLICATION NUMBER: US/10/609,515
CURRENT APPLICATION NUMBER: US/09/493,211
PRIOR APPLICATION NUMBER: US/09/493,211
PRIOR FILING DATE: 2003-07-01
PRIOR FILING DATE: 1997-07-31
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Pred. No. 2.5e+02;
1; Mismatches 3.
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CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US/09/493,211
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-609-515-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/10609515; Publication No. US20040049011A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10609515
Publication No. US20040049011A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
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4 KLFKKAFKKFLKI 16
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Matches 8; Conservative
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US-10-609-515-4
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Sequence 233572, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rittner, Karola
APPLICANT: Rittner, Karola
APPLICANT: Rittner, Karola
APPLICANT: Alacobs, Eric
TITLE OF INVENTION: Use of Non-Complexing Peptides for the Preparation of a
TITLE OF INVENTION: Cell and Compositions Useful in Gene Therapy
FILE REFRENCE: 029395-03.
FILE REFRENCE: 029395-03.
CURRENT APPLICATION NUMBER: US/10/467,513
FRIOR APPLICATION NUMBER: EP 01440049.3
FRIOR APPLICATION NUMBER: EP 01440049.3
FRIOR FILING DATE: 2001-03-23
FRIOR FILING DATE: 2001-03-24
FRIOR FILING DATE: 2001-03-27
FRIOR FILING DATE: 2001-05-15
FRIOR APPLICATION NUMBER: US 60/277,982
FRIOR FILING DATE: 2001-05-15
FRIOR PELING DATE: 2001-05-15
FRIOR PELING DATE: 2001-05-15
FRIOR FILING DATE: 2001-05-15
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FRATURE:

NAME/KEY: MISC_FEATURE

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

LOCATION: (40)

LOCATION: (40)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COTHER INFORMATION: And equals any of the naturally occurring L-amino acids

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-106-698-5301
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Pred. No. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                              query Match 50.0%;
Best Local Similarity 69.2%;
Matches 9; Conservative
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US-10-467-513-4
                                                                                                                                                                                                                                                                                                                                                                                                                         2 LYKKWKKKLLKLK 14
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Publication No. US2030109690A1

GENERAL INFORMATION:

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PADOSPI

CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SSCY ID NO 5301

LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 41
US-09-865-53-4
IS-09-865-53-4
| Sequence 4, Application US/0986553
| Patent No. US20020055174A1
| GENERAL INFORMATION:
| APPLICANT: Rittner, Karola
| APPLICANT: Jacobs, Eric
| TITLE OF INVENTION: Complex for Transferring an Anionic Substance of Interest
| TITLE OF INVENTION: Complex for Transferring an Anionic Substance of Interest
| TITLE OF INVENTION: Complex for Transferring an Anionic Substance of Interest
| TITLE OF INVENTION: Complex for Transferring an Anionic Substance of Interest
| TITLE OF INVENTION: Complex US/09/865,553
| CURRENT APPLICATION NUMBER: US/09/865,553
| PRIOR FILING DATE: 2001-05-26
| PRIOR FILING DATE: 2001-03-23
| PRIOR FILING DATE: 2001-03-23
| PRIOR FILING DATE: 2001-05-26
| PRIOR FILING DATE: 2001-02-27
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                                                                                                                       Score 37; DB 9; Length 29; Pred. No. 3.7e+02;
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Pred. No. 4.9e+02;
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                                                                                                                                                                               1; Mismatches
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      ; FEATURE:
; OTHER INFORMATION: Leucine zipper KK
US-09-853-897-7
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                                                                                                                       Query Match 50.0%;
Best Local Similarity 57.1%;
Matches 8; Conservative
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: JTS-1-K13
US-09-865-553-4
                                                                                                                                                                                                                                            1 KLYKKWKKKLLKLK 14
                                                                                                                                                                                                                                                                                                    13 KLAOKWKLNALKEK 26
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Best Local Similarity 77.0.
نمو 7; Conservative
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US-10-106-698-5301
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LENGTH: 40
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Sequence 48512, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL TOWN:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cano, Yongwei
APPLICANT: Cano, Yongwei
APPLICANT: APPLICANT: AN USCIPLE ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH TITLE OF INVENTION: Nucleic ACID MOLECULES AND OTHER ADDICATION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
SEQ ID NOS: 63128
LENGTH: 44
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                                                                                                                                                                                                                                                               Score 37; DB 15; Length 43;
Pred. No. 5.2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
CTHER INFORMATION: Clone ID: LIB3481-039-P1-K1-D11.pep
US-10-767-701-48512
                                                                                                                                                                       FEATURE:
GOTHER INFORMATION: Clone ID: PAT_MRT3847_43916C.1.pep US-10-424-599-223572
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 223572
LENGTH: 43
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72,7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Sorghum bicolor
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Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                             4 KKWKKKLLKLK 14
                                                                                                                                                                                                                                                                                                                                                                                        3 KKKKKKFVKLK 13
                                                                                                                           TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-767-701-48512
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Gaps ö

Search completed: May 16, 2005, 09:23:42 Job time : 53.6207 secs

1 KLYKKWKKKLLK 12 |::| : ||||| 7 KIFKYFNKKLLK 18

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version 5.1.6
- 2005 Compugen Ltd.
    GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 12.069 Seconds (without alignments) 111.611 Million cell updates/sec Run on:

US-09-648-816B-8

1 KLYKKWKKKLLKLK 14 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

22893 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 74 Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
3: pir2:*
: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	QI	Description
	41.5	56.1	55	2	H90520	hypothetical prote
7	40	54.1	57	7	C97937	
m	39	52.7	74	7	IS7554	interleukin-3 rece
4	36	48.6	54	7	S34541	hypothetical prote
S	36	48.6	62	0	C75106	ribosomal protein
9	36	48.6	62	~	C71028	ribosomal protein
7	34	45.9	34	7	E70239	hypothetical prote
80	34	45.9	9	7	140760	
6	33	44.6	22	~	A45913	æ
10	33	44.6	23	7	G69812	hypothetical prote
11	33	44.6	24	~	S42785	ра
12		44.6	25	0	S38425	ribosomal protein
13		44.6	25	~	T49214	_
14	33	44.6	48	٦	Q1BP87	gene 1.8 protein -
15		•	54	~	S46848	gene A52R protein
16	33	44.6	64	7	B90340	hypothetical prote
17	33	44.6	73	~	E90342	_
18	33	44.6	73	~	T00007	Q
19	32.5	43.9	33	~	S52107	
20	32	43.2	29	7	826229	ribosomal protein
	32	43.2	20	~	G97836	hypothetical prote
	32	43.2	57	~	JC5008	
	31	41.9	22	7	C64330	О
24	31	41.9	50	7	S14125	hypothetical prote
25	31	41.9	26	N	S31636	ical
		41.9	99	~	AH1492	н
27		•	57	~	S42778	1
	31	41.9	61	~	72	
29	31	41.9	67	~	T11393	H+-transporting tw

	ū	ribosomal protein	ribosomal protein	ribosomal protein	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	venom basic protei	conserved hypothet	venom protein C8S2	hypothetical prote	hypothetical prote	probable ribosomal	hypothetical prote	1SU ribosomal prot
•	V6EP2J	JC4278	JQ1617	JC4685	H95177	D90554	A05031	872280	TIEPVA	B69189	V6EP8A	D97862	AB0406	A71285	D97785	F90221
	н	-1	~	~	0	N	7	~	-4	~	н	~	7	~	~	7
	62	52	52	52	31	49	20	21	57	9	62	67	68	69	69	73
	41.2	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5
	30.5	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

hypothet	hypothetical protein MYPU_0720 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Specie C;Date:	C;Species: Mycopiasma pulmonis C;Date: 24-May-2001 #sequence revision 24-May-2001 #text change 09-Jul-2004
C;Access	C;Accession: H90520
R:Chamba	R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic A	kinds Kes. 29, 2145-2153, 2001 The commulet concer semisors of the mirine respiratory nathoned Myconlasma mil
A;Refere	A;Reference number: A99512; MUID:21267165; PMID:11353084
A; Access	A; Accession: H90520
A; Status	A;Status: preliminary
A; Molecu	A; Molecule type: DNA
A; Residu	A;Residues: 1-55 <kur></kur>
A; Cross-	A; Cross-references: UNIPROT: Q98RD7; GB: AL445566; PID: g14089485; PIDN: CAC13245.1; GSPDB: GR
A; Experi	A; Experimental source: strain UAB CTIP
C; Genetics:	:8:
A; Gene:	A;Gene: MYPU_0720
A;Geneti	A;Genetic code: SGC3
Query Match	
Best L	Best Local Similarity 66.7%; Pred. No. 12; Matches 10: Conservative 0: Mismatches 2: Indels 3: Gaos 1:
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ŝ	1 K.W K.K.W. 1.Z
ΩÞ	2 KKYKKWNINKKKLKK 16

transposase, uncharacterized, truncation [imported] - Streptococcus pneumoniae (strain R6 C;Species: Streptococcus pneumoniae (5Species: Cott-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 (5Species: Cott-2001 #sequence_revision 3.7 W. F. LeBanc, D.J.; Lee, N.E. L. J. Burgett, S.; DeHoff, B.S.; Efers, J. Bacteriol. 183, 5709-5717, 2001 (5Species: J. Manthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234 (5SPECIES) A;Status: C97837 (5SPECIES) A;Status: DNA A;Status: L-57 «KUR>
A;Rosidues: L-57 «KUR>
A;Rosidues: L-57 «KUR>
A;Cosesion: Cforest-references: UNIPROT:Q8DQS5; GB:AE007317; PIDN:AAK99327.1; PID:g15458097; GSPDB:GR C;Genetics: A;Genetics: A;Genet

Score 40; DB 2; Length 57; Pred. No. 20; 54.1%; 50.0%; Query Match Best Local Similarity

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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C75106
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct
A;Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: C71028
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A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. Accession: E70239

R. Fraser, C. M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, S. Fraser, C. M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Hanson, M.; Vugt, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, son, D.; Peterson, G.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997

A.Authors: Saith, H.O.; Venter, J.C.
A.Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A.Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A.Reference number: A70100; MuID:98065943; PMID:9403685
A.Reference number: A70100; MuID:98065943; PMID:9403685
A.Reference number: A70100; MuID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-62 < KAW>
A,Cross-references: UNIPROT:P62004; GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                  ribosomal protein L37 PAB7160 [similarity] - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein BBH39 - Lyme disease spirochete plasmid H/1p28-3
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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88;
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100.0%; Pred. No. 88;
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: rpl37E, PAB7160
C, Superfamily: rat ribosomal protein L37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-62 < KAW>
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                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
R;Hannemann, J: Hara, T: Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
Mol. Cell. Biol. 15, 2402-2412, 1995
MyTitle: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-s mediated by a truncated beta C subunit.
A;Reference number: 127554; MUD: 95257920; PMID: 7739524
A;Accession: 157554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-54 - HALL;
A; Residues: 1-54 - HALL;
A; Cross-references: UNIPROT: P31558; EMBL: X70810; NID: 9415327; PIDN: CAA50122.1; PID: 94157
A; Cross-references: UNIPROT: P31558; EMBL: X70810; NID: 94157; Monfort, A.; Orsat, B.; Spielman; Nucleic Acids Res. 21, 3537-3544, 1993
A; Title: Complete sequence of Euglena gracilis chloroplast DNA.
A; Reference number: S34862; MUID: 93347989; PMID: 8346031
A; Accession: S34908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:Q64110; GB:S78451; NID:g998544; PIDN:AAB34209.1; PID:g998545
C,Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypotherical protein 54 (psaC 3' region) - Euglena gracilis chloroplast
C;Species: chloroplast Euglena gracilis
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: 334541; 834908
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, submitted to the EMBL Data Library, January 1993
A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentati A;Reference number: 834494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50122.1; PID:g415778
Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
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Pred. No. 36;
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Pred. No. 77;
1; Mismatches 0; Indels
Indels
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157554
interleukin-3 receptor beta subunit - mouse (fragment)
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C;Superfamily: rice chloroplast ribosomal protein L32
C;Keywords: chloroplast
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Mismatches
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3
                                                                            2 LYKKWKKK-----LLKL 13
                                                                                                                                                     20 IWKOWKKKSRRLWGLLKL 37
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Matches 6; Conservative
Conservative
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65 RTYRKWKEKI 74
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A; Residues: 1-74 <RES>
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Matches
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc, E.P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laudhoois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Manada, S.; Maueel, N.; M.; Rivolta, G.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A,Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sakiguchi, J.; Sakowska, A.; Scanlon, A.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Yasumoto, V.; Uchiyama, T.; Wincers, Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida, K.; A; The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; A; Reference number: A69580; MulD:93844377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C; Accession: S42785
S; Evans, B.B.
submitted to the EMBL Data Library, November 1993
A; Reference number: S42776
A; Accession: S42785
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT: Q28780; EMBL: Z27246; NID: G416107; PIDN: CAA81759.1; PID: G41610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:034890; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12576.1
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-23 <KUN>
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C;Species: Gossypium hirsutum (upland cotton)
C;Species: Gossypium hirsutum (upland cotton)
C;Bate: 13-34n-1995 #sequence_revision 13-dan-1995 #text_change 09-Jul-2004
C;Accession: S38425
R;Turley, R.B.; Ferguson, D.L.; Meredith, W.R.
submitted to the EMBL Data Library, October 1993
A;Reference number: S38425
A;Accession: S38425
A;Accession: S38425
A;Accession: Systamary
A;Molecule type: mRNA
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C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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Pred. No. 97;
3; Mismatches 3; Indels
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C,Superfamily: insulin
C,Keywords: disulfide bond; hormone
F;1-24/Domain: relaxin chain B' (fr:
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Best Local Similarity 45.5.
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2 KWKEDVIKL 10
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Best Local Si
Matches 5;
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S38425
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C;Species: Bacillus subtilis
C;Date: OS-Dec-1997 #sequence_revision OS-Dec-1997 #text_change O9-Jul-2004
C;Accession: G69812
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein 3 - Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C; Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C; Augustion: 140760; 847318
B; Hani, B.K.; Chan, V.L.
J. Bacteriol: 177, 2396-2402, 1995
A; Atitle: Expression and characterization of Campylobacter jejuni benzoylglycine amidohyd
A; Accession: 140760
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A;Residues: 1-60 <RES>
A;Cross-references: UNIPROT:Q46117; EMBL:236940; NID:g535805; PIDN:CAA85393.1; PID:g5358
                                                        A;Cross-references: UNIPROT:O50694; GB:AE000784; NID:g2690041; PIDN:AAC66012.1; PID:g269 C;Genetics: A;Genome: plasmid
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C;Species: Lactobacillus plantarum
C;Species: Lactobacillus plantarum
C;Accession: A45913
R;Nissen-Meyer, J; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F.
submitted to the Protein Sequence Database, April 1993
A;Reference number: A45913
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                                                                                                                                                                                             Score 34; DB 2; Length 34;
Pred. No. 99;
2; Mismatches 3; Indels
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Pred. No. 93;
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Pred. No. 1.7e+02;
2; Mismatches 4; Indels
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A;Residues: 1-22 <NIS>
A;Cross-references: UNIPROT:P80214
C;Keywords: antibiotic; bacteriocin
                                                                                                                                                                                                  45.9%;
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Best Local Similarity 57.1%;
Matches 8; Conservative
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nes 5; Conservative
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Best Local Similarity
7; Conservē
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                                             Residues: 1-34 <KLE>
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                     A;Molecule type: DNA
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G69812
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SixOlykhalov, A.A.; Blinov, V.M.; Frolov, I.V.; Totmenin, A.V.; Shchelkunov, S.N.; Sandal submitted to the EMBL Data Library, April 1992
A; Description: Nucleotide sequence analysis of the region of variola virus HindIII-J genc A; Reference number: S46842
A; Reference number: S46848
A; Reference number: Stella A; Reference number: S46848
A; Reference number: S46848
A; Redecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-54 < KOL>
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A;Description: Sulfolobus solfataricus complete genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: variola virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S46848
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C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.6%; Score 33; DB 2; Length 54; ilarity 42.9%; Pred. No. 2.2e+02; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                               Length 48;
                                                                                                                                                                                                                                                          2; Indels
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                                                                                                                                                                               Score 33; DB 1; Dred. No. 1.9e+02; 2; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene A52R protein (C-terminal) - variola virus
                                 A;Gene: 1.8
A;Map position: 21.87-22.23
C;Superfamily: phage T7 gene 1.8 protein
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              38 KLYELWKSR 46
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Best Local Similarity
Matches 5; Conserva
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Matches 6; Conserv
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       C; Genetics:
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R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Bubmitted to the Protein Sequence Database, April 2000
A;Reference number: 225014
A;Accession: T49214
A;Status: preliminary
A,Residues: 1-25 <TUR>
A,Cross-references: UNIPROT.P62122; EMBL:X75423; NID:g407800; PIDN:CAA53175.1; PID:g4076
C,Superfamily: rat ribosomal protein L41
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R,Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 148, 303-330, 1981
A,Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the A;Reference number: A92866; MUID:82078034; PMID:7310871
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A, Reasidues: 1-48 cdD2.
A, Residues: 1-248 cdD2.
A, Residues: 1-48 cdD3.
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A, Rolecule type: DNA
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;Residues: 1-25 <BEN>
;Cross-references: UNIPROT:P62120; EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.200
;Experimental source: cultivar Columbia; BAC clone F27K19
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C,Species: phage T7
C,Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C,Accesion: B43003; B43005; S42297; A04419
R,Dunn, J.J.: Thomson k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternate names: protein F27K19.200 (Species: Arabidopsis thaliana (mouse-ear cress) (Abecies: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004)
                                                                                                                                                                                                                            Gaps
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submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A94615
A;Accession: B43003
A;Accession: BNA
A;Residues: 1-48 <DUN>
                                                                                                                                              Length 25;
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Pred. No. 1e+02;
                                                                                                                                          Score 33; DB 2;
Pred. No. 1e+02;
2; Mismatches
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A;Introns: 4/3
C;Superfamily: rat ribosomal protein L41
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Similarity 62.5%;
5; Conservative ;
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Best Local Similarity 62.5%;
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KWKKKRMR 11
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Best Local Similarity
Matches 5; Conserv
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Rischmidt, J.; Herfurth, E.; Subramanian, A.R. Plant Mol. Biol. 20, 459-465, 1992
A) Title: Purification and characterization of seven chloroplast ribosomal proteins: evide le pathways in chloroplasts.
A) Reference number: S26228; MUID:93043036; PMID:1421149
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C;Genetics:
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C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Bate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97836
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein, 6.5K - Leuconostoc mesenteroides insertion sequence IS1297 C; Species: Leuconostoc mesenteroides C; Date: 13-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 07-May-1999 C; Accession: JG5008 R; Ward, L.J.H.; Brown, J.C.S.; Davey, G.P. Gene 174, 259-263, 1996
                                                                                                                                                                                                                                                                                                                                                                                    ribosomal protein L32 - spinach chloroplast (fragment)
C;Species: chloroplast Spinacia oleracea (spinach)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 30-Sep-1993
C;Accession: S26229
                                                                   Gарв
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C;Superfamily: rice chloroplast ribosomal protein L32
C;Keywords: chloroplast; protein biosynthesis; ribosome
Pred. No. 1.6e+02;
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43.2%; Score 32; DB 2; Le
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 0;
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50.0%; Pred. No. 2.9e+02;
              53.8%; Pred. .v..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 IYKKRIRKNIWKKK 22
                                                                                                                                  1 KLYKKWKKKLLKL 13
                                                                                                                                                                                  18 KCY-QWQKKWRKL 29
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Best Local Similarity 50.0
Matches 5; Conservative
                             Best Local Similarity 53.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: S26229
A,Molecule type: protein
A,Residues: 1-29 <SCH>
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A; Status: preliminary
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Submitted to the EMBL Data Library, January 1998

Submitted to the EMBL Data Library, January 1998

A; Reference number: 214035

A; Reference number: 214035

A; Reterence number: By Company of the extremely thermophilic archaeon Acidianus ambit A; Reference number: 214035

A; Reterence numb
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;Cross-references: UNIPROT:057701; EMBL:AJ225333; NID:e1286971; PIDN:CAA12524.1; PID:e1
;Experimental source: strain Leil0
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q97XE5; GB:AE006641; NID:g13815052; PIDN:AAK41996.1; GSPDB:d
C;Genetics:
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R;Oian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Bjochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: S52107; MUID:95127729; PMID:7827104
                      C;Accession: E90342
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffitses, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Status: preliminary
A;Molecule type: DNA
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DNA-binding protein dbpA - Acidianus ambivalens process. Acidianus ambivalens
C;Species: Acidianus ambivalens
C;Date: 65-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
,Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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Pred. No. 2.9e+02;
3; Mismatches 0; Indels
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A;Residues: 1-33 <QIA>
A;Croser references: UNIPROT:Q9TR80
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2; Pred. No. 2.9e+02;
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57.1%;
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57.1%;
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Best Local Similarity 57.1-
Loc 4; Conservative
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48 IYRKWQK 54
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Best Local Similarity
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C; Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-73 <KUR>
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A;Gene: dbpA
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h 41.9%;
Similarity 57.1%;
4; Conservative 3
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ilarity 83.3%;
Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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20 ELYSEYKKVLAK 31
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20 WKRKVIK 26
                                                                                               6 WKKKLLK 12
                 Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S31636
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-56 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLYKKW 6
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                                                                                                                                                                                                                                                                                                                                                                           A;Title: Identification and sequence analysis of IS1297, an ISS1-like insertion sequence
A;Reference number: JC5007; MUID:97045822; PMID:8890744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P54025; GB:U67480; GB:L77117; NID:g2826265; PIDN:AAB98230.1;
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                                                                                                                                                                                           Length 57;
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Pred. No. 1.9e+02;
4; Mismatches 2; Indels
                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                         Score 32; DB 2; Pred. No. 3.3e+02;
                                                                                                                                                                                                                               4; Mismatches
                                   A,Accession: JCS008
A,Molacule type: DNA
A,Residues: 1-57 < WAR>
A,Cross-references: GB:U59101
A,Experimental source: strain NZDRI 2218
C,Genetics:
A,Mobile element: insertion sequence IS1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Map position: REV232198-232130
C,Superfamily: rat ribosomal protein L41
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50.0%;
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Best Local Similarity 38.5%;
Matches 5; Conservative
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31 IHGKWTKPISKLR 43
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Matches 6; Conservative
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C.Species: Latobacillus curvatus
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C.Accession: 831636
R.Rilein, J.; Ulrich, C.; Plapp, R.
submitted to the EMBL Data Library, August 1992
A.Bescription: Characterization and sequence analysis of a small cryptic plasmid from Lac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    **Siglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: AH1492
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-56 <GLA>
A,Cross-references: UNPROT:092EH9; GB:AL592022; PIDN:CAC95712.1; PID:g16412921; GSPDB:GNA;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q05642; EMBL:Z14234; NID:g43976; PIDN:CAA78601.1; PID:g43977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable secreted protein lin0480 [imported] - Listeria innocua (strain Clip11262)
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1492
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C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S42778; S42777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Score 31; DB 2; Length 50;
Pred. No. 4.1e+02;
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Pred. No. 4.5e+02;
0; Mismatches 1;
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Pred. No. 4.5e+02;
3; Mismatches 3.
                                                                  3; Mismatches
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A;Genome: mitochondrion
A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 8
C;Kepwords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A01678
R;Joubert, F.J.; Taljaard, N.
Hoppe-Seyler's Z. Physiol. Chem. 360, 571-580, 1979
A;Title: Snake venoms. The amino-acid sequence of protein S-2C-4 from Dendroaspis jamesor A;Reference number: A01678; MUID:79171275; PMID:437703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA
A,Residues: 1-25 <CHA>
A,CROSs-references: UNIPROT:P28751; EMBL:X82550; NID:g575383; PIDN:CAA57899.1; PID:g57538
C,Superfamily: rat ribosomal protein L41
C;Keywords: ribosome
A; Cross-references: UNIPROT: 063902; EMBL: AJ001562; NID: 93127895; PIDN: CAA04834.1; PID: 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P01407
A;Note: the functional molecule consists of two identical chains linked by at least two
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          venom protein S2C4 - eastern Jameson's mamba
C;Species: Dendroaspis jamesoni kaimosae (eastern Jameson's mamba)
C;Date: 31-Aug-1979 #sequence_revision 31-Aug-1979 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribosomal protein L41, cytosolic [similarity] - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul.2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: JC4278
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Pred. No. 3e+02;
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Biochem. Biophys. Res. Commun. 214, 810-818, 1995
A;Title: The primary structures of rat ribosomal proteins L4
A;Reference number: JC4277; MUID:96024571; PMID:7575549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.2%; Score 30.5; DB 1; 46.7%; Pred. No. 5.9e+02;
                                                                                                                                                                                                       Score 31; DB 2;
Pred. No. 5.4e+02;
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50.0%;
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25 FKGWKKGMGPKLYDVK 39
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                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                          4 KKWKKKLLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: snake toxin
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KWRKJCRMR 11
                                                                                                                                                                                                                                                                                                                                                              53 KKWTKSYLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 1-62 <JOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC4278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: venom
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C; Species: mitochondrion Myoxus glis (fat dormouse)
C; Species: mitochondrion Myoxus glis (fat dormouse)
C; Accession: T11393
R; Reyes, A.; Pesole, G.; Saccone, C.
Mol. Biol. Evol. 15, 499-505, 1938
A; Title: Complete mitochondrial DNA sequence of the fat dormouse, Glis glis: further evi
A; Reference number: Z17267; MULD: 98242079; PMID: 980978
A; Accession: T11393
A; Accession: T11393
                                                                                              A; Molecule type: DNA
A; Residues: 1-33 <EVA>
A; Cross-tatences: UNIPROT: Q28428; UNIPROT: Q28429; EMBL: Z27227; NID: g415950; PIDN: CAA81
A; Note: chain 1B
A; Accession: S42777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q97EJ1; GB:AE001437; PIDN:AAK81059.1; PID:g15026186; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein S14 [imported] - Clostridium acetobutylicum C.Species Clostridium acetobutylicum C.Species Clostridium acetobutylicum C.Species 14.5ep-2001 #sequence_revision 14.5ep-2001 #text_change 09-Jul-2004 C.Accession: H97283 R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A,Reference number: A96900, MUID:21359325, PMID:21359325
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A;Note: chain 1A
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                                                                                                                                                                                                                                                                                                                                                                                   C.Superfamily: insulin
C.Kaywords: disulfide bond; hormone
F8:1-3-Domain: relaxin chain 1B (fragment) #status predicted <RXBl>
F3:4-57/Domain: relaxin chain 1A (fragment) #status predicted <RXAl>
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Pred. No. 4.6e+02;
2; Mismatches 2; Indels
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C;Superfamily: Escherichia coli ribosomal protein S14
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62.5%; Pred. No. 4.9e+02;
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A;Molecule type: DNA
A;Residues: 1-67 <REY>
R;Evans, B.B.
submitted to the EMBL Data Library, November 1993
A;Reference number: $42776
A;Aceession: $42778
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nes 5; Conservative
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2 KWKDDVIKL 10
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6 LIEKWKKE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LYKKWKKK 9
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A; Residues: 34-57 < EVX>
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A;Molecule type: DNA
A;Residues: 1-61 <KUR>
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C;Genetics:
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A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-31 <KUR>
A;Residues: 1-31 <KUR>
A;Cross-references: UNIPROT:Q97PS3; GB:AE005672; PIDN:AAK75617.1; PID:g14973018; GSPDB:GN
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .Molecule type: DNA
.Residues: 1-49 «KUR»
.Cross-references: UNIPROT:0980M1; GB:AL445566; PID:g14089754; PIDN:CAC13513.1; GSPDB:GR
.Experimental source: strain UAB CTIP
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Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
Accession: 801587; A05031
Junesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T. Mol. Biol. 203, 299-331, 1988
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Residues: 1-50 «UME»

(Cross-references: UNIPROT:032618; EMBL:X04465; NID:911640; PIDN:CAA28075.1; PID:911662

;Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmors. Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: Structure and organization of Marchantia polymorpha chloroplast genome. II. Gene
Reference number: S01567; MUID:89068686; PMID:2974085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene organization deduced from complete sequence of liverwort Marcha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: D90554
;Chambaud, I.; Heilig, R.; Perris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer,
icleic Acids Res. 29, 2145-2153, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein MYPU 3400 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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Pred. No. 5.8e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                 Length 31
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                                                                                                                                                                                                                                                                             Score 30; DB 2; I
Pred. No. 3.7e+02;
1; Mismatches 1;
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5.7e+02;
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Pred. No.
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Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                 40.5%;
                                                                                                                                                                                                                                                                                                          ilarity 71.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLYKKWKKKLLKLK 14
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Best Local Similarity 50.0v
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A; Title: Chloroplast gene
                                                                                                                                                                                                                                                                                                                                                                                                         6 WKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WKKQLTK 10
                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 5; Conserv
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C;Keywords: chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: MYPU 3400
A;Genetic code: SGC3
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                                                                                                                                                                                                                       A; Gene: SP1528
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                                                                                                                                                                                           C;Genetics:
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H95177
Hypothetical protein SP1528 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: H95177
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
C,Accession: H95177
R;Tettelin, H.; Nelson, K.E.; Mitte, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                             A, Molecule type: mRNA
A, Molecule type: MLNA
A, Residues: 1-25 «KLA>
A, Residues: 1-25 «KLA>
A, Cross-references: UNDPROT: P28751; EMBL: Z12962; NID: 936135; PIDN: CAA78306.1; PID: 936136
R; Lee, J.H.; Kim, J.M.; Kim, M.S.; Lee, Y.T.; Marshak, D.R.; Bae, Y.S.
Bicchem, Biochyles Res. Commun. 289, 462-467, 1997
A, Title: The highly basic ribosomal protein L41 interacts with the beta subunit of protein A, Reference number: JC5659; MUID: 97446005; PMID: 9299532
                                                                                                                                                                                        걸
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z12962; NID:g36135; PIDN:CAA78306.1; PID:g36136
C;Comment: This protein stimulates phosphorylation of the beta chain of DNA topoisomeras
C;Superfamily: rat ribosomal protein L41
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;Alternate names: HG12 protein; ribosomal protein YL41
;Species: Homo sapiens (man)
;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
;Accession: JQ1617; JC5659; S31691
;Klaudiny, J.; von der Kammer, H.; Scheit, K.H.
;Acchem: Biophye, Res. Commun. 187; 901-906, 1992
jfttle: Characterization by cDNA cloning of the mRNA of a highly basic human protein ]
;Reference number: JQ1617; MUID:92412140; PMID:1326959
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C.Sate: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C.Accession: JC4685
R.Starkey, C.R.; Menon, R.P.; Prabhu, S.; Levy, L.S.
Blochem. Blophys. Res. Commun. Prabhu, S.; Levy, L.S.
A.Title: Primary sequence and evolutionary conservation of ribosomal proteir A.Reference number: JC4685; MUID:96183078; PMID:8607819
A.Accession: JC4685
A.Molecule type: mRNA
A.Residues: 1-25 <STA>
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C,Superfamily: rat ribosomal protein L41
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KWRKKRMR 11
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Matches 4; Conserv
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KWRKKRMR
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A; Residues: 1-25 < LEE>
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Query Match

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Genetics:

Query Match

Matches

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conserved hypothetical protein WTH67 / MTH82 - Methanobacterium thermoautotrophicum (strates) methanobacterium thermoautotrophicum (c.)species Methanobacterium thermoautotrophicum (c.)bate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 (c.)Accession: B69189; E69209
                                                                                                                                                                                              Cyaccession: Bobles; B
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R;Joubert, F.J.; Viljoen, C.C.
R;Joubert, F.J.; Viljoen, C.C.
R;Joubert, F.J.; Viljoen, C.C.
A;Reference number: A91679; MUID:80070629; PMID:511106
A;Accession: A01680
A;Accession: A01680
A;Molecule type: protein
A;Residues: 1-62 -450U>
A;Crossidues: UNIPROT:P01410
A;Crossicues: UNIPROT:P01410
A;Crossicues: Uniproductional molecule consists of two nonidentical chains, C852 chain 1 and che
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C;Species: Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              venom protein C8S2 chain 1 - eastern green mamba
C;Species: Dendroaspis angusticeps (eastern green mamba)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
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Pred. No. 6.9e+02;
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Pred. No. 7.1e+02;
2; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLYKKWKKKLLKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 RCFKKWTKMGPKL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 YKKWKKKLLKL
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Best Local Similarity
Matches 6; Conserva
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A;Gene: MTH82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: MTH67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fide bonds
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D97862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEEPBA
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                                                                                                                                                                                                                        hyporthetical protein 51 - Plasmodium falciparum plastid
C;Species: plastid Plasmodium falciparum
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
C;Accession: 572280
R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyt
J. Mol. Biol. 261, 155-172, 1996
A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fa
A;Reference number: 872277; MuID:96346169; PMID:8757284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       venom basic proteinase inhibitor K - eastern green mamba
N;Alternate names: dendrotoxin delta-DaTX
C;Species Dendroaspis angusticeps (eastern green mamba)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A91691; C32508; A01213
R;Joubert, P.J.; Taljaard, N.
Hoppe-Seyler's Z. Physiol. Chem. 361, 661-674, 1980
A;Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroaspi
A;Reference number: A91691; MUID:81045446; PMID:7429422
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A; Residues: 1-21 <BEN>
A; Nestidues: 1-21 <BEN>
A; Note: the amino acid composition of the inhibitor is identical with that predicted fro
C; Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological fu
C; Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q25800; EMBL:X95275; NID:g1171583; PIDN:CAA64570.1; PID:e22d
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Four polypeptide components of green mamba venom selectively block certain pota A;Reference number: A93137; MUID:88318591; PMID:2457792 A;Accession: C32508
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A;Molecule type: protein
A;Residues: 1-57 <JOU>
A;Cossidues: 1-57 <JOU>
A;Cross-references: UNIPROT:P00982
R;Benishin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaustein, M.P.
Mol. Pharmacol. 34, 152-159, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Genome: plastid
A,Note: this apparently degenerate plastid is referred to as the apicoplast
C,Keywords: plastid
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;5-55,14-38,30-51/Disulfide bonds: #status predicted
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5; Conservative 0; Mismatches 2; Indels
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Pred. No. 5.9e+02;
0; Mismatches 5; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 61.5
Matches 8; Conservative
                                                                43 LFSKWIKK 50
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Best Local Similarity
Matches 5; Conserv
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LYKKWKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-51 <WIL>
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Length 69;

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Score 30; DB 2; I
Pred. No. 7.8e+02;
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C,Superfamily: rat ribosomal protein L37a
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                                  40.5%;
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Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                     4; Conservative
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49 HKKWYESVIK 58
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28 IIREWKKK 35
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                                                        Best_Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-73 < KUR>
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-69 < KUR>
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                                     Query Match
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97862
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rc
Science 293, 2093-2098, 2001
A;Title: Mechaniams of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Yersinia peetis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0406
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0406
A;Status: preliminary
A;Residues: 1-68 «KUR»
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: A71285
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rison, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDG Science 281, 375-388, 1998
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A;Cross-references: UNIPROT:083739; GB:AE001247; GB:AE000520; NID:93323059; PIDN:AAC6572
A;Experimental source: strain Nichols
                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q92G25; GB:AE006914; PIDN:AAL03838.1; PID:g15620439; GSPDB:G
C;Genetics:
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C;Genetics:
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A,Gene: TP0758
C,Superfamily: Escherichia coli ribosomal protein S21
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 41.7
Matches 5; Conservative
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50 FKKIKNKFIEMK 61
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52 YEKWKE 57
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                                                                                                                                                                                           A; Status: preliminary A; Molecule type: DNA A; Residues: 1-67 < KUR>
                                                                                                                                                                   A; Accession: D97862
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                                                                                                                                                                                                                                                                                              C,Genetics:
A,Gene: RC1300
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A71285
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R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Vong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. Strett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:Q92HT7; GB:AE006914; PIDN:AAL03222.1; PID:g15619774; GSPDB:GR
                                                                                                                                                                                                                                                                                                                                                                                                       D.; Rot
                                                                                                                                                                                                                                                                  hypothetical protein RC0684 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Bate: 30-58p-2001
#sequence_revision 30-58p-2001 #text_change 09-Jul-2004
C;Accession: D97785
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, I Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F90221
1SU ribosomal protein L37AE (rpl37AE) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
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Pred. No. 7.8e+02;
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Pred. No. 8.3e+02;
2; Mismatches 3
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   3; Mismatches
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Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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MEDLINE=21429245; PubMed=11544234;
DOI=10.1128/JB.183.19.5709-5717.2001;
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01-MAR-2003 (
01-JUN-2003 (
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01-OCT-2001
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cauliflower
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chilo iride
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121,475 Million cell updates/sec
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                                                                                                        May 16, 2005, 08:21:21; Search time 59.0172 Seconds
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050596
091905
P31558
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P63312
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Q81gt8
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O50694
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Q91FR7
RL37 PYRAB
RL37 PYRFU
RL37 PYRHO
Q91801
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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091G05
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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seg length: 74
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Perfect score:
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STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mycoplasma pulmonis.";
Mycoplasma pulmonis.";
EMBL; AAcids Res. 29:2145-2153(2001).
EMBL; AL445563; CAC13245.1; --
PIR; H90520; H90520.
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxIb=2107;
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08j810
08j810
08j811
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Pred. No. 62;
0; Mismatches 2; Indels
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Complete proteome; Hypothetical protein.
SEQUENCE 55 AA; 7069 MW; FE0197BADCF9E677 CRC64;
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Hypothetical protein MYPU 0720.
Mycoblasma milmare.
Mycoplasma milmare.
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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.1 Similarity 66.7%;
10; Conservative
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   Query Match
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\begin{array}{c} \mathbf{4444} \\
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Bukaryota, Alveolata, Apicomplexa, Haemospoxida, Plasmodium.
NCBL_TaxID=73239;
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BMBL, S78451; AAB34209.1; -.
  Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz B.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R., Jr., Skatrud P.L.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                             "Genome of the bacterium Streptococcus pneumoniae strain R6.";

J. Bacteriol. 183:5709-5717(2001).

EMBL; AE008431; AAK99327.1; -.

PIR; C97937; C97937; C97937.
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MEDLINE=95257920; PubMed=7739524;
Hannemann J., Hara T., Kawai M., Miyajima A., Ostertag W.,
                                                                                                                                                                                                                                                                                                                                                                           54.1%; Score 40; DB 2; Length 57; 50.0%; Pred. No. 1.1e+02;
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Pred. No. 2e+02;
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                                                                                                                                                                                                                                                                                                                                57 AA; 6938 MW; 98016F1B93238913 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Hypothetical protein (Fragment).
Name=PY03824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Interleukin-3 receptor beta subunit (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 IWKOWKKKSRRLWGLLKL 37
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50.0%;
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SEQUENCE 57 AA;
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NCBI_TaxID=10095;
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"Gene arrangement in the upstream region of Clostridium botulinum type "Gene arrangement in the upstream region of Clostridium butyricum BL6340 progenitor toxin genes is different from that of other types.";
FEMS Microbiol. Lett. 158:215-221(1998).
BMBL, AB004778; BAA24886.1; -.
NON TER 51 51
SEQÜENCE 51 AA, 5998 MW; 834EB4A69DD1157F CRC64;
                                                                                                                                                                                                                                                                                                                          "Genome sequence and comparative analysis of the model rodent malaria
               Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Valdya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Carucci D.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                          parasite Plasmodium yoelli yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 2.1e+02;
2; Mismatches 3; Indels
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Pred. No. 2.7e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 AA; 4828 MW; CB57649EA8BB537E CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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PubMed=12368865; DOI=10.1038/nature01099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
EMBL; AABL01001128; EAA15595.1; -.
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MEDLINE-98126542; PubMed-9465394;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Matches 8; Conservative
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Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
"Chilo iridescent virus encodes a putative helicase belonging to a
distinct family within the 'DEAD/H' superfamily: implications for the
evolution of large DNA viruses.";
Virus Genes 8:151-158(1994).
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MEDILNE=9429206; PubMed=8021587;
Schnitzler P., Sonnteag K.C., Muller M., Janssen W., Bugert J.J.,
Koonin B.V., Darai G;
"Insect iridescent virus type 6 encodes a polypeptide related to the
largest subunit of eukaryotic RNA polymerase II.";
J. Gen. Virol. 75:1557-1567(1994).
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Bahr U., Tidona C.A., Darai G.;
"The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101 and 0.391; similarities in coding strategy between insect and vertebrate iridoviruses.";
Virus Genes 15:235-245(1997).
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MEDINE=86174607; PubMed=1959991;
Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
"Insect iridescent virus type 6 induced toxic degenerative hepatitis
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"DNA analysis of insect iridescent virus 6: evidence for circular permutation and terminal redundancy.";
J. Virol. 49:609-614(1984).
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MEDLINE-99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome
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MEDLINES-95213160; PubMed=7698884;
MEDLINES-95213160; PubMed=7698884;
Somnteag K.C., Schnitzler P., Janssen W., Darai G.;
"Identification of the primary structure and the coding capacit;
the genome of insect iridescent virus type 6 between the genome
coordinates 0.310 and 0.347 (7990 bp).";
Intervirology 37:287-297(1994).
                                                                           (CIV) (Insect iridescent virus type 6). no RNA stage; Iridoviridae; Iridovirus.
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MEDILYNE-87321126; PubMed=2820141;
Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
Delius H., Darai G.;
                                      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
  63 AA
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                          (TrEMBLrel. 19,
 PRELIMINARY;
                                                                                    Viruses; dsDNA viruses,
NCBI_TaxID=10488;
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Nucleic Acids Res. 22:158-166(1994).
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MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the first complete DNA sequence of an invertebrate iridovirus: coding strategy of the genome of Chilo iridescent virus."; virology 286:182-196(2001).
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Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6.";
"Molecular cloning and physical mapping of the genome of insect iridescent virus type 6: further evidence for circular permutation of the viral genome.";
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Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
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01-JUL-1993 (Rel. 26, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Chloroplast 50S ribosomal protein L32.
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MEDLINE=9118242; PubMed=1475907;
Sontrag K.C., Darai G.;
"Characterization of the third origin of DNA replication of the genome of insect iridescent virus type 6.";
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MEDLINE=9912523; PubMed=9926400; DOI=10.1023/A:1008017820941;
MALIBE X., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome of
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Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
"Chilo iridescent virus encodes a putative helicase belonging
distinct family within the 'DEAD/H' superfamily: implications
evolution of large DNA viruses.";
Virus Genes 8:151-158(1994).
                                            SEQUENCE FROM N.A.
STRAIN=Z / UTEX 753;
MEDLINE=93347989; PubMed=8346031;
Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,
Orbat B., Spielmann A., Stutz E.;
"Complete sequence of Euglana gracilis chloroplast DNA.";
Nucleic Acids Res. 21:3537-3544(1993).
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Euglenozoa; Euglenida; Euglenales; Euglena.
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53 AA; 6068 MW; BB61673532FB41B5 CRC64;
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Virus Genes 17:243-258(1998)
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MEDLINE-89073752; PubMed=3201750;
Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive DNA element in
the genome of insect iridescent virus type 6.";
Virology 167:485-496(1988).
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Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
"Insect iridescent virus type 6 induced toxic degenerative hepatitis
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SEQUENCE FROM N.A.

MEDLINE-24929206, PubMed=8021587;
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MEDLINE=93260401; PubMed=8492091;
Stohwasser R., Raab K., Schnitzler P., Janssen W., Darai G.;
Stohwasser R., Rab K., Schnitzler P., Janssen W., Darai G.;
"Identification of the gene encoding the major capsid protein of insect iridescent virus type 6 by polymerase chain reaction.";
J. Gen. Virol. 74:873-879(1993).
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Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
"Identification of the primary structure and the coding capacity
the genome of insect iridescent virus type 6 between the genome
coordinates 0.310 and 0.347 (7990 bp).";
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Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
Delius H., Darai G.;
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DG Name=T
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chromosomal HMG protein homologue, and a putative GTP phosphohydrolase in the genome of Chilo iridescent virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
Jakob N.J., Muller K., Bahr U., Darai G.;
"Analysis of the first complete DNA sequence of an invertebrate
iridovirus: coding strategy of the genome of Chilo iridescent virus.";
Virology 286:182-196(2001).
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iridescent virus encoding enzymes involved in viral DNA replication
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STRAIN=GES / Oreay;

MEDLINE=22511545; PubMed=12622808;

MEDLINE=22511545; Vo. Flament D., Galperin M., Heilig R., Lecompte (Cohen G.N., Barbe V.) Flament D., Galperin M., Thierry J.-C.,

Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,

Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;

"An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";

Mol. Mczrobiol. 47:1495-1512(2003).

-! SIMILARITY: Belongs to the ribosomal protein L37e family.
                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-99383793; PubMed=10456793; DOI=10.1023/A:1008072319875;
Muller K., Tidona C.A., Darai G.;
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P62004; O74015;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L37e.
Name=rpl37e; OrderedLocusNames=PXRAB06510; ORFNames=PAB7160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.6%; Score 36; DB 2; Length 59; 77.8%; Pred. No. 4.4e+02;
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SEQUENCE 59 AA; 6856 MW; 322CD7D6D95DC008 CRC64;
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Problom; PD005132; Ribosomal_L37B; 1.
PROSITE; PS01077; RIBOSOMAL_L37B; 1.
Complete protecome; Ribosomal_protein.
SEQUENCE 62 AA; 7298 MW; B236F77524208763 CRC64;
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HAMAP; MF 00547; -; 1.
InterPro; IPR001569; Ribosomal L37E.
                               in the genome of Chilo iridescent vi
Nucleic Acids Res. 22:158-166(1994).
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nes 7; Conservative
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FRB-2002) to the EWBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the ribosomal protein L37e family.
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BC505; 074015;
15-DBC-1998 (Rel. 37, Last sequence update)
15-DBC-1998 (Rel. 37, Last sequence update)
5-DBC-1004 (Rel. 45, Last annotation update)
50S ribosomal protein L37e.
Name=rpl37e; OrderedLocusNames=PH1518.1; ORFNames=PHS041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.6%; Score 36; DB 1; Length 62; 100.0%; Pred. No. 4.7e+02;
                      Length 62;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01907; Ribosomal L37e; 1.
ProDom; PD005132; Ribosomal L37E; 1.
PROSTTE; PS01077; RIBOSOWAL L37E; FALSE NBG.
Complete proteome; Ribosomal protein.
SEQUENCE 62 AA; 7223 MW; 99E0A2AF4954E439 CRC64;
                   DB 1; Le
4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-PEB-2003 (Rel. 41, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) 50S ribosomal protein L37e.
48.6%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=rpl37e; OrderedLocusNames=PF1541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00547; -; 1.
InterPro; IPR001569; Ribosomal L37E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE010255; AAL81665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     furiosus.
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40 KYYKKHEKKMIK 51

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MEDLINE-21927593; PubMed=11917108; DOI=10.1073/pnas.062526099; MEDLINE-21927593; PubMed=11917108; DOI=10.1073/pnas.062526099; Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beree S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.; Changell D.S., Smith T.M., Zhang C., Genur V., Daly J.A., Veasy L.G., Musser J.M.; Preptococcus and comparative microarray analysis of serctype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moerman L.F.A., Bosteels S., Noppe W., Willems J., Clynen E.,
Schoofs L., Thevissen K., Tytgat J., Van Eldere J., van der Walt J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Antibacterial and antifungal properties of alpha-helical, cationic peptides in the venom of scorpions from southern Africa.";

Eur. J. Biochem. 256:4799-4810(2002).

-i. FUNCTION: Induces a leak current in voltage-clamped dorsal root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthida, Buthoidea, Buthidae, Parabuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Verdonck F., Bosteels S., Desmet J., Moerman L.F.A., Noppe W., Willems J., Tytgat J., van der Walt J.; "A vovel class of pore-forming peptides in the venom of Parabuthus schlechteri Purcell (Scorpions: Buthidae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2; Length 66; Pred. No. 4.9e+02; Mismatches 3; Indels
                                                                                                                                                                                                                                                                              Streptococcus pyogenes (Berotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteome.
66 AA; 7772 MW; B9CA46BC7A5F4057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIRCULAR DICHROISM ANALYSIS, AND SYNTHESIS
                                                                                                                                                         01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein spyM18 1977.
OrderedLocusNames=spyM18_1977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002)
EMBL; AE010102; AAL98463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                     66 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22241537; PubMed=12354111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parabutoporin.
Parabuthus schlechteri (Scorpion)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cimbebasia 16:247-260(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLYKKWKKKLLKL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                Streptococcus.
NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=190110;
                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perdonck F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete |
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                   08NZE7
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PBPO_PARSC
                                                                      RESULT 13
Q8NZE7
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                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96198088; PubMed=8626421; DOI=10.1074/jbc.271.11.6273;
Puzianowska-Kuznicka M., Shi Y.B.;
"Nuclear factor I as a potential regulator during postembryonic organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                        -- SIMILARITY: Belongs to the ribosomal protein L37e family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2; Length 62;
Pred. No. 4.7e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 1; Length 62; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shi Y.-B.;
Submirted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L43150; AAB38018.1; -.
NON_TER 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; C71028; C71028.

HAMARP: MF 00547; -; 1.

InterPro; IPR001569; 1.

Pfam; PR01907; Ribosomal L37e; 1.

ProDom; PD005132; Ribosomal L37E; 1.

PROSITE; PS01077; RIBOSOMAL L37E; 1.

COMPLETE PS01077; RIBOSOMAL L37E; 1.

SEQUENCE 62 AA; 7298 MW; B236F77524208763 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 62
62 AA; 7591 MW; 0A17DBC1D105F4C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel: 01, Created)
01-NOV-1996 (TrEMBLrel: 01, Last sequence update)
01-OCT-2003 (TrEMBLrel: 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 271:6273-6282(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear factor I-C2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP000006; BAA30627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.68;
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Best Local Similarity 58.3-7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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                                                                                                                                                                                     5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae, Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 KKWKKK 58
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                                                                                                                                                                                          DNA Res.
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09160

Matches

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Gaps

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2 KKFKNFSKKLLK 13
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 61 AA;
                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=H1100;
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                                                                       STRAIN=MB4;
        [1]
SEOUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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           SERRERERES
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ganglion cells of rats by forming pores. Degranulates human granulocytes and has a weak hemolytic activity against human red blood cells. Has antibacterial activity against Gram-negative bacteria but is less active against Gram-positive bacteria. Has antifungal activity.
--- SUBUNIT: Monomer and homodimer.
--- SUBURIT: Monomer and homodimer.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUB SPECIFICITY: Expressed by the venom gland.
--- TASS EFECTROMETRY: MW=5030.3; METHOD=MALDI; RANGE=1-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Taudien S., Dagand B., Delabar J., Orti R., Nordsiek G., Drescher B. Weber J., Schattevoy R., Yaspo M.-L., Rosenthal A.;
Submitted (NOV-1998) to HEMBL/GenBank/DDBJ databases.

EMBL; AF107259; AAD04931.1; -..

GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                           NOTE=Ref.1.
Antibiotic; Direct protein sequencing; Fungicide; Hemolysis; Neurotoxin; Toxin.
INSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2; Length 51;
Pred. No. 5.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35; DB 1; Length 45; Pred. No. 4.8e+02; 0; Mismatches 4; Indels
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44 44
45 45 45
45 AA; 4995 MW; 3EEPP71425FA14FA CRC64;
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51 51
51 AA; 5846 MW; BDB014D694FF5C54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Glutamate receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.3%;
85.7%;
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OrderedLocusNames=TTE2173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.38;
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Best Local Similarity 63...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=GLUR5;
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NON TER
NON TER
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071UA
AC 071UA
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DT 05-JU
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DF 05-JU
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DF 01
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PubMed=14752164; DOI=10.1126/science.1093027;
Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
Socket R.B., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio' bacteriovorus from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schwudke D., Strauch B., Appel B., Linscheid M.; "Putentive pilus encoding gene cluster of Bdellovibrio bacteriovorus DSM 50701."; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302; Bao O. Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.; M., Chen R., Ling L., Chen R., Chen R., Ling L., Experimente sequence of the T. tengcongensis genome."; Genome Res. 12:689-700(202).

EMBL; AR013164; AAAN2332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Plp1 pilus subunit) (Flp1 protein).
Name=flp1, OrderediocusNames=Bd0119;
Bdellovibrio bacteriovorus.
Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionaceae;
Bdellovibrionaceae;
Bdellovibrionaceae;
Bdellovibrionaceae;
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                                                                                                                                                                                                                                                                                                                                         47.3%; Score 35; DB 2; Length 61; 61.5%; Pred. No. 6.5e+02; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 2; Length 62;
Pred. No. 6.6e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                61 AA; 7096 MW; 1F7B325AB545F606 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 61.5%;
nes 8; Conservative
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Science 303:689-692(2004).
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49 KKYKEKIKKILKL 61
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=13 (Type Ab)
MEDLINE=21664773; PubMed=11792842; DOI=10.1073/pnas.022493799;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 2; Length 71;
Pred. No. 7.5e+02;
2; Mismatches 0; Indels
  Score 35; DB 2; Length 68; Pred. No. 7.2e+02;
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                                                 3; Indels
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003187; BAB80251.1; -.
Complete proteome.
SEQUENCE 71 AA; 8643 MW; 3B61EB6CAD1CA3F9 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                 71 AA.
                                               2; Mismatches
                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last seq 01-MAR-2004 (TrEMBLrel. 26, Last ann Hypothetical protein CPB045.
                                                                                                                                                                                                                                                                   PRT;
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EMBL; AE017006; AAP09536.1; -.
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50.0%;
Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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16 KLVQKWKFALLQ 27
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                                                                                              1 KLYKKWKKKLLK 12
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Q8XMZ3;
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Q81D06
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-!- SIMILARITY: Belongs to the ATPase protein 8 family.
-!- SIMILARITY: Belongs to the ATPase protein 8 family.
-!- SIMILARITY: Belongs to the ATPase protein 8 family.
-!- SIMILARITY: Belongs to the ATPase protein 8 family.

GO; GO:0005799; C:mitochondrion; IEA.
GO; GO:0016569; C:mitochondrion; IEA.
GO; GO:0046591; F:hydrogen-transporting ATP synthase activity. ..; IEA.
GO; GO:0015986; P:ATP synthasis coupled proton transport; IEA.
GO; GO:0015992; P:proton transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Natl. Acad. Sci. U.S.A. 99:8151-8156(2002).
FUNCTION: This is one of the chains of the nonenzymatic component
(CF(0) subunit) of the mitochondrial ATPase complex (By
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22056019; PubMed=12034869; DOI=10.1073/pnas.102164299;
Arnason U., Adegove J.A., Bodin K., Born E.W., Esa Y.B., Gullberg A.,
Nilsson M., Short R.V., Xu X., Janke A.;
"Mammalian mitogenomic relationships and the root of the eutherian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Yu W.-Q., Sun B.-Z., Chai Y.-B., Zhu F., Liu X.-S., Li Z., Lu F.,

Yan W., Yang H., Zhao Z.-L.;

Submitted (JUN-2000) to He EMBL/GenBank/DDBJ databases.

EMBL; AR279899; AAKO754.1;

SEQUENCE 68 AA; 8161 MW; D7B93A9E144F4E96 CRC64;
                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Pinnipedia, Otariidae, Eumetopias.
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CF(0); Hydrogen ion transport; Ion transport; Mitochondrion;
Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2; Length 67;
Pred. No. 7.1e+02;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PNAS-145.
                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                        Eumetopias jubatus (Steller sea lion).
Mitochondrion.
                                                                                                                         Created)
                                                                          PRT;
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                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
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46 KTYTPWEKKWTKI 58
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                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                    01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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                                                                                                                                                                                              ATPase subunit 8.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=34886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
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                                                                                                  Q8LX44;
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                           RESULT 18
Q8LX44
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Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K., Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D., Richardson. D.L., Peterson J.D., Kerlavage A.R., Quackenbush J., Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D., Artiach J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A., Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K., Roberts K.M., Hatch B., Smith H.O., Venter J.C.; "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90320145; PubMed=2371775;
Vaden V.R., Melcher U.K.;
"Recombination sites in cauliflower mosaic virus DNAs: implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                                                                            Score 35; DB 2; Length 73;
Pred. No. 7.7e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 34;
Pred. No. 5.2e+02;
2; Mismatches 3; Indels
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Cauliflower mosaic virus.
Viruses, Retroid viruses; Caulimoviridae, Caulimovirus.
                                                                    73 AA; 8669 MW; F4FA4DB259451D52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FD687CA065B19056 CRC64;
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Last annotation update)
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Last annotation update)
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  Pfam; PF00507; Oxidored q4; 1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
NON TEN 1
SEQUENCE 73 AA; 8669 MW; F4FA4DB259451D52 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia burgdorferi (Lyme disease spirochete).
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EMBL; AE000784; AAC66012.1; -.
PIR; E70239; E70239.
                                                                                                                47.3%;
54.5%;
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7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLral. 06, 01-JUN-1998 (TrEMBLral. 06, 01-JUN-2003 (TrEMBLral. 24, Hypothetical protein BBH39.
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                                                                                                                                                           6; Conservative
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61 LYHEWKSNALK 71
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                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
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Matches 7; Conserv
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01-NOV-1996
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050694
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Q83175
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-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SIMILARITY: Balongs to the complex I subunit 3 family.
EMBL; AF484025; AAL88660.1; -..
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.
InterPro; IPR000440; Oxidored_q4.
    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kaparral V., Bottacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Bhilich S.D., Goverbeek R., Kyrpides N.C.
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Neoptera, Endopterygota, Diptera, Brachycera, Asilomorpha,
Nemestrinoidea, Acroceridae, Ogcodes.
NCBI_TaxID=188258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; Length 72; Pred. No. 7.6e+02; 5; Mismatches 0; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                            Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 423:87-91(2003).
EMBL, AE017001; AAP08084.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 72 AA, 8030 MW; DEF6B66451ACA507 CRC64;
                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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7
                                                                                                                                                                                                     72 AA
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    Mismatches
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01-JUN-2002 (TrEMBLrel. 21, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotation)
NADH dehydrogenase subunit 3 (Fragment).
                                                                                                                                                                                                                                                    Created)
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                                                                    | | | | | | | | 40 YPKWIIKKKMTEMK 53
                                            3 YKKW--KKKLLKLK 14
                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
OrderedLocusNames=BC1097;
7; Conservative
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23 QIYRQWKEK 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus anthracis.
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STRAIN=Ames / isolate Porton;

KEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;

KEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;

KEAG T.D., Peterson S.N., Tourasse N.J., Bailia L.W., Paulsen I.T.,

Nelson K.E., Tettelin H. Fouts D.E., Eisen J.A., Gill S.R.,

Holtzapple B.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

Kolonay J.F., Meanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

DeBoy R.T., Madpu R., Dodson R.J., Brinkac L.M., Gwinn M.L.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

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A Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

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Hanna P.C., Kolstoe A.-B., Fraser C.M.;

"The genome sequence of Bacillus anthracis Ames and comparison to

closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
                                 truncated and overlaps a cytochrome
Zhuo D., Nguyen-Lowe H.T., Subramanian S., Bonen L.;
"The S7 ribosomal protein gene is truncated and overlaps s
c biogenesis gene in pea mitochondria.";
Plant Mol. Biol. 40.91-97 (1999).
EMBL, Y18317; CA843001.1; -.
GO, GO:0003735; F:structural constituent of ribosome; IEA.
Ribosomal protein.
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Pred. No. 7.4e+02;
1; Mismatches 0; Indels
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Pred. No. 7.2e+02;
0; Mismatches 2; Indels
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Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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6276 MW; 543274DE6EFF15FB CRC64;
                                                                                                                                                                                                                                                                         48 AA; 5804 MW; E262EEFE50C66EB4 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                              45.9%;
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Local Similarity 83.3%;
les 5; Conservative
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Matches 6; Conserv
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MEDIATRE=27-09201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
MEDIATRE=27-09201; PubMed=12810954; DOI=10.1073/pnas.1332093100;
S. Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Koenig J., Macko L., Mandz G.I., Nyakatura G.;
Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter hepaticus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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MEDLINE=99320871; PubMed=10394948; DOI=10.1023/A:1026499906338;
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35 AA; 4552 MW; ·472F3CE98D4C46A6 CRC64;
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                           Virology 177:717-726(1990).
EMBL, M32814, AA46352.1; -.
GO, GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
87 ribosomal protein (Fragment).
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Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003)
EMBL; AE017147; AAP77730.1; -.
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Pred. No. 5.3e+02;
2; Mismatches 1;
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            mechanisms of recombination.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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4 KWTKRALKL 12
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18 KVYKPYKKK 26
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SEQUENCE FROM N.A.
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Gaps

RESULT 29 Q9UC64

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Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R.; Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome."; Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).

BMBL, AE017165; AAQ00438.1; -. Complete proteome.

SEQUENCE S4 AA; 6680 MW; 8B3P7AED122ABCD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; rosids; NCBI_TaxIb=85636;
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"Complete nucleotide sequence of the Oenothera elata plastid chromosome, representing plastome I of the five distinguishable euoenothera plastomes."

EMBL: AJ71079; CAB67181.1; -
GO: 0009507; C:chloroplast; IEA.
Chloroplast; Hypothetical protein.

SEQUENCE S5 AA; 6656 MW; EIPAC733FBDC5AEA CRC64;
                                                                                                                                                                                                                                                                                                                                                               STRAIN=SARG / CCMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
                                                                                                                                                                                               Prochlorococcus marinus.
Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                               Last sequence update)
Last annotation update)
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54 AA.
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PRT;
                                               01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 101-0CT-2003 (TrEM
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Best Local Similarity 72...
Best Local 8; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                  NCBI_TaxID=1219;
                 OTVAR3;
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Q9MTJ9
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MEDLINE=2111149; PubMed=11160885; DOI=10.1093/nar/29.3.644;
Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
Analysis of six prophages in Lactococcus lactis IL1403: different genetic structure of temperate and virulent phage populations.";
Nucleic Acids Res. 29:644-651(2001).

EMBL, ARX08366.1; -.
SEQUENCE 54 AA; 6398 MW; 3DB8C06A7503B61A CRC64;
                                                                                                          DIMAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PP 4-derived endothelial cell growth inhibitor PEAK II (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Viruses; daDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=151537;
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Pred. No. 8.1e+02;
3; Mismatches 3; Indels
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Last annotation update)
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MEDLINE=95372366; PubMed=764496;
Gupta S.K., Hassel T., Singh J.P.;
Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; F:chemokine activity; IEA.
GO; GO:0006955; F:chemokine ILB.
InterPro; IPR001811; Chemokine ILB.
InterPro; IPR00189; CXC_chmkine_smll.
Pfam; PF00048; ILB; 1.
PRINTS; PR00436; INFERICKINB.
                                                                               54 AA
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 50.0.
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les 8; Conservative
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RESULT 30 Q9AZP4

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RESULT 31 Q7VAR3

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Pediatr. Infect. Dis. J. 0:0-0(2002).
EMBL; AF474920; AAN03362.1; -.
InterPro; IPR004337; Astro_capsid.
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Pediatr. Infect. Dis. J. 0:0-0(2002).
EMBL; AF474919; AAN03361.1; -.
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Mamastrovirus.
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Pred. No. 9e+02;
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Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauquier A.;
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Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauquier A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 AA; 6350 MW; 612AF4A3F71E2293 CRC64;
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                                                                                                                                                                                                                                                                                                                                                         01-077-2002 (TrEMBLrel. 22, Created)
01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Capsid protein (Fragment).
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 9e+02;
1; Mismatches
                                                                                                                                                                                                                                                                                                   60 AA.
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   Mismatches
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   2;
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                                                                   1 KLYKKWKKKLLKLK 14
                                                                                                                                46 KSNKKIYKKIIKLK 59
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Best Local Similarity 50.0
Matches 6; Conservative
   8; Conservative
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Best Local Similarity
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01-OCT-2002
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Q8JSS8
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Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
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MEDILNE=95247673; PubMed=7730270;
Hani E.K., Chan V.L.;
"Expression and Characterization of Campylobacter jejuni
Bencoylglycine Amidohydrolase Gene (Hippuricase) in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
                                                                                                                                                                                                                                                                                                Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2; Length 59;
Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 2; Length 60;
Pred. No. 9e+02;
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BMB1, AABLO1000596, EAA21604.1; -.
Hypothetical protein.
SEQUENCE 59 AA, 6819 MW, 39D0FD94A7C11E30 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12368865; DOI=10.1038/nature01099;
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EMBL; 236940; CAA85393.1; -.
PIR; 140760; 140760.
Hypothetical protein.
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Best Local Similarity. 57.1%;
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Matches 7; Conservative
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                                                                       PRELIMINARY;
                                                                                                                                                                                                                                      Hypothetical protein.
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Q7RMKS
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Q8JST2;
01-OCT-2002 (TrEWBLrel. 22, Created)
01-OCT-2002 (TrEWBLrel. 22, Last sequence update)
01-OCT-2004 (TrEWBLrel. 26, Last annotation update)
Capsid protein (Fragment).
Human astrovirus.
Viruses; SENNA positive-strand viruses, no DNA stage; Astroviridae;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauquier A.;
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Q8JST4
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Pediatr. Infect. Dis. J. 0:0-0(2002).
BMBL, ARYA917; AAN03359.1;
InterPro; IPR004337; Astro. capsid.
Pfam; PP03115; Astro. capsid; 1.
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EMBL; AF474918; AAN03360.1; -.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
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Pred. No. 9e+02;
1; Mismatches 5; Indels
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Pred. No. 9e+02;
1; Mismatches 5; Indels
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Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauquier A.;
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Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauguier A.;
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                                                                                                                                                                                                01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Capsid protein (Fragment).
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pfam; PR03115; Astro capsid; 1.
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NCBI_TaxID=12702;
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SEQUENCE
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Pediatr. Infect. Dis. J. 0:0-0(2002).
EMBL; AF474915; AAN03357.1; -.
InterPro; IPR004337; Astro_capsid.
Pfam, PF03115; Astro_capsid.
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"Astrovirus acute gastroenteritis among children in Madrid, Spain."; Pediatr. Infect. Dis. J. 0:0-0(2002).
BMBL, AR749916; ARN03358.1; -
InterPro; IPR004337; Astroc capsid.
Pfam; PF03115; Astroc capsid.
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Pred. No. 9e+02;
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Dalton R., Roman B., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauquier A.;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Capsid protein (Fragment).
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01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Best Local Similarity 50.0
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nes 6; Conservative
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NCBI_TaxID=12702;
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Sanchez-Fauquier A.;
Sanchez-Fauquier A.;
Batrovirus acute gastroenteritis among children in Madrid, Spain.";
Pediatr. Infect. Dis. J. 0:0-0(2002).
EMBL; AR474914; AAN03356.1;
InterPro; IPR004337; Astro_capsid.
Pfam; PF03115; Astro_capsid.
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Dalton R., Roman B., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauquier A.;
Sanchez-Fauquier A.;
Satrovirus acute gastroenteritis among children in Madrid, Spain.";
Pediatr. Infect. Dis. J. 0:0-0(2002).
EMBL, AF474913; AAN03355.1; -.
EMBL, PF03115; ASTROQA37; ASTROCASPIG.
Pfam, PF03115; ASTROCASPIG, 1.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-Mara protein (Fragment).
Human astrovirus.
Viruses; SERNA positive-strand viruses, no DNA stage; Astroviridae;
                     Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 9e+02;
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                                              Mamastrovirus.
NCBI_TaxID=12702;
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                                                                  "Astrovirus acute gastroenteritis among children in Madrid, Spain.";
Pediatr. Infect. Dis. J. 0:0-0(2002).
EMBL; AF474912; AAN03354.1; -.
InterPro; IPR004337; Astro capsid.
Pfam; PF03115; Astro capsid, 1.
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Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauquiez A.;
Astrovirus acute gastroenteritis among children in Madrid, Spain.";
Pediatr. Infect. Dis. J. 0:0-0(2002).
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EMBL; AF474911; AAN03353.1; -.
InterPro; IPR004337; Astro_capsid.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
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Pred. No. 9e+02;
1; Mismatches 5; Indels
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Pred. No. 9e+02;
1; Mismatches 5; Indels
SEQUENCE FROM N.A.
Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Fauquier A.;
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Dalton R., Roman E., Negredo A., Wilhelmi I., Glass R.,
Sanchez-Pauquier A.;
                                                                                                                                                                                                                                                              60 AA; 6336 MW; 612AF4A3F71E3003 CRC64;
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Q8JST8;
Q1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Capsid protein (Fragment).
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amocation update)
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50.0%;
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Best Local Similarity 50.0
Matches 6; Conservative
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DR EMBL; AF474910; AAN03352.1; -.
DR InterPro; IPR004337; Astro_capsid.
DR Pfam; PF03115; Astro_capsid; 1.
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FT NON TER 60 60
SQ SEQÜENCE 60 AA; 6336 MW; 612AP4A3F71E3003 CRC64;
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CRC6	Len	·	
) SEQUENCE 60 AA; 6336 MW; 612AF4A3F71E3003 CRC64;	45.9%; Score 34; DB 2; Length 60; 50.0%; Pred. No. 9e+02;	1) Atomacones	
6336 MW;		CK 14	:  fvk 37
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SEQUENCE	a th	maccines 3	26
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Gaps

Search completed: May 16, 2005, 08:30:28 Job time : 61.0172 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	Aay57471 Antimicro	Abg69895 Rabbit pl	2 Antimic	w		4			Aay57501 Antimicro		Abg69923 Rabbit pl	Rabbit	2 Antimic		5 Antimic		Adl70275 Peptide a	7 Antimic		w	7	Adl70278 Peptide a	Abg69990 Rabbit pl	Rabbit	Aay57500 Antimicro
SUMMARIES		A.	AAY57471	ABG69895	AAY57472	ABG69896	AAY57470	ABG69894	AAY57465	ABG69889	AAY57501	AAY57499	ABG69923	ABG69925	AAY57502	ABG69926	AAY57496	ABG69920	ADL70275	AAY57497	ABG69921	ADL70276	ADL70277	ADL70278	ABG69990	ABG69992	AAY57500
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## ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

Database :

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi. Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. (HARB-) HARBOR-UCLA RES & EDUCATION INST. Antimicrobial peptide RP-7 SEQ ID NO:9. AAY57471 standard; peptide; 13 AA. 99WO-US003350. 98US-00025319. (first entry) Oryctolagus cuniculus. Shen AJ; WPI; 1999-527417/44. 18-FEB-1998; WO9942119-A1. 17-FEB-1999; 25-FEB-2000 26-AUG-1999. Yeaman MR, Synthetic. AAY57471; AAY5747. 

Disclosure; Page 110; 166pp; English.

activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXKB and its derivatives selected from XZBBZBXBXB, BXZXB, XBBXZXBX and its derivatives selected from XZBBZBXBXB, BXXZXB, XBBXZXBX and BBXZBBXZ; and (b) a second peptide template XBBX.XBX, XBBXZXBX and elected from the group consisting of XBBXBBX, BXXXBXB, XBBXXXB, ABBXXXBBX, and Capton of XBBXZBXBX, by a selected from the axial capton of XBBZBXXBXBX, by a selected from the axial capton of XBBZXXBBXXBBX; where B = at least one positively charged amino acid; X = at least one aromatic amino acid. and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of The present invention describes an antimicrobial peptide (AP) for direct

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, runcations, extensions, combinations, funions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial appriate or potentiation and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial for the foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                           Gaps
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbit platelet.microbicidal protein, PMP-2, based peptide #7.
                                                                                                                              100.0%; Score 69; DB 2; Length 13; 100.0%; Pred. No. 0.0013; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 130; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                      ABG69895 standard; peptide; 13 AA
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                                                                                                          Query Match
Best Local Similarity luv...
Conservative
Conservative
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                                                                                                                                                                                                                                                           1 ALYKKWKNKLLKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-590659/63.
                                                                                      Sequence 13 AA;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against or crivity or for potentiating antimicrobial agents active against or gramisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting cessentially of a first peptide template XZBEBXXB and its derivatives cesentially of a first peptide template XZBEBXXB and BBXZBBX; and (b) a second peptide template XBBXZBB, WXBXXBBX and BBXZBBX; and (b) a second peptide template XBBXXBBX, MXBBXXBBX, MABZXBBX, MABZZBBX, MABZBBX, MABZZBBX, MABZZBBX, MABZZBBX, MABZZBBX, MABZZBBX, MABZZBBX, MABZBBX, MABZZBBX, 
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                       half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
considered to have undesirable toxicity, immunogenicity and short
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                          Length 13;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                       100.0%; Score 69; DB 5;
100.0%; Pred. No. 0.0013;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial peptide RP-8 SEQ ID NO:10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY57472 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      Sequence 13 AA;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial agents, agents such as individual antimicrobial against bacteria and fungi, agents in combination with other conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in the foods and cosmetics and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants of profer art have generally been considered to have undesirable toxicity, immunogenicity and short convention natural antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short convention natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibicitic resistance. They exhibit lower inherent mammalian cell toxicities and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
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preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rabbit platelet microbicidal protein, PMP-2, based peptide #8
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   Length 18;
                                                                           1; Indels
                                                                       1; Mismatches
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   Score 56;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                ABG69896 standard; peptide; 18 AA
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   81.2%;
83.3%;
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                                                                       10; Conservative
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Query Match
Best Local Similarity
Matches 10; Conserv
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overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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Pred. No. 0.17;
0; Mismatches 1; Indels
                                                                                                     DB 5; Length 18;
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                                                                                                     Score 56; DB 5,
Pred. No. 0.16;
                                                                                                                                      1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial peptide RP-6 SEQ ID NO:8.
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                                                                                                                                                                                                                                                                                       AAY57470 standard; peptide; 14 AA.
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                                                                                                                   Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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                                                                    Sequence 18 AA;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers,
truncations, extensions, combinations, funions and their derivatives. The possible structures are fully described in the specification. Also concluded are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fungion; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial agents (2) antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial activity of functions of leukocytes, as disinfectants or preservatives for use in commercional antimicrobial peptides of protentiate or restore efficacy of foods and cosmetics and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in commercions and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic creatstance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness due to biodegradation, recipience prepages of the present sequence is a rabbit pWP based antimicrobial peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                       Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                              Rabbit platelet microbicidal protein, PMP-2, based peptide #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 130; 221pp; English.
                                                                                                                                    ABG69894 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-2001; 2001WO-US041877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-2000; 2000US-00648816
                                                                                                                                                                                                                               (first entry)
2 LYKKWKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                 mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200255554-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeaman MR,
                                                                                                                                                                                   ABG69894;
                                                                                        RESULT 6
                                                                                                                ABG69894
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXEBXB and its derivatives selected from XZBBZBXBXB, BXXXXXB, XBBXXBBXB and BBXZBBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXBBX, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and contain acid, and where B = at least one positively charged amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7463 to AAXS757 represent sequences used in the exemplification of the present invention
                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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 DB 5; Length 14;
                                      1; Indels
                   0.17;
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
Score 55;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide RP-1 SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 106; 166pp; English.
                                                                                                                                                                                                       AAY57465 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US003350.
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 79.7%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              against bacteria and fungi
                                                                                                                                                                                                                                                                               25-FEB-2000 (first entry)
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 Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                          2 LYKKWKNKLLK 12
                                                                                                             2 LYKKWKKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-527417/44.
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                           AAY57465;
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Sequence 14 AA

1 ALYKKFKKKLLKS 13

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide contentining a 7-13 amino acide core sequence (desirved from PMP-1 and PMP-2, platelet microbicalal protein), and retromers.

Every sequence sere fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents bacteria and fungi, agents in combination with other antimicrobial peptides and seafors that enhance the antimicrobial armicrobials, agents that enhance the antimicrobial for conventional antimicrobials, agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in the foods and cosmetics and as agents to improve efficiency of molecular belongy techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibictic resistance. They exhibit lower inherent mammalian cell toxicities and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                 Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                     Rabbit platelet microbicidal protein, PMP-2, based peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.8%; Score 53; DB 5; Length 18; 84.6%; Pred. No. 0.43; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                ABG69889 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; Page 71; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-2000; 2000US-00648816.
                                                                                                                                       (first entry)
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeaman MR, Shen AJ
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                                                                                            ABG69889;
RESULT 8
ABG69889
                                              8X6X6CCCCCCCCCCCCCCCCCCCCCCCCX
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXXBXS and BRXZBXZing selected from the group consisting a second peptide template XBZXB, XBXXBXS, XBXXBXS, AM (BXZBBXZBXZ) and (b) a second peptide template XBBXXBBX, XBXXBXXB, XBXXBBX, and their derivatives selected from the group consisting of XBBXXBBX, XBBXXBBX, BBXZBBX; where B = at least one positively charged amino acid, at least one non-polar hydrophobic amino seld; Z = at least one aromatic amino acid, and where B, and Z may be separated by one or more other camino acids. The peptides can be used to treat bacterial and fungal amino acids. The peptides also increase the antimicrobial activity of intections. The peptides overall effect cellular disruption and rapid application of application and rapid application of application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid application and rapid ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                        metapeptide; PMP-2; platelet microbicidal protein;
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Pred. No. 0.46;
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                                                                                                                                                                                                     Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 59; 166pp; English.
                                             AAY57501 standard; peptide; 19 AA
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Local Similarity 84.6%;
es 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shen AJ;
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                                                                                                                                                                                                                                                        Antimicrobial;
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                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                  AAY57501;
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RESULT 9
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84.68;

25-FEB-2000 (first entry)

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Gaps

microbicidal protein;

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBKB and its derivatives selected from KXBBZBRXB, BXXZXB, XBBXZXBB, and BBXZBBXZ; and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXZXBB, and consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXBBX, BAXZBB, and ABZBXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX57463 to AAX5757 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial peptides for potentiating antimicrobial agents active
                                                 Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein
antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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Pred. No. 0.46;
1; Mismatches 1; Indels
                 Antimicrobial peptide OC-RP-1 SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 58; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              against bacteria and fungi.
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Best Local Similarity 84.6
Marches 11; Conservative
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                                                                                                                            Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                   Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527417/44
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                                                                                                                                                                                                                                                                                                                                                    Yeaman MR,
                                                                                                           Synthetic
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers.

Cruncations, extensions, combinations, funions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations of the peptides described above, and retromers, extensions, such as bacteria and fungion; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial for the foods and cosmetics and as agents to improve efficiency of molecular (cods and cosmetics and as agents to improve efficiency of molecular (cods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that that half-lives and considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that the partial and considered to have undesirable exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicity and short or effective proper due to hidder the entition of effective and produced and considered where the entition of effective and an approach and produced and considered 
                                                                                                                                                                                                                                                                                                                                                                New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbit platelet microbicidal protein, PMP-2, based peptide #37.
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Pred. No. 0.46;
1; Mismatches 1; Indels
                                                                                                                                                                                                                     (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Page 71-72; 221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                multiple antibiotic resistance.
                                                                                                                       24-AUG-2001; 2001WO-US041877.
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84.6%;
                                                                                                                                                                    25-AUG-2000; 2000US-00648816
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                  WPI; 2002-590659/63
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                         WO200255554-A2
                                                                       18-JUL-2002.
                                                                                                                                                                                                                                                                     Teaman MR,
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Synthetic

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Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40.
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                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acida contening a 7-13 amino acid acore sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and recromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as or for potentiating antimicrobial agents active against organisms such as core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents that enhance the antimicrobial for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undestrable to private art have generally been considered to have undestrable to fire private in memoral considered to have undestrable to fire private in the constant to the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the
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 preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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                                                                                                                                                                                                                                                          (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY57502 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 72; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          multiple antibiotic resistance.
                                                                                                                                                                                    24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                      25-AUG-2000; 2000US-00648816
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Best Local Similarity 84.6
Matches 11; Conservative
                                                        Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                WPI; 2002-590659/63
                    mutant; mutein.
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                                                                                                            WO200255554-A2
                                                                                                                                              18-JUL-2002
                                                                                                                                                                                                                                                                                              Yeaman MR,
                                                                         Synthetic.
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AAY57502
1D AAY57
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activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide estantially of a first peptide template XEBZENKER and its derivatives selected from XEBZENKER, BXXXE, XEBZENKER and its derivatives selected from XEBZENKER, BXXXE, XEBZZENKER and BENZENKZ; and (b) a second peptide template XEBXX and their derivatives selected from the group consisting of XEBXENK, and their derivatives selected from the group consisting of XEBXENKER, BXXENXE, XEBZXENE, and (b) at least one positively charged amino acid; x at least one aromatic amino acid, and where B, x and Z may be separated by one or more other infections. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAVS7463 to AAVS7557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an antimicrobial peptide (AP) for direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 59; 166pp; English.
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                                                                                                                                                                                                                                                                                                                                                    99WO-US003350,
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|| Similarity 84.6%;
| 11; Conservative
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                                                                                                                                           Oryctolagus.cuniculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (eaman MR, Shen AJ;
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Best Local Similarity
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ABG69920
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150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also core sequence selected from truncations of the specification. Also core sequence selected from truncations of the specifies described above, and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the specifies described above, and retromers, extensions, combinations of the specifies described above, and retromers, extensions, combinations and fungi. And retromers, extensions, combinations and fungi, agents in combination with other antimicrobial peptides are useful as individual antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as dishifectants or preservives for use in the functions of leukocytes, and as agents to improve efficiency of molecular conventions of leukocytes, and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short has a based upon natural antimicrobial peptides of prior art have generally espectum activity against pathogens exhibiting multiple antibiotic sections of spectrum activity against pathogens exhibiting multiple antibiotic converceme problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and constructions of effectiveness due to biodegradation, retaining activity and shortness of duration of effectiveness due to biodegradatio
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                                                                                                                                                                                                                                         New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                   The invention relates to an antimicrobial peptide composition for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.
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                                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
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                                                                                                                                                                                                                                                                        multiple antibiotic resistance.
                                                                              24-AUG-2001; 2001WO-US041877
                                                                                                             25-AUG-2000; 2000US-00648816
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84.6%;
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Best Local Similarity 84.0
Best Local Similarity
Local Similarity
Local Similarity
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                                                                                                                                                                                                           WPI; 2002-590659/63.
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                WO200255554-A2
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                                              18-JUL-2002
                                                                                                                                                                             Yeaman MR,
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activity or for potentiating antimicrobial agence active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZENENE and its derivatives selected from XZBZENENE, BXZXZB, XBBXZXBENE and its derivatives selected from XZBZENENE, BXZXZB, XBBXZXBEN, and BBXZBBXZ, and (b) a second peptide template XBBX and their derivatives selected from the group consisting of XBBXENENE, and XBBXXBBN, BXXBXB, XBBXZXBB, and (b) at least one positively charged amino acid; at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal ninfections. The peptides overall effect cellular distription and rapid apoptosis of microbial cells. AAVS7567 represent sequences
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bacterial infection; fungal infection; fungicide; disinfectant;
preservativė; foods; cosmetic; multiple antibiotic resistance; rabbit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabbit platelet microbicidal protein, PMP-2, based peptide #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53; DB 2; Length 25; Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes an antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                     (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 126; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG69920 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                   99WO-US003350
                                                                                                                                                                                                                                                                                                      98US-00025319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.8%;
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALYKKWKNKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALYKKFKKKLLKS 13
                                   Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200255554-A2
                                                                                                                                                                                                                                                                                                      18-FEB-1998;
                                                                                                                                                                                                                                   17-FEB-1999;
                                                                                                  WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2002
                                                                                                                                                                 26-AUG-1999
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG69920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 16
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Brass EP;

Edwards JE,

Yount NY,

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New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                               20-AUG-2003; 2003WO-US026405.
                                                                                            :0-AUG-2002; 2002US-00225562
                                                                                                                                                                                        WPI; 2004-226740/21
   WO2004017985-A1
                                                                                                                                                          Teaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY57497
   a
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                                                                                                                                                                                                                           The invention relates to an antimulational peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derivatives from
150 amino PMP-1 and PMP-2, platelet microbical protein), and retromers,
150 core for potentiating antimicrobial agents active against organisms such as
151 core sequence selected from truncations of the peptides described above,
152 core sequence selected from truncations of the peptides described above,
153 core sequence selected from truncations of the peptides described above,
154 containing an amino acid
155 core sequence selected from truncations of the peptides described above,
156 core sequence selected from truncations of the peptides described above,
157 core sequence selected from truncations of the peptides described above,
158 core sequence selected from truncations and fusions; and (2)
159 core sequence selected from truncations and fusions; and (2)
150 core sequence selected from truncations and fusions, and (2)
150 core sequence selected from truncations and fusions, and (2)
150 core sequence selected from truncations and fungi. The
150 core sequence against bacteria and fungi, agents in combination with other
151 conventional antimicrobials, agents that enhance the antimicrobial
150 core sequence to have undesirable to improve efficiency of molecular
151 considered to have undesirable to improve efficiency of molecular
151 considered to have undesirable toxicity, immunogenicity and short
151 considered to have undesirable toxicity, immunogenicity, and short considered to have undesirable toxicity, immunogenicity, and short considered to have to biodegradation. The peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibials of toxicity, immunogenicity, and short core problems of toxicity, immunogenicity, and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                           peptide composition for the prevention and treatment of by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                       invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protide; antibiotide; antimicrobial; interleukin-8; Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 5; Length 25; Pred. No. 0.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15. .16
/note= "Cleaved by V8 protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL70275 standard; peptide; 33 AA.
                                                                                                                                                                                      Example; Page 70; 221pp; English
                                                                                                                                                         multiple antibiotic resistance
 25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALYKKWKNKLLKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide antibiotide PT-1.
                                                                                                                          New antimicrobial per
infections caused by
                                                             Shen AJ;
                                                                                            WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Cleavage-site
                                                               Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL70275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The present sequence is that of Protide-1 (PT-1), a peptide antibiotide with distinct effector and activator domains. PT-1 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokina-like peptide effector (Interleukin-8 domain) and an activator site specific peptide effectors in the presence of VB protease. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of VB protease. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of VB protease produced by Staphylococcus ansueus. Thus, PT-1 was designed to exert optimal antimicrobial activity in the context of infections due to staphylococcal cells elaborating the virulence factor WB protease. PT-1 was synthesised by Solid-phase synthesis It is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 8; Length 33;
Pred, No. 0.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide RP-1:RP-13 SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
Claim 1; SEQ ID NO 1; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY57497 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.8%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US003350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 ALYKKFKKKLLKS 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKKWKNKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000
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Example; Page 71; 221pp; English.

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activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XBBXZBBXB and its derivatives selected from XZBBZBXBB, BXZXB, BXZXZB, XBBXZBBX and BBXZBBXZ; and (b) a second peptide template XBBXXBB, BXXBXBBX and BBXZBBXZ; and (b) group consisting of XBBXBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, BXXBXBB, and XBBXXBBXXBBX, WBBXXBBXXBBX, and a least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acid, and where B, X and Z may be separated by one or more other amino acid, and where B, X and Z may be separated by one or more other amino acid, and peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAX57537 to AAX57537 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                         invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                              Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 2; Length 35;
Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                    Disclosure; Page 126; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69921 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.8%;
84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 84.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-590659/63.
                                                                                         WPI; 1999-527417/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200255554-A2.
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                                                      Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG69921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 19
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, antimicrobial peptides for potentiatings antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobials agents that enhance the antimicrobial agents that enhance the antimicrobial attimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and commettes and as agents that enhance the antimicrobial peptides of prior art have generally believely techniques, antimicrobial peptides of prior art have generally believely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 5; Length 35;
Pred. No. 0.85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL70276 standard; peptide; 36 AA.
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35 AA;
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(HARB-) HARBOR-UCLA RES & EDUCATION INST. WPI; 2004-226740/21. WPI; 2004-226740/21. Sequence 36 AA; WO2004017985-A1 Cleavage-site 20-MAY-2004 04-MAR-2004 condition. Yeaman MR, Synthetic. ADL70277; 8 qq

The present sequence is that of Protide-2 (PT-2), a peptide antibiotide with distinct effector and activator domains. PT-2 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific cordinates, a complement fixing protease. PT-2 is cleaved into 2 distinct effectors in the presence of C3 convertase. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of C3 convertase. PT-2 was designed to exert optimal antimicrobial activity in PT-2 was designed to exert optimal activity in the context of activation of one of the inner end activity in the context of activation of one of the context-activated protides of the innate immune response to antigen exposure. PT-2 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more effectors with individual distinct biological functions and one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory Claim 1; SEQ ID NO 2; 103pp; English range of pathological conditions.

Gaps ö 8; Length 36; 1; Indels Score 53; DB 8; Pred. No. 0.87; 1; Mismatches 76.8%; 84.6%; Query Match
Best Local Similarity 84.6'

1 ALYKKWKNKLLKS 13  ADL70277 standard; peptide; 37 AA. Peptide antibiotide PT-3.

Protide; antibiotide; antimicrobial; interleukin-8.

/note= "Cleaved by thrombin" Location/Qualifiers 18. .19

20-AUG-2003; 2003WO-US026405

20-AUG-2002; 2002US-00225562

Edwards JE,

New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.

with distinct effector and activator domains. Pr.3 contains a C-remainal antimorcobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (RP-1), an N-terminal chemokine-like peptide effector (Interleukin-8 domain) and an activator site specific for thrombin. Pr-3 was designed to be cleaved into 2 distinct effectors in the presence of thrombin. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of thrombin. Thus, PT-3 exerts optimal antimicrobial activity in the context of thrombin as would be present in the setting of vascular injury or infection. PT-3 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological sequence is that of Protide-3 (PT-3), a peptide antibiotide Claim 1; SEQ ID NO 3; 103pp; English. conditions 

Sequence 37 AA;

Gaps ; 0 Score 53; DB 8; Length 37; Pred. No. 0.9; 1; Mismatches 1; Indels 76.8%; 84.6%; Query Match 76.8 Best Local Similarity 84.6 Matches 11; Conservative

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ADL70278 standard; peptide; 39 AA. (first entry) 20-MAY-2004 ADL70278; RESULT 22

Peptide antibiotide PT-4.

Protide; antibiotide; antimicrobial; interleukin-8; cytostatic. 17. .18
/note= "Cleaved by MMP-9" Location/Qualifiers Cleavage-site Synthetic. 

WO2004017985-A1. 04-MAR-2004 20-AUG-2003; 2003WO-US026405. 20-AUG-2002; 2002US-00225562 (HARB-') HARBOR-UCLA RES & EDUCATION INST.

Brass EP; Edwards JE, Yeaman MR, Yount NY,

WPI; 2004-226740/21.

New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition

Claim 1; SEQ ID NO 4; 103pp; English.

The present sequence is that of Protide-4 (PT-4), a peptide antibiotide with distinct effector and activator domains. PT-4 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like

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peptide effector (interleukin-8 domain) and an activator site specific for matrix metalloproteinase MMP-9, which is produced to dissolve the tissue in front of the growing blood vessel tip to allow for its continued tissue invasion. PT-4 was designed to be cleaved into 2 distinct effectors in the presence of MMP-9. In particular, PT-4 exerts antineoplastic and/or antimicrobial activity less than that of RP-1 in the absence of MMP-9, but equivalent to or exceeding that of RP-1 in the presence of MMP-9, thus, PT-4 exerts optimal antineoplastic and/or antimicrobial activity in the context of new blood vessel formation. PT-4 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         broad range of pathological conditions.
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Score 53; DB 8; Length 39;
Pred. No. 0.95;
                        1; Indels
                      1; Mismatches
76.8%;
84.6%;
                                                            22 ALYKKFKKKLIKS 34
                                              1 ALYKKWKNKLLKS 13
                        11; Conservative
Query Match
Best Local Similarity
                         Matches
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Gaps

RESULT 23

ABG69990 standard; peptide; 40 AA.

21-OCT-2002 (first entry)

ABG69990;

Rabbit platelet microbicidal protein, PMP-2, based peptide #102

Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.

Oryctolagus cuniculus. Synthetic.

WO200255554-A2. 18-JUL-2002 24-AUG-2001; 2001WO-US041877

25-AUG-2000; 2000US-00648816

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

WPI; 2002-590659/63.

New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

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Example; Page 67; 221pp; English.

The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acide sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as ABG69990

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bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukcoytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, bacteria and fungi, agents in combination with other antimicrobials, agents that enhance the antimicrobial agents of conventional antimicrobials, agents that enhance the antimicrobial functions of leukcoytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of prior art have generally care based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic conservations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from
                                                                                                                                                                                                                                                                                                                                                    overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.8%; Score 53; DB 5; Length 40; 84.6%; Pred. No. 0.97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG69992 standard; peptide; 40 AA.
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-2002
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Theritate and fundicrobial gents active against organisms such as bacteria and fundicrobial agents active against organisms such as bacteria and fundi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fundions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fundi. The entimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fundi. The estore efficacy of conventional antimicrobials, agents that enhance the antimicrobial conventions of leukocytes, as disinfectants or preservatives for use in functions of leukocytes, as disinfectants or preservatives for use in commerces and cosmetics and as agents to improve efficiency of molecular blology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short of spectrum activity against pathogens exhibiting multiple antibiotic are based upon natural antimicrobial peptides to the present invention are based upon natural antimicrobial peptides to the present and broad overcome problems of toxicity, immunogenicity, and shortness of duration. The present estimicrobial peptides the resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration. Of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit pwp based antimicrobial peptide
                                        truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also
                                                                                                                included are (1) an antimicrobial peptide composition for direct activity
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and PMP-2, platelet microbiocidal protein), and retromers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-1998;
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The present invention describes an antimicrobial peptide (AP) for direct

Disclosure; Page 58; 166pp; English.

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             corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting selected from XZBAZBASB, BXZXXB, XBBXZBBS and its derivatives selected from XZBAZBASB, BXZXXB, XBBXZBBS and BBXZBBXZ; and baccod from XZBAZBASB, BXZXXB, XBBXZBBX and BBXZBBXZ; and (b) a second peptide template XBBXX and their derivatives selected from the XBBXXXBBXXBBX; where B = at least one positively charged amino acid, x = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acid, and where B, X and z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AMYS7463 to AAYS7557 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
activity or for potentiating antimicrobial agents active against
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                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB 2; Length 18; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide RP-1-10F SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY57504 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US003350
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.0%;
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid core sequence (derived from
150 amino acids containing a 7-13 amino acid retromers,
150 possible structures are fully described in the specification. Also
150 possible structures are fully described in the specification. Also
150 core sequence selected from truncations of the peptides described as bacteria and fungi comprising a peptide of 13-74 containing an amino acid
150 core sequence selected from truncations of the peptides described above,
151 core sequence selected from truncations of the peptides described above,
152 core sequence selected from truncations of the peptides described above,
153 continucobial peptides for potentiating antimicrobial activity of
154 conventional peptides are useful as individual antimicrobial agents,
155 conventional antimicrobials, agents that enhance the antimicrobial
155 conventional antimicrobials, agents that enhance the antimicrobial
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amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAX57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungacide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabbit platelet microbicidal protein, PMP-2, based peptide #36.
                                                                                                                                                        Length 18;
                                                                                                                                                                                                 2; Indels
                                                                                                                                                        Score 49; DB 2;
Pred. No. 1.7;
                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-AUG-2000; 2000US-00648816
                                                                                                                                                          71.0%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-2002 (first entry)
                                                                                                                                                    Query Match
Best Local Similarity 76.9°
Matches 10, Conservative
                                                                                                                                                                                                                                     1 ALYKKWKNKLLKS 13
                                                                                                                                                                                                                                                          Oryctolagus cuniculus.
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                                                                                                                      Sequence 18 AA;
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ABG69924
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foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and
                                                                                                                                               overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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Pred. No. 1.7;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                               71.0%;
83.3%;
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Best Local Similarity 83.3
***rhes 10; Conservative
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                                                                                                                                                                                                                                      Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG69928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8888888888888
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antimicrobial peptides are useful as individual antimicrobial agents,

specifically against bacteria and fungi, agents in combination with other

curtimicrobials, agents that enhance, potentiate or restore efficacy of

conventional antimicrobials, agents that enhance the antimicrobial

functions of leukocytes, as disinfectants or preservatives for use in

code and cosmetics and as agents to improve efficiency of molecular

biology techniques. Antimicrobial peptides of prior art have generally

been considered to have undesirable toxicity, immunogenicity and short

are based upon natural antimicrobial peptides that have potent and broad

spectrum activity against pathogens exhibiting multiple antibiotic

spectrum activity against pathogens exhibiting multiple antibiotic

resistance. They exhibit lower inherent mammalian cell toxicities and

overcome problems of toxicity, immunogenicity, and shortness of duration

covercome problems of toxicity, immunogenicity, and shortness of duration

covercome problems of sequence is a rabbit PMP based antimicrobial peptide
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Sequence 18 AA;

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Gaps
                        ö
  Length 18;
                        2; Indels
Score 49; DB 5;
Pred. No. 1.7;
1; Mismatches
  71.0%;
76.9%;
                                            1 ALYKKWKNKLLKS 13
                                                                  1 ALYKKFKKKFLKS 13
            Local Similarity 76.9
nes 10; Conservative
  Query Match
                      Matches
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                                                                  셤
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RESULT 29

AAY57468 standard; peptide; 13 AA. 25-FEB-2000 (first entry) AAY57468; 

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

Antimicrobial peptide RP-4 SEQ ID NO:6.

Oryctolagus cuniculus. Synthetic

WO9942119-A1

26-AUG-1999.

99WO-US003350 17-FEB-1999; (HARB-) HARBOR-UCLA RES & EDUCATION INST.

98US-00025319

18-FEB-1998;

Shen AJ; Yeaman MR,

WPI; 1999-527417/44

Disclosure; Page 108; 166pp; English. against bacteria and fungi.

Antimicrobial peptides for potentiating antimicrobial agents active

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against conganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XEBERENEB and its derivatives a selected from XEBERENES, BXZXZB, BXZXZBB, WEBXZXBBS, and (b) a second peptide template XEBXX and their derivatives selected from the group consisting of XEBXEBS, XEBXXBB, BXXEBS, XEBXXBB, and (b) as second peptide template XEBXXBBS, BXXBXSB, MENCES, where B = at least one positively charged amino acid, x = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other

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amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7463 to AAYS7557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                     ö
                                                                                                                                                       Score 48; DB 2; Length 13;
Pred. No. 1.7;
3; Mismatches 1; Indels
                                                                                                                                                             69.6%;
69.2%;
                                                                                                                                                                                                       9; Conservative
                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                        Sequence 13 AA;
                                                                                                                                                                                                     Matches
    88888888
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1 ALYKKWKNKLLKS 13 | |:|:|||:||| 1 ARYRKFKONKILKS 13

ઠે g RESULT 30 ABG6989;

ABG69892 standard; peptide; 13 AA. ABG69892;

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(first entry) 21-OCT-2002

bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit; Rabbit platelet microbicidal protein, PMP-2, based peptide #4 Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;

mutant; mutein.

Oryctolagus cuniculus. Synthetic. 

WO200255554-A2

18-JUL-2002

24-AUG-2001; 2001WO-US041877.

& EDUCATION INST. (HARB-) HARBOR-UCLA RES

25-AUG-2000; 2000US-00648816

Yeaman MR, Shen AJ;

WPI; 2002-590659/63.

ఠ New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

Disclosure; Page 129; 221pp; English.

distributions are particular properties of State or and Fundio compositions of State or against organisms such as bacteria and fundi compositions of State or and PMP-2, platelet microbiocidal protein), and retromers from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers The truncations, extensions, combinations, funding and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as or for potentiating antimicrobial agents active against organisms such as antimicrobial peptides of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fundions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fundi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other specifically against that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial for leukocytes, as disinfectants or preservatives for use in The invention relates to an antimicrobial peptide composition for use

Gaps

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Mismatches

Score 48; Pred. No.

69.6%;

Conservative 2 LYKKWKNKLLK 12 ||:|:|||||| 2 LYRKFKNKLLK 12

Local Similarity nes 9; Conserv

Query Match Matches

Sequence 14 AA;

X S

2; Length 14; 0; Indels

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foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apopto8is.
                                                                                                                                                                                            ö
                                                                                                                                                                Score 48; DB 5; Length 13;
Pred. No. 1.7;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide RP-3 SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                        AAY57467 standard; peptide; 14 AA.
                                                                                                                                                                   69.6%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00025319
                                                                                                                                                                                                                                                                                                                                                           25-FEB-2000 (first entry)
                                                                                                                                                                                                                    1 ALYKKWKNKLLKS 13
                                                                                                                                                                                                                                 1 ARYRKFKNKILKS 13
                                                                                                                                                                              Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus.
                                                                                                                                           Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L8-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                   AAY57467;
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                 RESULT 31
                                                                                                                                                                                                                                                                                              AAY57467
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Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;

Oryctolagus cuniculus.

Synthetic.

WO200255554-A2.

18-JUL-2002.

mutant; mutein.

(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

24-AUG-2001; 2001WO-US041877. 25-AUG-2000; 2000US-00648816.

Rabbit platelet microbicidal protein, PMP-2, based peptide #3

21-OCT-2002

ABG69891;

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ABG69891 standard; peptide; 14 AA.

RESULT 32

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ABG69891

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The invention relates to an antimicrobial peptide composition of the invention relates to an antimicrobial peptide composition of the invention relates to an antimicrobial protein), and retroners, the ind PMP-1, platelet microbiocidal protein), and retroners, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (i) an antimicrobial peptide composition for direct activity or or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retroners, extensions, combinations and fungions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual activity of leukocytes against organisms such as bacteria and fungi. The attimicrobials agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance the antimicrobial committions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable operiodes of prior art have generally been considered to have undesirable the present invention are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 129; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-590659/63.
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXB, XBBXZXBBX and BWZZBBXZ; and (b) a second peptide template XBBXXBX, BXBXXBBX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and CXBZXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AMY57463 to AAY5757 represent sequences used in the exemplification of the present invention

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure; Page 108; 166pp; English.

(HARB-) HARBOR-UCLA RES & EDUCATION INST

WPI; 1999-527417/44

Yeaman MR,

Gaps

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Indels

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Mismatches

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10; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZEMENS and its derivatives selected from XZBZEMENS, BXZXZB, XBBZXZBBX and BBXZBBXZ; and (b) a second peptide template XBBXXXB, XBBXZKBBX and backering of XBBXZBBX; Where B = at least one positively charged amino acid; X = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of infections.
spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAV57463 to AAV57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                           ö
                                                                                                                                         5; Length 14;
                                                                                                                                                                         0; Indels
                                                                                                                                         Score 48; DB Pred. No. 1.9;
                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide RP-2 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 107; 166pp; English
                                                                                                                                                                                                                                                                                                                                 AAY57466 standard; peptide; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-00025319
                                                                                                                                         69.6%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                             2 LYRKFKNKLLK 12
                                                                                                                                                                                                           2 LYKKWKNKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen AJ;
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13 AA;
                                                                                                       Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9942119-A1
                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                  AAY57466;
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                 RESULT 33
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DB 2; Length 13;

Score 47; DB; Pred. No. 2.4;

68.1**\$**; 76.9**\$**;

Query Match Best Local Similarity

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-10 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbicidal protein), and retromers.

Eventuations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are to 1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as acteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi, agents in combination with other, appending antimicrobial agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial and companied and as agents to improve efficiency of molecular conventions of leukocytes, as disinfectants or preservatives for use in the conventions and comments and as agents to improve efficiency of molecular and comments and as agents to improve faritation of proversely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                     Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection; fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and
                                                                                                                                                                                                                                                                                          Rabbit platelet microbicidal protein, PMP-2, based peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 128; 221pp; English.
                                                                                                                                                     ABG69890 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                (first entry)
                     1 ARYKKFKKKLLKS 13
1 ALYKKWKNKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                          mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200255554-A2.
                                                                                                                                                                                                                                                21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8-JUL-2002
                                                                                                                                                                                                     ABG69890;
                                                                                                             RESULT 34
                                                                                                                                  ABG69890
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Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,

Oryctolagus cuniculus.

Synthetic.

WO200255554-A2.

18-JUL-2002.

mutant; mutein.

Rabbit platelet microbicidal protein, PMP-2, based peptide #39.

(first entry)

21-OCT-2002

ABG69927;

ABG69927 standard; peptide; 18 AA.

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RESULT 36
                        ABG6992
                                                      %XCCCCCCCCCCCCCCCCCCCCCCCCX8X444X8X1XX8XX1XX8XX8XX8XX8XX8XX8XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XCBBZBXBXB, BXZXXB, XBBXZXBB, and BMXZBBXZ, and (b) a second peptide template XBBXXXB, XBBXXXBB, and their derivatives selected from the group consisting of XBBXBBX, XBBXXXBB, BXXXBB, and and consisting of XBBXBBX, XBBXXXBB, BXXBXXB, AXBBXXBB, and activatives one non-polar hydrophobic amino acid, 2 = ar least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AMX57463 to AAX5757 represent sequences
                                           ö
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47; DB 2; Length 18;
Pred. No. 3.4;
1; Mismatches 2; Indels
                      Length 13;
                                           2; Indels
                     Score 47; DB 5;
Pred. No. 2.4;
                                                                                                                                                                                                            Antimicrobial peptide RP-1-2R SEQ ID NO:41.
                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 59; 166pp; English.
                                                                                                                                           AAY57503 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.1%;
76.9%;
                     68.1%;
76.9%;
                                                                                                                                                                                                                                                                                                                                              99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                   98US-00025319
                                                                                                                                                                                      (first entry)
                                                                 1 ALYKKWKNKLLKS 13
                                                                                     1 ARYKKFKKKLLKS 13
                               Local Similarity 76.5
                                                                                                                                                                                                                                                                          Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                             Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                             17-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                             Yeaman MR,
                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                  AAY57503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                     Query Match
                                          Matches
                                                                                                                      RESULT 35
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(HARB-) HARBOR-UCLA RES & EDUCATION INST.

Yeaman MR, Shen AJ;

24-AUG-2001; 2001WO-US041877. 25-AUG-2000; 2000US-00648816.

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-10 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and recromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 contendining an amino acid core sequence selected from truncations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The attimicrobial peptides are useful as individual antimicrobial agents, agents that enhance the antimicrobial antimicrobials, agents that enhance the antimicrobial for conventional antimicrobials, agents that enhance the antimicrobial for conventional antimicrobials, agents to improve efficiency of conventional antimicrobials, agents to improve efficiency of mortions of leukocytes, as disinfectants or preservatives for use in conventional antimicrobials. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short
New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and
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                                                                                                                                                                                                                                                                 Example; Page 72; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
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Score 47; DB 5; Length 18; Pred. No. 3.4;

68.1%; 76.9%;

Query Match Best Local Similarity

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Gaps

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Best Local Similarity 76.9 Matches 10; Conservative

Panasik N;

Pugh C,

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The present sequence is an antibacterial peptide C18G, which was modified by adding a Cys-amide to the carboxy terminus. This was used to produce an immunoadapter conjugate. Making a conjugate comprises covalently.

Inking a surface-binding ligand (SBL) to a hapten via a spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the compound with munoadapter of the Igand-spacer-hapten of the compound. The conjugate can be used for the ig to the hapten of the compound. The conjugate can be used for the diagnosis, prevention and treatment of microbial infections, e.g. sepsis, influenza, viremia or fungemia. They can also be used in neurology, cancer and endocrinology, where Ig targeting can provide desired therapeutic effects. The methods for producing a conjugate can use small molecule targeting ligands to efficiently direct otherwise unreactive Ig to microbial targets. This targeting allows Ig to react with microbial structures that may not normally be accessible to Ig, or are incapable of stimulating antibody production
                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial compans. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
                                                                                                                                                                                                                                                                                                              Williams JA, Shekhani MS, Firca JR, Schatz RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 39; Page 150; 227pp; English.
antibodiotic; antibody; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY57505 standard; peptide; 18 AA.
                                                                                                                                                                                                                          95US-00482191,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US003350.
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76.9%;
                                                                                                                                                                                                                                                                  (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 76.3.
Local 10; Conservative
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Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-077224/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-1999;
                                                                                      WO9640251-A1
                                                                                                                                                                              07-JUN-1996;
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                                                                                                                                  19-DEC-1996
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                                                                                                                                                                                                                                                                                                                                      Stafford D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY57505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphabilation structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; cancer; endocrinology;
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
  ö
                                                                                                                                                                                                                                                                                                                                                                                                       human platelet factor 4 C-13 fragment; amphipathic alpha helix.
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial peptide C18G for immunoadapter synthesis.
  2;
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  Mismatches
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Pred. No.
                                                                                                                                                                                                 AAR13927 standard; protein; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cosand WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW10351 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; Page 44; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRIM ) BRISTOL-MYERS SQUIBB CO.
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91US-00655321.
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76.9%;
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(first entry)
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                                            1 ALYKKWKNKLLKS 13
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1 ARYKKPKKKLLKS 13
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10; Conservative
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                                                                                                                                                                                                                                                                                                                                                          Cationic oligopeptide #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-281214/38.
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26-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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Gaps

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Indels

Mismatches

Score 43; DB 2; Length 18; Pred. No. 13;

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting cessentially of a first peptide template XZBZBXXBX and its derivatives selected from XZBZBXZBX. BXXXZBX XBBXXBBX and BBXZBBXZ, and (b) a second peptide template XBBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, XBBXXBBX, XBBXXBBX, ABBXXBBX, ABBXXBBX, ABBXXBBX, ABBXXBBX, BXXBXXB, ABBXXBBX, and (b) a least one non-polar hydrophobic amino acid, Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other camino acid, and where B, X and Z may be separated by one or more other amino acid, and where B, and Z may be separated by one or more other controphils. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7537 to AAX57537 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
                                                                                                                                                             Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 2; Length 18;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                    (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial peptide C18G SEQ ID NO:2.
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                                                                                                                                                                                                                  Disclosure, Page 59, 166pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY68001 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.3%;
69.2%;
                98US-00025319
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                                                                                                                                                                              against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OPHI-) OPHIDIAN PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALYKKWKNKLLKS 13
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1 ARYKKFKKKFLKS 13
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Matches 9; Conservative
                                                                                                                          WPI; 1999-527417/44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shekhani MS,
                  18-FEB-1998;
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                                                                                        Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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(phenylalanyl)-4-aninophenyl-alpha-mannopyranoside (I). Also described is a method of treatment for bacterial disease comprising: (a) providing a method of treatment for bacterial disease comprising: (a) providing can subject with symptoms of bacterial disease comprising: (a) providing can propounds comportising a mannose of an anomeric configuration, an alpha-aromatic or heteroaromatic ring attached to the mannose by a alycosidic or pseudoglycosidic linkage and a functional group which provides a site for chemical modification remote from the mannose and provides a site for chemical modification remote from the mannose and characteristic and (b) administration of one or more finbriae-binding compounds can be used for treating subjects with symptoms of and for subjects at risk from bacterial diseases. Treatment of and prevention of blood-borne and toxin mediated diseases in particular sepsis in humans and other animals can be carried out and the in vivo neutralisation of the identify bacteria according to their cell binding specificity's through conjugation to reporter substances such as dyes, luminescent or fluorescent molecules and enzymes. The compounds also inhibit the agglutination of yeast cells induced by type I pili bearing bacteria. The present sequence is used in the exemplification of the present invention
                                                                              invention describes a therapeutic formulation comprising N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbit platelet microbicidal protein, PMP-2, based peptide #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 3; Length 18;
Pred. No. 13;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HARB-). HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG69929 standard; peptide; 18 AA.
                                          Example 39; Col 84; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.3%;
76.9%;
treating bacterial diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALYKKWKNKLLKS 13
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 41
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Gaps

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New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

Example; Page 72; 221pp; English

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The invention relates to an antimicrobial peptide composition for the invention relates to an antimicrobial peptide composition for the invention relates to an antimicrobial period core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from 150 amino acids containing a 7-13 amino acid core sequence (derived from possible structures are fully described in the specification. Also core for potentiating antimicrobial peptide composition for direct activity or included are (1) an antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions, and (2) antimicrobial peptides are useful as individual activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that chhance, potentiate or restore efficacy of conventional antimicrobials, agents that chance, preservatives for use in foods and cosmetics and as agents that enhance the antimicrobial peptides of prior art have generally considered to have undesirable toxicity, immunogenicity and short belongy techniques. Antimicrobial peptides of prior art have generally considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present and broad are based upon natural antimicrobial peptides that have potent and broad appertance and activity against pathogens exhibiting multiple antibiotic and are perior art have generally considered. resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradelion, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; cancer; endocrinology; antibodiotic; antibody; antibiotic. ö antimicrobial peptide composition Pugh C, Score 43; DB 5; Length 18; Pred. No. 13; 1; Mismatches 3; Indels Antibacterial peptide C19G for immunoadapter synthesis. Shekhani MS, Firca JR, Schatz RW, /note= "In amide form" Location/Qualifiers AAW10352 standard; peptide; 19 AA. 95US-00482191. 96WO-US010227 62.3%; 69.2%; invention relates to an (OPHI-) OPHIDIAN PHARM INC. (first entry) Query Match Best Local Similarity 69.2' 1 ALYKKWKNKLLKS 13 1 ARYKKFKKFLKS 13 Sequence 18 AA; Wodified-site Williams JA, Stafford D; 22-SEP-1997 WO9640251-A1 07-JUN-1996; 07-JUN-1995; 19-DEC-1996 Synthetic AAW10352; RESULT 42 **AAW10352** X555555555555555555555555555555555 ò 셤

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The present sequence is a peptide designated C19G. This was used to produce an immunoadapter conjugate. Making a conjugate comprises covalently linking a surface-binding ligand (SBL) to a hapten via a spacer to form a ligand-spacer-hapten (LSH) compound, and reacting the compound with immunoglobulin (Ig) under conditions that allow for non-covalent binding of the Ig to the hapten of the compound. The conjugate can be used for the diagnosis, prevention and treatment of microbial infections, e.g. sepsis, influenza, viremia or fungemia. They can also be used in neurology, cancer and endocrinology, where Ig targeting can provide desired therapeutic effects. The methods for producing a conjugate can use small molecule targeting ligands to efficiently direct otherwise unreactive Ig to microbial targets. This targeting allows Ig to react with microbial structures that may not normally be accessible to Ig, or are incapable of stimulating antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (I). Also described is a method of treatment for bacterial disease comprising: (a) providing
                                                                                           Antimicrobial compans. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin;
bacterial infection; antibacterial; fimbriae-binding compound; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 14;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial peptide C19G SEQ ID NO:3.
                                                                                                                                                                                                                                  Example 39; Page 150; 227pp; English.
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76.9%;
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treating bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shekhani MS, Anderson B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2000 (first entry)
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                            WPI; 1997-077224/07.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 AA;
                                                                                                                                                                  immunoglobulin
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binding compounds comprising a mannose of an anomeric configuration, an alpha-aromatic or heteroaromatic ring attached to the mannose by a alpha-aromatic or heteroaromatic ring attached to the mannose by a glycosidic or pseudoglycosidic linkage and a functional group which provides a site for chemical modification remote from the mannose and a pharmaceutically carrier; and (b) administering the fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compounds can be used for treating subjects with symptoms of and for subjects at risk from bacterial diseases. Treatment of and prevention of blood-borne and toxin mediated diseases in particular sepsis in humans and other animals can be carried out and the in vivo neutralisation of the effects of endotoxin is also possible. The compounds may also be used to identify bacteria according to their cell binding specificity's to identify bacteria according to their cell binding specificity's through conjugation to reporter substances such as dyes, luminescent or fluorescent molecules and enzymes. The compounds also inhibit the agglutination of yeast cells induced by type 1 pili bearing bacteria. The present sequence is used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against corganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, MEXZXBX, KBBXZBBX and BBXZBBXZ; and (b) a second peptide template XZBXZB, KBBXZXBS and BBXZBBXZ; and (b) group consisting of XBBXZBBX, MEXEBXXB, XBBZXXBB, and XBBZXXBBX, Where B = at least one positively charged amino acid; X =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 3; Length 19;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial peptide RP-5 SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 109; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY57469 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial peptides for against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALYKKWKNKLLKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-2000
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbicidal protein), and recromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid ore sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents. Specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of
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  at least one aromatic
                amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. ANYS7463 to AAXS7557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rabbit platelet microbicidal protein, PMP-2, based peptide #5
                                                                                                                                                                                             2; Length 13;
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  one non-polar hydrophobic amino acid; Z =
                                                                                                                                                                                           Score 42; DB Pred. No. 14; 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          ABG69893 standard; peptide; 13 AA.
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53.8%;
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1 ARYRKFRNKILRS 13
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conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cometries and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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Sequence 13 AA;

ò Gaps ö 60.9%; Score 42; DB 5; Length 13; 53.8%; Pred. No. 14; 1; Indels tive 5; Mismatches 1; Indels 1; Indels Query Match
Best Local Similarity 53.8
Matches 7; Conservative

Search completed: May 16, 2005, 08:38:31 Job time : 54.1293 secs

1 ALYKKWKNKLLKS 13 | |:|:||:||:| 1 ARYRKFRNKILRS 13

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69.833 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/ReZOMB.pep:*

(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
         version 5.1.6
- 2005 Compugen Ltd.
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US-09-525-269A-9
US-08-233-203-7
US-08-182-191-2
US-08-182-191-2
US-08-182-191-3
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US-08-233-203-8
US-08-233-203-8
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US-09-453-605-37
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
         GenCore (c) 1993
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12, Appl
23756, A
214, App
135, App
135, App
111, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09525269A;
Patent No. 6743769;
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shean, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025(HRS644)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
FRIOR APPLICATION NUMBER: US 09/025,319
FRIOR PEDICATION NUMBER: US 09/025,319
FRIOR PEDICATION NUMBER: US 09/025,319
SOFTWARE: FRASESEQ for Windows Version 4.0
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UG-09-225-269A-10
; Sequence 10, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.;
; APPLICANT: Shen, Alexander J.;
; TITLE OF INVENTION: Metapeptides
; TITLE OF INVENTION: Metapeptides
; TITLE OF INVENTION: Metapeptides
; TITLE OF INVENTION: Metapeptides
; CURRENT APPLICATION NUMBER: US/09/525,269A
; CURRENT FILING DATE: 1998 02-18
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998 02-18
; NUMBER OF SEQ ID NOS: 39
                               US-09-453-826-37
US-09-453-840-37
US-09-85-989-37
US-09-525-269A-12
US-09-525-269A-12
US-09-248-796A-23756
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US-09-106-568E-135
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US-08-127-351-53
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ORGANISM: Artificial Sequence
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Pred. No. 0.04;
0; Mismatches 1; Indels
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APPLICANT: Yeaman, Michael R.; APPLICANT: Shen, Alexander J.; TITLE OF INVENTION: Antimicrobial Peptides and Derived; TITLE OF INVENTION: Metapeptides; FILE REFERENCE: 66742-025(HR5614); CURRENT APPLICATION NUMBER: US/09/525,269A; CURRENT APPLICATION NUMBER: US/09/525,269A; PRIOR PILLING DATE: 2000-03-13; PRIOR PILLING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapoptides
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525, 269A
CURRENT FILING DATE: 2000-03-13
PRIOR PILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                      1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 14
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SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6743769
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ORGANISM: Artificial Sequence
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LENGTH: 18
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Antimicrobiccidal peptide designed in part upon
OTHER INFORMATION: microbiccidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial

OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-6
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84.6%; Pred. No. 0.1;
ive 1; Mismatches 1; Indels
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Sequence 6. Application US/09525269A;
Patent No. 6743769;
GENERAL INFORMATION:
APPLICANT: Seman, Michael R.;
APPLICANT: Seman, Michael R.;
TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HRS614);
CURRENT APPLICATION NUMBER: US/09/525,269A;
CURRENT APPLICATION NUMBER: US 09/025,319;
PRIOR APPLICATION NUMBER: US 09/025,319;
PRIOR FILING DATE: 1998-02-18;
NUMBER OF SEQ ID NOS: 39;
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6;
LENTH: 13
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APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SEQ ID NOS: 39
SEQ ID NO 5
IENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                               1 ALYKKFKKKLLKS 13
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                                                                                                                                                                                                                   Best_Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-525-269A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-525-269A-5
                                                                                                                                      US-09-525-269A-3
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PatentIn Release #1.0, Version #1.25
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Patent No. 5998381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALYKKWKNKLLKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94104
    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-233-203-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-760-903-2
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Patent No. 5409898

GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
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                                                                                                                                                              Gaps
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; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon interpretation: microbiocidal domains from platelet microbial corner information: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon interpretation microbiocidal domains from platelet microbial Transformation: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-4
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Pred. No. 0.59;
1; Mismatches 2; Indels
                                                                                                               Score 48; DB 4; Length 14;
Pred. No. 0.45;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09525269A; Patent No. 6743769; Fatent No. 6743769; GENERAL INFORMATION:
APPLICANT: Seman, Michael R.; APPLICANT: Shem, Alexander J.; TITLE OF INVENTION: Metapetides
TITLE OF INVENTION: Metapetides
TITLE OF INVENTION: Metapetides
TITLE OF INVENTION: Metapetides
TILLE REFRERNCE: 66742-025 (HRS614); CURRENT APPLICATION NUMBER: US/09/525,269A; CURRENT TILNG DATE: 1908-03-13
FRIOR APPLICATION NUMBER: US 09/025,319
FRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                 69.6%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.1%;
Best Local Similarity 76.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3005 First Avenue
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                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                2 LYRKFKONKLLK 12
                                                                                                                                                                                                      2 LYKKWKNKLLK 12
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CITY: Seattle
STATE: Washington
                                                                                                               Query Match
Best Local Similarity
Matches 9, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                     RESULT 7
US-09-525-269A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-233-203-7
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Gaps
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APPLICANT: SHEKHANI MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: PIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
ITILE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES: 9
NUMBER OF SEQUENCES: 9
NUMBER OF SEQUENCES: 9
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUNOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION 10705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFECATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FBB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 13-FBB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
TELEPHONE: 206/728-4800
TELEPHONE: 206/748-4800
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                                                                                                                                          FUGUATION PECTUS SEQUENCE 2, Application PC/TUS9610227
; Sequence 2, Application PC/TUS9610227
; GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: PRATZ, ROBERT W.
APPLICANT: PARAZ, SOBERT W.
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
APPLICANT: STAFFORD, DOUGLAS C.
AITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ALIPORNIA
COUNTRY: SAN FRANCISCO
STATE: CALIFORNIA
COMPUTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTRY: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PCT/US96/1027
FILING DATE: PRICATION DATA:
APPLICATION NUMBER: PCT/US96/1027
FILING DATE: 17-DEC-1993
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/482,191
FILING DATE: 17-DEC-1993
FILING DATE: 17-DEC-1993
FILING DATE: 17-DEC-1993
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FILING DATE: 17-DEC-1993
FILING DATE: 18-DEC-1993
FILING DATE:
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Pred. No. 3.2;
0; Mismatches
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US-08-760-903-3
'Sequence 3, Application US/08760903
; Patent No. 5998381
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76.9%;
1 ALYKKLLKKLLKS 13
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                    Score 43; DB 2; Length 18; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: PIGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: POGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:

ZIP: 94104

ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: DEATH SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FTLING PATE: 07-JUN-1995
FTLING PATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                 Query Match 62.3%; Score 43; DB Best Local Similarity 76.9%; Pred. No. 3.2; Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-070-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-08-482-191-2
; Sequence 2, Application US/08482191
; Patent No. 6579696
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               1 ALYKKWKNKLLKS 13
                                                                                                                                                                                                                                                                                                     1 ALYKKLLKKLLKS 13
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Best Local Similarity 76.9
Matches 10; Conservative
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-760-903-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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STRANDEDNESS: 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WILLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-482-191-2
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Gaps

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APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: SCHALES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFPORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
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                                                 FILING DATE: 07-001-1995
CLASSIFICATION 514
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA: 21-DEC-1993
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTONEN/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
RELECOMONICATION INFORMATION:
TELECOMONICATION INFORMATION:
TELECO
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PELLING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
UMBER: US/08/482,191
07-JUN-1995
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application PC/TUS9610227 GENERAL INFORMATION:
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76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 amino acida
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Best Local Similarity 76.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKKWKNKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ALYKKLLKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-482-191-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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APPLICANT: WILLIAMS, WOHAWMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
                                                         FIRCA, JOSEPH R.
ANDERSON, BYRON
NVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
                                                                                                                                                                                                                                                                                                                                                           CUNTRY: UNITED STATES OF AMERICA
ZULP: 94104
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEHLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: SOUNDOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION: ACCOUNTED TO THE
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ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                         E: MEDLEN & CARROLL, LLP
220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 n ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08482191
Patent No. 6579696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.3%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 19 amino acids
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Matches 10; Conservative
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                                                 APPLICANT: FIRCA, JÓSEPH
APPLICANT: ANDERSON, BYR
TITLE OF INVENTION: COMP
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CA
STREET: 220 MONTGOMERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                           CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sin
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APPLICANT: WILLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-760-903-3
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GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
COMPOSITONS AND METHODS FOR TREATING INPECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
       TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SET ITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beristol-Myers Squibb Company, Patent ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
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FILING DATE:
CLASSIFCATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321

FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020

FILING DATE: 23-FEB-1990
ATTORNEY AGENT INFORMATION:
NAMME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-233-203-8; Application US/08233203; Patent No. 5409898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: ON TELECOMMUNICATION: TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALYKKWKNKLLKS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
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STATE: Washingt
COUNTRY: USA
                                                                                                                                                                                                                                                               ZIP: 98121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 3.3;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7.4 Application US/09525269A; Batent No. 6743769; GENERAL INFORMATION: 6743769; GENERAL INFORMATION: APPLICANT: Seman, Michael R.; APPLICANT: Seman, Michael R.; TITLE OF INVENTION: Metapoptides TIVE OF INVENTION: Metapoptides; FILE REFERENCE: 66742-025 (HRS614); CURRENT APPLICATION NUMBER: US/09/525,269A; CURRENT APPLICATION NUMBER: US 09/025,319; PRIOR APPLICATION NUMBER: US 09/025,319; PRIOR PILING DATE: 1998-02-18; NUMBER OF SEQ ID NOS: 39; SOFTWARE: PastSEQ for Windows Version 4.0; SEQ ID NO 7; LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                              FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
PELIGATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
           APPLICATION NUMBER: US 08/164,067
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Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.9%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.3%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | |:|::||:|
1 ARYRKFRNKILRS 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.3
Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALYKKLLKKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US96-10227-3
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US-09-525-269A-7
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US-08-233-203-6
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Washington
COUNTEY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: INP PC COMPALIE
                                          REFERENCE/DOCKET NUMBER: ONOI
TELECOMPUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELERAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                   REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.5%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                           18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPB: peptide
; HYPOTHETICAL: YES
US-08-233-203-11
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                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                           LENGTH:
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Sequence 10, Application US/08233203
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Sequence 10. Sequence 10. Application US/08233203
Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequence 10. Sequenc
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAARE: Patentin Release #1.0, Version #1.25
SUBTRANE PATENTIN RAISE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W 32,928
REGISTRANCE/DOCKET NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Sattle Arenae
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FLING DATE: US-FEB-1991
PRIOR APPLICATION NUMBER: US/07/655,321
PRIOR APPLICATION NUMBER: US/07/655,321
PRILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOF, Brian W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Bristol-Myers Squibb Company, Patent
E: Department
3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,928
REPRENCE/POCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 206/448-4775
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.(
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKKWKNKLLK 12
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APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
                                   ö
Score 39; DB 1; Length 18;
Pred. No. 13;
                                   Indels
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CADRESSER: Bristol-Myers Squibb Company, Patent
ADDRESSER: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                   Mismatches
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US-09-525-269A-11
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APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                 Gaps
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      DB 1; Length 20;
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                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
    Score 39; DB 1
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-525-269A-11
; Sequence 11, Application US/09525269A
; Patent No. 6743769
; GENERAL INFORMATION:
                                                                                                                                                                                                                      Sequence 12, Application US/08233203 Patent No. 5409898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
....hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 amino acids
                      Best Local Similarity 75.0
Matches 9; Conservative
                                                                                    2 LYKKWKNKLLKS 13
                                                                                                                         4 LYKKLLKKLLKS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LYKKLLKKLLKS 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-233-203-12
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      Query Match
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METHODS FOR TREATING
3D BY ORGANISM SENSITIVE TO BETA-LACTAM
                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 4; Length 13;
Pred. No. 13;
0; Mismatches 3; Indels
APPLICANT: Shen, Alexander J.

TITLE OF INVENTION: Antinfcrobial Peptides and Derived;
TITLE OF INVENTION: Metapetides

TITLE OF INVENTION: Metapetides

FILE REFERENCE: 66742-025 (HRS614)

CURRENT APPLICATION NUMBER: US/09/525,269A

CURRENT APPLICATION NUMBER: US 09/025,319

FRIOR APPLICATION NUMBER: 1988-02-18

NUMBER OF SEQ ID NOS: 39

SEQ ID NOS: 39

SEQ ID NO 11

LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0,.Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHO,
TITLE OF INVENTION: INFECTIONS CAUSED BY
TITLE OF INVENTION: ANTIBIOTICS
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOR: Brian W
REGISTRATION NUMBER: 32,928
REPERENCE/DOCKET NUMBER: ON0063A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/07/655,321
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08233203 Patent No. 5409898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALYKKLFKKLLK 12
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SINLL...
CITY: Seattle
STATE: Washington
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GENEKAL.

APPLICANT: Date. Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Gornut, Isabelle
APPLICANT: Gornut, Isabelle
APPLICANT: Metz, Gunther
ITILE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
ITILE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds Lip
STREET: 1155 Avenue of the Americas
CITY: New York

NY
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TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/940,093
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,09
CLASSIFICATION DATA:
PRICH APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-
                                                                                                              Sequence 37, Application US/08940093
Patent No. 6037323
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 37, Application US/08940096
Patent No. 6046166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louir
APPLICANT: Sexul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: No. 6037323e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LYKKWKNKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LFREWLNELLEA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                        US-08-940-093-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-940-093-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/08940095

Sequence 37, Application US/08940095

Patent No. 6004925

GENERAL INFORMATION:

APPLICANT:

APPLICAN
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                                                                                                                                                                                                       53.6%; Score 37; DB 1; Length 18; 69.2%; Pred. No. 26; 7ative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 44;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: DISKCLE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRELSC Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,095
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 0091:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: No. 6004925e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.2%;
Best Local Similarity 41.7%;
                                                                                                                                                                                                                                                                                                                                  1 ALYKKWKNKLLKS 13
18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        1 ALYKKIIKKLLES 13
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:::| |:||:
5 LFREWLNELLEA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette
                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                         amino acid
GY: linear
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                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-940-095-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-940-095-37
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Sequence 37, Application US/09453605

Batent No. 6329341

GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sexul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.2%; Score 36; DB 3; Length 22; 41.7%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IRM Compatible
OPERATING SYSTEM: DOS
SOFTWARB: FRATESQ VEFRION 2.0
CURRENT APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-No. 6323941-1999
CLIASSIFICATION NUMBER: 08/940,095
RILING DATE: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: «Unknown»
TILING DATE: «Unknown»
REGISTRACE/COKET UNFORMATION:
NAME: COTTAXI, LAMIR A
REGISTRACE/COKET UNBERR: 30,742
RESTERRACE/COKET UNBERR: 30,742
                                                                                                 REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 009196-0006-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
TELEFAX: 6514 PENNIR
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: No. 6265377e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 258
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/9
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 41.7
Matches 5; Conservative
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S LFREWLNELLEA 16
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                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-465-719-37
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Rabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 3; Length 22;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                       CURREATING SYSTEM: DOS
SOFTWARE: FASTESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT:
APPLICATION NUMBER:
ATTORNEY AGENT:
ARGITSTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAK: 660-493-5556
TELERAK: 66141 PENNIE
INFORMATION FOR SEG ID NO: 37:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                  ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FARLSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
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Patent No. 6265377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: No. 6046166e
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MEDIUM TYPE: Diskette
                                                                                                                      ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 22 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.2
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:::| |:||::
5 LFREWLNELLEA 16
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CORRESPONDENCE ADDRESS:
                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                          USA
                                                                                 STATE: NY COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 26
US-09-465-719-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I ACONISTS AND THEIR
TITLE OF INVENTION: 274
CORRESPONDENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,136
FILING DATE: 29-SEP-1997
CLASSIFICATION: 514
                                                                                                                                                    Sequence 37, Application US/08940136 Patent No. 6518412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/09453841
Patent No. 6573239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 0091:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAK: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEGUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:::| |:||::
S LFREWLNELLEA 16
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   5 LFREWLNELLEA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                   US-08-940-136-37
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                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dascux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Kļaus
APPLICANT: Buttner, Isabelle
APPLICANT: Metz, Gunther
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APPLICANT: Sekul, Rear
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APPLICANT: Metz, Gunther
APPLICANT: Me
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                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATE:
FILLOR DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEPRAK: 650-493-5556
                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                            TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 37: US-09-453-605-37
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEB: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 37, Application US/09453838; Patent No. 6376464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
LENGTH: 22 amino acids
                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: No. 6376464e
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                      2 LYKKWKNKLLKS 13
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| LFREWINELLEA 16
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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US-09-453-838-37
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NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                SOFTWARE: FREESRO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY AGENT: INFORMATION:
NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 Avenue of the Americas CITY: New York
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COMPUTER: DE Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/09453826
Patent No. 6630450
GENERAL INFORMATION:
                                                                                                                                                                                                NAME: COTUZZI, LAUKA A
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 00915
TELECOMMUNICATION INFORMATION:
TELEFAX: 660-493-556
TELEFAX: 660-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: No. 6602854e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.2%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 41.7.
France 5; Conservative
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5 LFREWLNELLEA 16
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Patent No. 6602854
GENERAL INFORMATION:
APPLICANT: Betul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Buttner, Klaus
APPLICANT: Metz, Gunther
APPLICANT: Motourog, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                    TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
TUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 4; Length 22; Pred. No. 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                        AUDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMFUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,841
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFCATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAULA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
LEMEGHAY: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.2%;
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ZIF: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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Best Local Similarity 41.7:
--- hes 5; Conservative
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5 LFREWLNELLEA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
Dufourcq,
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US-09-453-833-37
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Gaps
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Outher
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
                                                    ö
Score 36; DB 4; Length 22; Pred. No. 44;
                                                    Indels
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Sequence 37, Application US/09865989

Patent No. 6734169

GENERAL INFORMATION:
APPLICANT: Danseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther, Labelle
Metz, APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I THEAT DYSLIPIDEMIC DISORDERS
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: 1BM COMPATIBLE
COMPUTER: 1BM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARRE: FASISEQ Vereion 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
FILING DATE: 17-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: No. 6734169e
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/09453834 Patent No. 6753313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE
N FOR SEQ ID NO: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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APPLICANT: Sekul, Renate
    5; Conservative
                                                               |:::| |:||:
| LFREWLNELLEA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYKKWKNKLLKS 13
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                                        2 LYKKWKNKLLKS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                           US-09-865-989-37
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    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Metz, Gunther
APPLICANT: Difourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                       DB 4; Length 22;
                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORWATION:
NAME: COTUZZI, LAURER: 30,742
REGISTRATION NUMBER: 009196-0004-999
TELECHONNIACATION INFORMATION:
TELECHONNIACATION INFORMATION:
TELECHONNE: 650-493-5556
                                                                                                                                                                                                                                     Score 36; DB 4
Pred. No. 44;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/453,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/09453840 Patent No. 6716816
TELEFAX: 650-493-5556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.2%;
                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: No. 6630450e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRIE COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: No. 6716816e
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5 LFREWLNELLEA 16
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                                                                                                                                         single
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 5; Conserva
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Best Local Similarity
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                                                                                                                    TYPE: amino a STRANDEDNESS:
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Sequence 214, Application US/09288143
Patent No. 6433139
GENERAL INFORMATION:
APPLICANT: Brewe et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT AFFILING DATE: 1999-04-08
EARLIER FILING DATE: 1999-04-08
EARLIER FILING DATE: 1998-04-08
EARLIER FILING DATE: 1990-0-08
EARLIER PRILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/661, 529
EARLIER APPLICATION NUMBER: 60/661, 529
EARLIER APPLICATION NUMBER: 60/61, 529
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
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EARLIER FILING DATE: 1997-10-09
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Best Local Similarity 66.7-
Thes 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                            2 LYKKWKNKLLKS 13
                                                                                                                                                                                                                                                                                              2 LYKRLFKKLIKS 13
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49 KQYKNKILK 57
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Best Local Similarity
Matches 6; Conserv
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US-09-248-796A-23756
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US-09-288-143-214
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APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
APPLICANT: Dufourcq, Jean
APPLICANTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
OF SEQUENCES: 258
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Sequence 12, Application US/09525269A

Sequence 12, Application US/09525269A

GENERAL INFORMATION:
APPLICANT: Seman, Michael R.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR564)
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12
LENTH: 13
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PRIOR APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION NUMBER: 009196-0004-999
TELECHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELERAX: 650-493-5556
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acide
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Pred. No. 44;
6; Mismatches
                                                                                                                                                                                                                                E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRREESQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 41.7
Matches 5; Conservative
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5 LFREWLNELLEA 16
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ADDRESSEE: Pennie &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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CITY: New York
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US-09-525-269A-12
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Sequence 23756, Application US/09248796A

Sequence 23756, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PAPLICATION NUMBER: US 60/074,725

PRIOR PAPLICATION NUMBER: US 60/096,409

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 23756

LIENGTH: 60
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                                                                                                                                                                                                                          Gaps
; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial ; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-569A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                           ZIP: 19899
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                       RESULT 41
US-08-985-526-11
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Sequence 135, Application US/09106568E

GENERAL INFORMATION:
APPLICANT: Bhattacharjee, J.
APPLICANT: Bhattacherjee, J.
APPLICANT: Bhattacherjee, Vasker
TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
TITLE OF INVENTION: METHODS AND REAGENTS
CURRENT APPLICATION NUMBER: US/09/106,568E
CURRENT APPLICATION NUMBER: US/69/106,568E
CURRENT FILING DATE: 1999-06-29
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Microsoft Word 97
LENGTH: 10
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Sequence 59280, Application US/09270767

GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Pacentin Ver. 2.0
SEQ ID NO 59280
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PEATURE:
; OTHER INFORMATION: Polypeptide segment of TYCA_BACBR shown in Pigure 4.
US-09-106-568E-135
                                                                                                                  Gaps
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                                                             Score 35; DB 4; Lengtn /v, Pred, No. 1.9e+02;
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Pred. No. 41;
1; Mismatches 2; Indels
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Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 3;
                                                                           Query Match
Best Local Similarity 42.1%; Pred. No. 1.96
Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Drosophila melanogaster US-09-270-767-59280
                                                                                                                                                                                 43 AIQKKWPLYMSTKNTILKA 61
                                                                                                                                                      1 ALYKKW-----KNKLLKS 13
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Best Local Similarity 66.7"
----hes 6; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-288-143-214
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US-09-106-568E-135
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James A
CARRIER: DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
THERAPY
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Batent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BNTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT FILLIG DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.8e+02;
2; Mismatches 3
                                                                TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC FITTLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STREE: Delaware
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.3%; Score 34; DB 3; 61.5%; Pred. No. 1.8e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-UUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCMORTOW Jr., RODERT G
TELECOMMUNICATION:
Sequence 11, Application US/08985526
Patent No. 6080728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6642
EBNCTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (302) 658-9141
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16 SLYKKIIKKLLES 28
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Matches 8; Conservative
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US-08-127-351-53
; Sequence 53, Application US/08127351
; Sequence 53, Application US/08127351
; Patent No. 5449761
; Patent INFORMATION:
; APPLICANT: BELINKA Jr, BENJAMIN A. APPLICANT: CUGGHLIN, DANIEL J. APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: ALVAREZ, VERNON L.
; TITLE OF INVENTION: CONSTRUCTS
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & ADDRESSEE: NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 13;
Pred. No. 74;
1; Mismatches 3; Indels
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STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 19-FEB-1990
ATTORNEY AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 0N0063A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAȚING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                              3005 First Avenue
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                                                    CITY: Seattle
STATE: Washington
COUNTRY: USA
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INFORMATION F
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Patent No. 526251

CENERAL INFORMATION:
CENERAL INFORMATION:
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CENERAL INFORMATION:
CENERAL OF INVENTION:
CONTRIBUTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
CENERAL CAN MAINTION:
CORRESPONDENCE ADDRESS:
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VERYTION: COMPOSITONS AND METHODS FOR TREATING
VERYTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
VENTION: ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                    Gaps
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    Pred. No. 2.7e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUNTERT SEADABLE FORM:

MEDIUM TYRE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: 19910607
CLEASTRICATION NUMBER: US/07/714,540
FILING DATE: 19910607
CLEASTRICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 31,292
REGISTRATION NUMBER: 31,292
REGISTRATION NUMBER: 31,292
REGISTRATION NUMBER: 31,292
REGISTRATION NUMBER: 31,292
REGISTRATION NUMBER: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.8%; Score 33; DB 66.7%; Pred. No. 69; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AN TITLE OF INVENTION: INFECTIONS AN TITLE OF INVENTION: ANTIBIOTICS AND A
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTICS:
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                   33 KKWKNR 38
                                                                                                                                              4 KKWKNK 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 44
US-08-233-203-1
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Gaps

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### APPLICATION NUMBER: US/08/127,351
| PILING DATE: 28-SEP-1993 |
| CLEASSIFICATION: 28-SEP-1993 |
| ATCORNEY/AGENT INFORMATION: NAME: Villacorta, Gilberto M. |
| REGISTRATION NUMBER: 34,038 |
| REFERENCE/DOCKET NUMBER: 4980-004-44 |
| TELECOMMUNICATION INFORMATION: |
| TELEPHONE: (703) 413-3000 |
| TELEPHONE: (703) 413-3000 |
| TELEPHONE: (703) 413-220 |
| TELEPHONE: (703) 413-220 |
| TELEPHONE: (703) 413-200 |
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| TELEPHONE: (703) 413-300 |
| TENEMINE: (703) 413-300 |
| TELEPHONE: (703) 413-300 |
| TENEMINE: ```

Search completed: May 16, 2005, 08:40:41 Job time : 14.8966 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:38:44; Search time 48.8621 Seconds (without alignments) 88.876 Million cell updates/sec Run on:

1 ALYKKWKNKLLKS 13 US-09-648-816B-9 69 Title: Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

1432185 segs, 334051727 residues Searched:

527782 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description                      | Sequence 158393,     | Sequence 125, App  | Sequence 125, App | 124,               | Sequence 124, App | equence 48620, A    | Sequence 37, Appl | Sequence 37, Appl | Sequence 37, Appl | Sequence 37, Appl | Sequence 37, Appl | Sequence 37, Appl | Sequence 37, Appl |
|----------------------------------|----------------------|--------------------|-------------------|--------------------|-------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| Dec                              |                      | ٠,                 | ٠,                | ٠,                 | 0,                | Š                   | 0,1               | ٠,                | 0,                | ٠,                | ٠,                | ٠,                | •,                |
| ID                               | US-10-424-599-158393 | US-09-820-053A-125 | US-10-109-171-125 | US-09-820-053A-124 | US-10-109-171-124 | US-09-864-761-48620 | US-09-865-989-37  | US-09-865-989-37  | US-10-099-574A-37 | US-10-099-836B-37 | US-10-283-599-37  | US-10-802-080-37  | US-10-801-897-37  |
| BB                               | 15                   | 10                 | 14                | 70                 | 14                | σ                   | 2                 | ==                | 14                | 15                | 15                | 16                | 9†                |
| *<br>Query<br>Match Length DB ID | 73                   | 16                 | 16                | 17                 | 17                | 37                  | 22                | 22                | 22                | 22                | 22                | 22                | 22                |
| &<br>Query<br>Match              | 6.09                 | 55.1               | 55.1              | 55.1               | 55.1              | 55.1                | 52.2              | 52.2              | 52.2              | 52.2              | 52.2              | 52.2              | 52.2              |
| Score                            | 42                   | 38                 | 38                | 38                 | 38                | 38                  | 36                | 36                | 36                | 36                | 36                | 36                | 36                |
| Result<br>No.                    |                      | 7                  | m                 |                    | S                 | 9                   | 7                 | ω                 | თ                 | 10                | 11                | 12                | 13                |

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| 7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 15442,<br>Sequence 50, Appl<br>Sequence 31, Appl<br>Sequence 9, Appli<br>Sequence 1, Appli<br>Sequence 31, Appli<br>Sequence 8, Appli<br>Sequence 8, Appli              |
| 7 US-10-937-767-37<br>7 US-10-937-767-37<br>5 US-10-424-599-2206<br>5 US-10-424-599-2206<br>5 US-10-424-599-22443<br>5 US-10-424-599-22443<br>6 US-10-424-599-2443<br>6 US-10-424-599-2243<br>6 US-10-424-599-22443<br>1 US-09-84-429-214<br>4 US-10-124-599-2613<br>1 US-09-864-761-4094<br>1 US-09-864-761-4013<br>1 US-09-864-761-4013<br>1 US-09-864-761-4013<br>1 US-09-864-761-4013<br>2 US-10-424-599-2269<br>5 US-10-424-599-2269<br>6 US-10-424-599-2269<br>6 US-10-424-599-2269<br>6 US-10-424-599-2269<br>6 US-10-424-599-2269<br>6 US-10-424-599-2269<br>6 US-10-424-599-2269 | 16 US-10-38-03-156452<br>16 US-10-38-037-50<br>9 US-09-765-6148-31<br>9 US-09-925-715-27<br>13 US-10-036-865-9<br>15 US-10-382-20-1<br>16 US-10-722-075-31<br>14 US-10-131-546-8 |
| 0.000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 69<br>74<br>113<br>113<br>113<br>118                                                                                                                                             |
| 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 3.34<br>3.33<br>3.33<br>3.33<br>3.34<br>4.44<br>4.47<br>4.47                                                                                                                     |
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## ALIGNMENTS

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Sequence 158333, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21 (5323) B
CURRENT FILING DATE: 2003-04-28
UNDER OF SEQ ID NOS: 285684
SEQ ID NO 158393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 15; Length 73;
Pred. No. 82;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_114047C.1.pep
US-10-424-599-158393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.9%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max
US-10-424-599-158393
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Sequence 125, Application US/09820053A; Publication No. US20030083243A1 :|||:|||: | 52 IYKKFKNKIKRS 63 US-09-820-053A-125 RESULT 2 a

2 LYKKWKNKLLKS 13

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55.1%;
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Similarity 63.6%;
7; Conservative
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                  ; OTHER INFORMATION: AMIDATION US-09-820-053A-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (17)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                          2 LYKKWKNKLLK 12
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                                                                              Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-864-761-48620
LOCATION: (17)
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Publication No. US20030109452A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE FILE REFERENCE: HELX028
FILE REFERENCE: HELX028
CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT PILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO. 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 82;
                                                                                                                                                                                                                                                                                                                    55.1%; Score 38; DB 10; Length 16; 63.6%; Pred. No. 82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-109-820-053A-124
Sequence 124, Application US/09820053A
Publication No. US20030083243A1
GENERAL INFORMATION:
TILE OF INVENTION: SHORT BIOACTIVE PEPTIDES
TILE REPRENCE: HELXO27
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT PILIG DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 124
LENGTH: 17
                APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELXO27
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                          ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-09-820-053A-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: SYNTHETIC SEQUENCE US-10-109-171-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: SYNTHETIC SEQUENCE NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                               TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.1%;
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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2 LWKKWAKKWLK 12
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2 LWKKWAKKWLK 12
GENERAL INFORMATION:
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                                                                                                                                                       SEQ ID NO 125
LENGTH: 16
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US-91-814-714-48620, Application US/09864761

j Sequence 48620, Application US/09864761

j Patent No. US20020048763A1

j GENERAL INFORMATION:

j APPLICANT: Penn, Sharron G.

j APPLICANT: Rank, David R.

j APPLICANT: Hannel, David R.

j APPLICANT: Hannel, David R.

j APPLICANT: Hannel, David R.

j APPLICANT: Hannel, David R.

j APPLICANT: Hannel, David R.

j TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FRICK APPLICATION NUMBER: US 60/180,312

PRIOR PILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30
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Sequence 124, Application US/10109171

Sequence 124, Application US/10109171

Sequence 124, Application US/10109171

GENERAL INFORMATION:

TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE

TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE

CURRENT APPLICATION UNMBER: US/10/109,171

CURRENT FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 165

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 124

LENGTH: 17
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Pred, No. 86;
   Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
Score 38; DB 10;
Pred. No. 86;
1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD_RES
```

```
Butther, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROPEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPEDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                009196-0006-999
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.2%; Score 36; DB 10;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRACSCO VEFION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <u >
CUASSIFICATION: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: No. US20030008827Ale
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                            APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT: 6
US-09-86-37
Sequence 37, Application US/09865989
; Publication No. US20040029807A9
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
Sexul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 22 amino acide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S LPREWLNELLEA 16
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Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: MAP TO AC007225.2
CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
OTHER INFORMATION: BST HUMAN HIT: AU118020.1, EVALUE 4.00e-15
CTHER INFORMATION: SWISSPROT HIT: Q9Y5NG, EVALUE 3.00e-16
US-09-864-761-48620
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PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
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FILING DATE: 25-May-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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Publication No. USZO0030008827A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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21 YEEWKRKILEN 31
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ORGANISM: Homo sapiens
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Best Local Similarity
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TITLE OF INVENTION:
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APPLICANT:
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                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
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                                                                                                                                       Score 36; DB 11; Length 22; Pred. No. 2.1e+02; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            009196-0005-999
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  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. US20040029807A9e
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-865-989-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,574A
FILING DATE: 29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: No. US20030060604Ale
                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/10099574A Publication No. US20030060604A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGHMAN AND TANK TO THE TELEPHONE: G0021, LBUTA A REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET UNBER: 005
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                         Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
TYPE: amino acid
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LFREWLNELLEA 16
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LFREWLNELLEA 16
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APPLICATION NUMBER:
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Best Local Similarity
Matches 5; Conserv
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                                                        APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPEDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Metz, Gunther
Nofourcq, Jean
NYENTION: GENE THERAPY APPROACHES TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099, 836B
FILLING DATE: 28-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: «Unknown»
                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: No. US20030203842Ale

SEQUENCE DESCRIPTION: SEQ ID NO: 37

US-10-099-836B-37
Sequence 37, Application US/10099836B Publication No. US20030203842A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/10283599 Publication No. US20030208059A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LYKKWKNKLLKS 13
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APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Suture, Klaus
APPLICANT: Suture, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 22;
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                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/COCKET NUMBER: 009196-0004-999
TELECOMPUNICATION INFORMATION:
TELEFAX: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 650-493-556
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TELEFAX: 650-493-556
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TELEFAX: 650-493-556
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Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 6; Mismatches 1.
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/802,080
FILING DATE: 15-Mar-2004
CLASSIFICATION: «Inknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE: 01-DEC-1999
APPLICATION NUMBER: 08/940,095
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-802-080-37
         FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/801,897
FILING DATE: 15-Mar-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 37, Application US/10801897; Publication No. US20040198662A1; GENERAL INFORMATION:
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5 LFREWLNELLEA 16
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-801-897-37
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Publication No. US20040181034A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
    SUPPLY APOLIPOPROTEIN A-1 AGONISTS AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS. 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 15; Length 22;
Pred. No. 2.1e+02;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,136
FILING DATE: 29-58P-1997
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAUZE A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0007-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
TITLE OF INVENTION: SUPPLY APOLIPOPROTEI
TITLE OF INVENTION: USE TO TREAT DYSLIP!
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                    ZUP: 10136-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-0CT-2002
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: No. US20030208059Ale
US-10-283-599-37
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 amino acids
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TOPOLOGY: linear
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US-10-425-114-37094
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      US-10-937-767-37
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Publication No. US20050080013A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                Score 36; DB 16; Length 22;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                          1; Indels
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKGT NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-556
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/ASENT INFORMATION:
NAME: COTUZZI, LABLE A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/937,767
FILING DATE: 08-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENČE ADDRESS:
ADDRESSES: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 08-SEP-2004
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/940,096
FILING DATE: 29-SEP-1997
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 41...
Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  2 LYKKWKNKLLKS 13
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5 LFREWLNELLEA 16
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STRANDEDNESS: single
                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                               MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: None
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US-10-937-767-37
                                                                                                                                                                                                                                                                                       US-10-801-897-37
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Sequence 37094 Application US/10425114

Sequence 37094 Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zoreen, Serven E

APPLICANT: Soreen, Serven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Part Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 37094
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     Length 22;
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                                                                                                                                                                                                                                                          Sequence 126. Application US/10884355A

Publication No. US20050058689A1

GENERAL INPORMATION:
APPLICANT: Reactive Surfaces, Ltd.
TILLE OF INVENTION: Antitungal Paints and Coatings
FILE REFRENCE: RACT-00400

CURRENT APPLICATION NUMBER: US/10/884,355A

CURRENT FILING DATE: 2004-07-02

PRIOR APPLICATION NUMBER: 60/485,234

PRIOR FILING DATE: 2003-07-03

NUMBER OF SEQ ID NOS: 199

SOFTWARE: Patentin Version 3.3

SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: LIB3242-107-C6_FLI.pep
US-10-425-114-37094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 17;
Pred. No. 3.9e+02;
1; Mismatches 3;
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Pred. No. 4.7e+02;
2; Mismatches 3;
Score 36; DB 17;
Pred. No. 2.1e+02;
6; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Scorpion Parabutoporin US-10-884-355A-126
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity, 63.6%;
Matches 7; Conservative
  Query Match 52.2
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                 2 LYKKWKNKLLKS 13
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S LFREWLNELLEA 16
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7 LKKAWKSKLAK 17
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ORGANISM: Glycine max
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US-10-424-599-231840
US-10-424-599-231840
US-10-424-599-231840, Application US/10424599
Sequence 231840, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 231840
LENGTH: 64
                     APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Exovalic David K
APPLICANT: Tou Vihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 244348
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Pred. No. 5.3e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT3847_62673C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Clone ID: PAT_MRT3847_51374C.1.pep
US-10-424-599-231840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 15;
Pred. No. 5.2e+02;
2; Mismatches 3
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; Sequence 108293, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.5%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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Li, Ping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 YVOWKNKCSKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | | | | | 46 MYNKWKN 52
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-424-599-244348
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APPLICANT:
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Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovala Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
TITLE Acid Molecules Associated With
TITLE Acid Molecules Associated With
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TITLE Acid Molecules Associated With
TITLE Acid Molecules Associated With
TITLE Acid Molecules Associated With
TITLE Acid Molecules Associated With
TITLE Acid Molecules Associated With
                 RESULT 17
US-10-424-599-220615
Sequence 220615, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(53223)8
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.2%; Score 36; DB 15; Length 62; 40.0%; Pred. No. 5.2e+02; ative 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_41246C.1.pep
US-10-424-599-220615
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US-10-424-599-191534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(62)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 244348, Application US/10424599
; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.2
Best Local Similarity 40.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.9
Matches 6; Conservative
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47 LYRDWQNRII 56
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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US-10-424-599-244348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
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LENGTH: 62
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                                                                                                                                                                Length 73;
                                                                                                                                                                                                                         2; Indels
                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_97882C.1.pep
US-10-424-599-283343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROBER et al.

APPLICANT: ROBER et al.

TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REPERENCE: P5018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-10-09
PRIOR PILING DATE: 1999-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
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PRIOR PILING DATE: 1997-10-09
                                                                                                                                                             DB 15;
6e+02;
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Publication No. US20030078386A1
GENERAL INFORMATION:
APPLICANT: Rubin et al.
TITLE OF INVENTION: Secreted Protein HPEAD48
FILE REPERENCE: PZ018P1D1
CURRENT APPLICATION NUMBER: US/10/150,111
CURRENT FILING DATE: 2002-05-20
FRIOR APPLICATION NUMBER: 09/288,143
PRIOR APPLICATION NUMBER: 09/288,143
PRIOR APPLICATION NUMBER: PCT/US98/21142
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                      1; Mismatches
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                                                                                                                                                             Score 36;
Pred. No. 6
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US-09-984-429-214
Sequence 214, Application US/09984429
Publication No. US20040010132A1
GENERAL INFORMATION:
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Best Local Similarity 42.1%;
Matches 8; Conservative 3
                                                                                                                                                             52.2%;
70.0%;
                                                                                                                                                                Query Match 52.2
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                    3 YKKWKONKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                  ORGANISM: Glycine max FEATURE:
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US-10-150-111-214
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21/53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 108293

LENGTH: 64
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 283343
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cov vinus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFREENCE: 38-21(53233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 165089
LENGTH: 66
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Pred. No. 5.5e+02;
0; Mismatches 1; Indels
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pred. No. 5.3e+02;
2; Mismatches 4; Indels
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US-10-424-599-165089
                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_12560C.1.pep
US-10-437-963-108293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 ALFOKWGNPFFK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALYKKWKNKLLK 12
                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 LYKKWGN 59
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Gaps

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GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Polypeptide segment of TYCA_BACBR shown in Figure 4. US-09-994-595-135
                                                                                                                                                                                                                                                                                                                                                                                            49.3%; Score 34; DB 10; Length 10; 66.7%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR PELLING DATE: 2001-05-23
PRIOR PELLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-06-36
PRIOR PLING DATE: 2000-06-36
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
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PRIOR PLING DATE: 2001-01-30
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PRIOR PELICATION NUMBER: PCT/USO1/00668
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: ZOO1-01-30
PRIOR PELING DATE: ZOO1-01-30
PRIOR PELING DATE: ZOO1-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PELING DATE: ZOO1-01-30
PRIOR PELING DATE: ZOO1-01-30
PRIOR PELING DATE: ZOO0-06-30
PRIOR PELING DATE: ZOO0-06-31
PRIOR PELING DATE: ZOO0-06-31
PRIOR PELING DATE: ZOO0-06-31
PRIOR PELING DATE: ZOO0-06-30
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PRIOR PELING DATE: ZOO0-06-30
PRIOR PELING DATE: ZOO0-06-30
PRIOR PELING DATE: ZOO0-06-30
PRIOR PELING DATE: ZOO1-01-29
PRIOR PELING DATE: ZOO1-01-29
PRIOR PELING DATE: ZOO1-01-29
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         CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION WUMBER: 08/650,809
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Microsoft Word 97
SEQ ID NO 135
LENGTH: 10
                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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US-09-864-761-40944
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Sequence 266178, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Acvalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 266178
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US-09-994-595-135
Sequence 135, Application US/09994595
Publication No. US2003003981A1
GENERAL INFORMATION:
APPLICANT: Bhatcacharjee, J.
APPLICANT: Bhattacherjee, Vasker
TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
TITLE OF INVENTION: A BIOLOGICAL SAMPLE
FILE REFERENCE: 96,247-A
CURRENT APPLICATION NUMBER: US/09/994,595
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Pred. No. 8.2e+02;
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US-10-424-599-266178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
PRIOR PRILING DATE: 1997-10-09
PRIOR PRILING DATE: 1997-10-09
PRIOR PRILING DATE: 1997-10-09
PRIOR PLILING DATE: 1997-10-09
PRIOR PLILING DATE: 1997-10-09
PRIOR PLILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR PRILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SEQ ID NO 214
LENGTH: 70
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43 AIQKKWPLYMSTKNTILKA 61
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42.1%;
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Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Glycine max
FEATURE:
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US-10-424-599-266178
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APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yonganing
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 31
US-09-864-761-47136
US-09-864-761-47136
Sequence 47136, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, Benome-Derived Single Exon NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acountica-X-1.
CURRENT PILING DATE: 2001-05-23
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                     Length 30;
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OTHER INFORMATION: MAP TO AC006084.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.44
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ 1D NOS: 49117
SEQ TANNOMAX Sequence Listing Engine vers. 1.1
SEQ 1D NO 48193
LENGTH: 30
                                                                                                                                                                                                                                                                                                                  Score 34; DB 9;
Pred. No. 5.3e+02;
1; Mismatches 2
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Pred. No. 6.2e+02;
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CURRENT APPLICATION NUMBER: US/10/001,835

CURRENT FILING DATE: 2001-11-20

FRIOR APPLICATION NUMBER: 60/249,997

PRIOR APPLING DATE: 2000-11-20

NUMBER OF SEQ ID NOS: 228

SEQ ID NO 119

LENGTH: 36
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PRIOR APPLICATION WUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION WUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 119, Application US/10001835 Publication No. US20020160387A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     49.3%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 41.7
Matches 5; Conservative
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                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                     US-09-864-761-48193
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US-10-001-835-119
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APPLICANT: Rank, David R.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                              OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.81
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EST_HUMAN HIT: AM875651.1, EVALUE 2.10e-02
US-09-864-761-40944
                                                                                                                                                                                                                                                                                                                                                                                        49.3%; Score 34; DB 9; Length 29; ilarity 50.0%; Pred. No. 5.1e+02; Conservative 3; Mismatches 2; Indels
  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 40944
LENGTH: 29
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DR FILING DATE: 2000-08-03
DR APPLICATION NUMBER: GB 24263.6
DR APPLICATION NUMBER: US 60/236,359
DR FILING DATE: 2000-09-27
DR APPLICATION NUMBER: US 60/236,359
DR FILING DATE: 2000-09-27
DR APPLICATION NUMBER: PCT/US01/00666
DR APPLICATION NUMBER: PCT/US01/00666
DR APPLICATION NUMBER: PCT/US01/00667
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00669
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APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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APPLICATION NUMBER: US 60/207,456
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                           MAP TO AL137248.4
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10 IMKQWRNSLL 19
                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                           OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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US-09-864-761-48193
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Sequence 226920, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Stou Yihua
APPLICANT: Stou Yihua
APPLICANT: Cavorongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
FILE REFERENCE: 2003-04-28
CURRENT PILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
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                                                           COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION APPLICATION APPLICATION NUMBER: US/08/985,526
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY AGENT INFORMATION:
NAME: MCMOXION JT., ROBERT G
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 49.3%; Score 34; DB 13; Length 46; Best Local Similarity 61.5%; Pred. No. 7.7e+02; Matches 8; Conservative 2; Mismatches 3; Indels
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US-10-424-599-226920
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Pred. No. 8.3e+02;
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; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 46 amino acids
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55.6%;
                  COMPUTER READABLE FORM:
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16 SLYKKIIKKLLES 28
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Best Local Similarity 55.6
Matches 5; Conservative
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34 FLRWENKLL 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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US-10-424-599-226920
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US-10-424-599-236980
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Publication No. US2002015156A1
GENERAL INFORMATION:
APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
THERAPY
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.63
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN PLACEMYA, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.63
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Pred. No. 7e+02;
2; Mismatches 2; Indels
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-07
PRIOR PILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.3%;
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ZIP: 19899
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

GURRENT APPLICATION NUMBER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 156452

LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: SITE
LOCATION: (12)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-1414
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US-10-437-963-156452
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                                                                                                                                                                                                           TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-1.2
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR PILING DATE: 2000-12-21
PRIOR PILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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Sequence 50, Application US/10398037
Publication No. US20040138414A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS; YUE, Henry;
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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61 LYKKYKN 67
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US-10-437-963-156452
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us-09-648-

APPLICANT: La Rosa Thomas J
APPLICANT: Acvalic David K
APPLICANT: Acvalic David K
APPLICANT: Cao Vihua
APPLICANT: Cao Vinua
ATILE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 235980
LENOTH: 52
TYPE
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Yahua
APPLICANT: Zhou, Yahua
APPLICANT: Zhou, Yahua
APPLICANT: Gao, Yongwei
APPLICANT: Wai wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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US-10-424-599-236980
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OTHER INFORMATION: Clone ID: PAT_MRT4530_28529C.1.pep
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OTHER INFORMATION: ungure at all Xaa locations
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; Publication No. US20040010134A1
; GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 125933
LENGTH: 66
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Best Local Similarity 58.3
Matches 7; Conservative
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17 KRWRRLLSS 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
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US-10-437-963-125933
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FILING DATE: <URKNOWN>
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
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ORGANISM: Artificial Sequence
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                                   Ouery Match
Best Local Similarity 66.7-
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 13
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STATE: Delaware
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            US-09-765-614B-31
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TANG, Y. Tom; NGUYEN, Danniel B.;
YAO, Monique G.; XU, Yuming;
TRIBOULEY, Catherine M.; SANJANWALA, Madhusudan M.;
CHAWLA, Narinder K.; BAUGHW, Mariah R.;
SAPPERSTEIN, Stephanie K.; LAL, Preeti G.;
THORNTON, Michael B.; GANDHI, Ameena R.;
RAWKUMAR, Jayalaxmi; ELLIOTT, Vicki S.;
RAWKUMAR, Jayalaxmi; ELLIOTT, Vicki S.;
ARVIZU, Chandra S.; THANGAVELU, Kavitha;
GIETZEN, Kimberly J.; DING, Li,
ALVOUNG, Janice K.; TRAN, Bao;
POLICKY, Jennifer L.; LEE, Sally;
LU, Dyung Aina M.; BURCRAD, Mell;
WARKEN, Bridget A.; GURURAJAN, Rajagopal;
DUGGAN, Brendan M.; HONCHELL, Cynthia D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.3%; Score 34; DB 16; Length 74; 85.7%; Pred. No. 1.2e+03;
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Patent No. US20020102215A1
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT PILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 31
SEQ ID NOS: 31
SEQ ID NOS: 31
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:Platelet
OTHER INFORMATION: binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 4102938CD1
US-10-398-037-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT PILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30042
PRIOR PILING DATE: 2001-09-25
PRIOR PLING DATE: 2001-09-25
PRIOR PELICATION NUMBER: US 60/24,218
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-09-29
PRIOR PLING DATE: 2000-10-11
PRIOR PLING DATE: 2000-10-11
PRIOR PLING DATE: 2000-10-11
PRIOR PLING DATE: 2000-10-12
PRIOR PLING DATE: 2000-10-12
PRIOR PLING DATE: 2000-10-17
PRIOR PRILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PERL PROGRAM
SSOFTWARE: PERL PROGRAM
SSOFTWARE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HAFALIA, April J.A.
TITLE OF INVENTYON: SECRETED PROTEINS
TITLE REFERENCE: PI-0240 USN
CURRENT APPLICATION NUMBER: US/10/398,037
CURRENT FILING DATE: 2003-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:||
68 LYKKYKN 74
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Matches 6; Conserv
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US-09-765-614B-31
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Sequence 9, Application US/10036869
Publication No. US2002015156A1
GENERAL INFORMATION:
APPLICANT: Mixson, James A
TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/09925715
Patent No. US20020102217A1
GENERAL INFORMATION
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/206
CURRENT APPLICATION NUMBER: US/09/925,715
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:Platelet
OTHER INFORMATION: binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 47.8%; Score 33; DB 9; Length 13; Best Local Similarity 66.7%; Pred. No. 3.5e+02; Matches 8; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/036,869
FILING DATE: 29-No. US20020151516A1-2001
CLASSIFICATION: <u >Unknown></u>
Score 33; DB 9; Pred. No. 3.5e+02;
                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/985,526
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Gaps

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Sequence 8, Application US/10131546
; Sequence 8, Application US/20030103955A1
; GENERAL INFORMATION:
; APPLICANT: CYT, John E.
; APPLICANT: CYT, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: USING HYDROPHILC THIOETHERS AND HYDROPHILC 6-HYDROXY
; TITLE OF INVENTION: USING HYDROPHILC THIOETHERS AND HYDROPHILC 6-HYDROXY
; TITLE OF INVENTION: USING HYDROPHILC THIOETHERS AND HYDROPHILC 6-HYDROXY
; TITLE OF INVENTION: USING HYDROPHILC THIOETHERS AND HYDROPHILLC 6-HYDROXY
; FILLE REFERENCE: 09744-018001
; CURRENT PELLON NUMBER: US/02-04-24
PRIOR FILLING DATE: 2000-10-24
; PRIOR FILLING DATE: 2001-10-24
; PRIOR FILLING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PRESENCE for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
                                                                                                                                                                                                                                                                                          Length 18;
                                                                             Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                             Score 33; DB 16;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 14;
Pred. No. 4.7e+02;
1; Mismatches 3
                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic construct US-10-131-543-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
; OTHER INFORMATION: Sequence:Platelet; OTHER INFORMATION: binding peptide US-10-722-075-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 47.8%;
Similarity 66.7%;
8; Conservative
                                                                                  47.8%;
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                                                                             Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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Sequence 1, Application US/10382240;
Bublication No. US20030216298A1;
GENERAL INFORMATION:
APPLICANT: BIOSIGHT LTD.;
TITLE OF INVENTION: PEPTIDE CONJUGATED ANTI-CANCER PRODUCTS;
TITLE REFREENCE: 85189-4400;
CURRENT APPLICATION NUMBER: US/10/382,240;
CURRENT FILING DATE: 2003-03-05;
PRIOR APPLICATION NUMBER: PCT/1L01/00839;
PRIOR APPLICATION NUMBER: PCT/1L01/00839;
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                Score 33; DB 13; Length 13;
Pred. No. 3.5e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.8%; Score 33; DB 15; Length 13; 66.7%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31. Application US/10722075
Publication No. US20040141922A1
GENERAL INFORMATION:
APPLICANT: Wycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: agence
TITLE OF INVENTION: agence
FILLE REFERENCE: REF/Klavenes8/054
CURRENT APPLICATION NUMBER: US/10/722,075
CURRENT PILING DATE: 2003-11-26
PRIOR PILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-10-036-869-9
                       NAME: MCMOrrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
                                                             TELEPHONE: (302) 658-9141
TELEFAR: (302) 658-5613
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                               LENGTH: 13 amino acids TYPE: amino acid
      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 13
                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                          8; Conservative
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          2 LYKKIIKKLLES 13
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 43
US-10-722-075-31
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US-10-382-240-1
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US-10-131-546-8
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0; Gaps Query Match

47.8%; Score 33; DB 14; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 8; Conservative 1; Mismatches 3; Indels

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2 LYKKWKNKLLKS 13 |||| |||| ||||| 7 LYKKIIKKLLES 18

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Search completed: May 16, 2005, 09:23:42 Job time : 48.8621 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 11.2069 Seconds (without alignments) 111.611 Million cell updates/sec Run on:

US-09-648-816B-9 69 Title: Perfect score: Sequence:

1 ALYKKWKNKLLKS 13

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

22893 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        |       | d     |              |   | 074    |                    |
|--------|-------|-------|--------------|---|--------|--------------------|
| Result |       | Query |              |   |        |                    |
| No.    | Score | Match | Match Length | 8 | ΩI     | Description        |
| -      | 37    | 53.6  | 34           | ~ | 70239  |                    |
| 7      | 37    | 53.6  | 74           | 0 | IS7554 |                    |
| e      | 34    | •     | 67           | N | T40218 | probable ATP synth |
| 4      | 33.5  | 48.6  | 55           | ~ | H90520 | _                  |
| 5      | 33    | 47.8  | 20           | 7 | G97836 | _                  |
| 9      |       | 47.8  | 63           | N | AG1703 | _                  |
| 7      | 32    | 46.4  | 63           | 7 | AG1332 | _                  |
| 80     | 32    | 46.4  | 69           | 7 | A05061 | hypothetical prote |
| σ      | 32    | 46.4  | 74           | ~ | B42517 |                    |
| 10     |       | ٠     | 37           | ~ | JU0329 | hypothetical 4.4K  |
| 11     | 31    | 44.9  | 51           | ~ | G69133 | ribosomal protein  |
| 12     |       | 44.9  | 53           | ~ | I59604 | glutamate receptor |
| 13     | 31    | 44.9  | 54           | ~ | S34541 | _                  |
| 14     | 31    | 44.9  | 26           | ~ | AH1648 | hypothetical prote |
| , 15   | 31    | 44.9  | 57           | ~ | C97937 |                    |
| 16     | 31    |       | 62           | ~ | C75106 | ribosomal protein  |
| 17     | 31    | 44.9  |              | 7 | C71028 | ribosomal protein  |
| 18     | 31    | 44.9  |              | ~ | S61085 | M protein precurso |
| .19    | 31    | ٠     | 99           | ~ | 815538 | n.                 |
| 20     | 31    | •     | 67           | 7 | A25188 | H+-transporting tw |
| 21     | 31    | 44.9  | 70           | ~ | S61080 | M protein precurso |
| 22     | 30    |       | 57           | Н | TIEPVA | venom basic protei |
| 23     | 30    | •     | 57           | N | C97813 | hypothetical prote |
| 24     | 30    | •     | 61           | ~ | H97283 | S                  |
| 25     | 30    | 43.5  | 61           | ~ | 872338 | hypothetical prote |
| 56     | 30    |       | 62           | ~ | F70442 | æ                  |
| 27     | 30    |       | 63           | 7 | G96517 |                    |
| 28     | 30    | 43.5  | 65           | 7 | S78743 | protein YCR099c -  |
| 29     | 29    | 42.0  | 20           | 7 | PC2248 | lambda 112 protein |

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0; Gaps

Query Match 53.6%; Score 37; DB 2; Length 74; Best Local Similarity 62.5%; Pred. No. 35; Matches 5; Conservative 2; Mismatches 1; Indels

| link protein - rat<br>gene 1.8 protein - | hypothetical prote<br>relaxin - gorilla | hypothetical 8K pr<br>ribosomal protein | hypothetical prote<br>hypothetical prote | hypothetical prote<br>type I restriction | hypothetical prote<br>hypothetical prote | hypothetical prote<br>1SU ribosomal prot | plantaricin A - La<br>relaxin - baboon ( |
|------------------------------------------|-----------------------------------------|-----------------------------------------|------------------------------------------|------------------------------------------|------------------------------------------|------------------------------------------|------------------------------------------|
| S56756<br>018987                         | S14125<br>S42778                        | JN0652<br>B72248                        | F97099<br>D97862                         | AB0406<br>D82933                         | C72262<br>D97785                         | T31142<br>F90221                         | A45913<br>'S42785                        |
| 7 7                                      | 0 0                                     | 0 0                                     | 0 0                                      | 00                                       | 0 0                                      | 0 0                                      | 0 0                                      |
| 20 4                                     | 50                                      | 66<br>67                                | 67                                       | 6<br>6<br>8<br>9<br>9                    | 69                                       | 71                                       | 22                                       |
| 42.0                                     | 42.0                                    | 42.0<br>42.0                            | 42.0<br>42.0                             | 450.0<br>0.0                             | 42.0                                     | 42.0<br>42.0                             | 40.6                                     |
| 5 6                                      | 5 6                                     | 7<br>7<br>7<br>7                        | 5<br>7<br>7<br>8                         | 7<br>7<br>7<br>8<br>7<br>8               | 5<br>7<br>7<br>8                         | 5 7<br>7 7<br>7 8                        | 58<br>58<br>78                           |
| 30                                       | 332                                     | 3.4<br>3.5                              | 36<br>37                                 | 3 8<br>3 6<br>8 6                        | 4<br>41<br>41                            | 42                                       | 44<br>45                                 |

## ALIGNMENTS

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A;Cross-references: UNIPROT:Q92GM8; GB:AE006914; PIDN:AAL03633.1; PID:g15620218; GSPDB:GR C;Genetics:
A;Gene: RC1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          **Siglaser. F.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, S.; Jones, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; L.M.; Karset, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Sinoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;cross-references: UNIPROT:0929V4; GB:AL592022; PIDN:CAC97399.1; PID:g16414683; GSPDB:G1A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H., D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.

**Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT: Q8Y5J7; GB:NC_003210; PIDN: CAD00141.1; PID:g16411533; GSPDB:C
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein lin2169 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Listeria innocua
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C.Accession: AG1703
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C,Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                               C; Superfamily: virulence protein, RhuM type
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 53.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 YKKWKNKLLK 12
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17 FRKWATNLLK
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A; Residues: 1-63 <GLA>
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A;Residues: 1-63 <GLA>
                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-50 < KUR>
                                                                                   A; Accession: G97836
A; Status: preliminary
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A; Status: preliminary
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C'Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C'Accession: G97836
R'Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rd
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T40218
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule: 1-67 - WOOD>
A; Cross-references: UNIPROT: P87316; EMBL: Z97204; PIDN: CAB10091.1; GSPDB: GN00067; SPDB: SF
A; Experimental source: strain 972h-; cosmid c31F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: H90520
A;Status: preliminary
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A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                   robable ATP synthase epsilon chain, mitochondrial - fission yeast (Schizosaccharomyces;Species: Schizosaccharomyces pombe;Decies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein MYPU 0720 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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G97836
hypothetical protein RC1095 [imported] - Rickettsia conorii (strain Malish 7)
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                                                                                                                                                                                                                                                                                                            C;Accession: T40218
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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Pred. No. 98;
1; Mismatches
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Pred. No. 97;
0; Mismatches
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Best Local Similarity 71.4%;
Matches 5; Conservative
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nes 8; Conservative
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C;Keywords: mitochondrion
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                                                                                   67 YRKWKEKI 74
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LYTRWKN 49
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                               YKKWKNKL
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A;Residues: 1-55 <KUR>
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A,Gene: MYPU 0720
A,Genetic code: SGC3
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Matches
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C;Species: Streptococcus pneumoniae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
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44 YTEWKOR 50
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                                                                                                                                                                                                                                                                                                    hypothetical protein 69 - liverwort (Marchantia polymorpha) chloroplast (Species: chloroplast Marchantia polymorpha (Species: chloroplast Marchantia polymorpha (Space: 05-Unn-1987 #sequence_revision 05-Unn-1987 #text_change 09-Unl-2004 (Spacession: S01514; A05061 Regular (Spacession: S01514; A05061 Regular (Spacession: S01514; A05061 Regular (Spacession: S01514; A) Regular (Spacession: S01512; MUD: B9068688; PMID: 3199437 A) Reference number: S01512; MUD: 89068688; PMID: 3199437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P12196; EMBL:X04465; NID:g11640; PIDN:CAA28131.1; PID:g11720 R;Ohyama, K.; Pikuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi Wature 322, 572-574, 1986 A;Mature 322, 572-574, 1986 A;Title: Chloroplast gene organization deduced from complete sequence of liverwort March A;Reference number: A38014 A;Contents: annotation; gene organization, sites, features
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B42517
C.ORF-I protein - vaccinia virus (strain Copenhagen)
C.Species: vaccinia virus
A.Note: host Homo sapiens (man)
C.Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
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JU0329
hypothetical 4.4K protein (lytA 5'region) - Streptococcus pneumoniae
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                                                                     Length 63
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C;Superfamily: rice chloroplast ribosomal protein L32
C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 2; I Pred. No. 2.1e+02;
                                                                Score 32; DB 2;
Pred. No. 1.9e+02;
3; Mismatches 4
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A;Residues: 1-74 <JOH>
A;Cross-references: UNIPROT:P20553
                                                                     46.48;
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C, Accession: B4257
R, Johnson, G.P.
Bubmitted to Gensank, June 1990
A, Reference number: A33172
A, Accession: B42517
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                                                                Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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LYKRWFN 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-69 < KOH>
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C;Genetics:
A;Gene: lmo2063
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C;Accession: JU0329
R;Diaz, B.; Gazcia, J.L.
Gene 90, 157-162, 1990
A;Title: Characterization of the transcription unit encoding the major pneumococcal auto)
A;Reference number: JU0329; MUID:90337339; PMID:1974230
A;Accession: JU0329
A;Molecule type: DNA
A;Residues: 1.37 - DNA>
A;Cross-references: DNA>
A;Cross-references: DNA>
A;Cross-references: DNA>
A;Experimental source: strain M31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tibosomal protein S27a - Methanobacterium thermoautotrophicum (strain Delta H)

C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F.; Smith, D.R.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
J; Bacteriol. 179, 7135-7155, 1997
A;Tilla: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct; A;Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: G69133
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Residues: 1-51 <MTA
A, Residues: 1-51 <MTA
A, Cross-references: UNIPROT: 026368; GB: AE000812; GB: AE000666; NID: G2621298; PIDN: AAB8477
A, Experimental source: strain Delta H
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C,Accession: IS9604

E, Bubanks, J.H.; Heinemann, S.F.; McNamara, J.O.
Somat. Cell Mol. Genet. 19, 581-588, 1993

A,Title: Chromosomal localization of gene for human glutamate receptor subunit-7.

A,Reference number: IS9604; MUID:94174381; PMID:8128318
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: ribosomal protein S27a; ribosomal protein S27a homology
F;2-48/Domain: ribosomal protein S27a homology <RIB>
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C;Reywords: neurotransmitter receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 2; 1 Pred. No. 1.7e+02;
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Pred. No. 2.3e+02;
2; Mismatches 1
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Finoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHofff, B.S.; Es e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc y, P.; Sun, P.M.; Winkler, M.E.

y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Reference number: A97872; MulD:21429245; PMID:11544234

A; Reference number: A97872; MulD:21429245; PMID:11544234

A; Reference number: DNA

A; Residues: 1-57 < KUR>
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submitted to the EMBL Data Library, July 1999
AjDescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
AjReference number: A75001
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C;Species: Pyrococcus horikoshii
Cjate: 14 Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: C71028
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q8DQSS; GB:AE007317; PIDN:AAK99327.1; PID:g15458097; GSPDB:GPCG:C;Genetics:
                                                                                                                                                                                                                                                            uncharacterized, truncation [imported] - Streptococcus pneumoniae (strain R6
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                                                                                                                                                                                                                                                                                             C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: C97937
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C75106
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   Indels
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Pred. No. 2.6e+02;
3; Mismatches 1; Indels
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Mismatches
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C,Superfamily: rat ribosomal protein L37
3;
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Similarity 50.0%;
4; Conservative
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Matches 5; Conservative
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A;Gene: transposase H-truncation
   4; Conservative
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4 YKKWLDSMM 12
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20 IWKQWKKK 27
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Best Local Similarity
Matches 4; Conserv
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-62 < KAW>
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Jonninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Joninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Kuhn, M.; Tarerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                           hypothetical protein 54 (paaC 3' region) - Buglena gracilis chloroplast
C;Species: chloroplast Euglena gracilis
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S34541; S34908
R;Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann, Bubhitted to the EMBL Data Library, January 1993
A;Description: The complete sequence of the Euglena gracilis chloroplast genome (tentati
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A, Residues: 1-54 - GHALI.
A, Residues: 1-54 - GHALI.
A, Cross-references: UNIPROT: P31558; EMBL: X70810; NID: 941537; FIDN: CAA50122.1; PID: 94157
B, Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielman
Nucleic Acids Res. 21, 3377-3544, 1993
A, Title: Complete sequence of Euglena gracilis chloroplast DNA.
A, Reference number: $34862; MUID: 93347989; PMID: 8346031
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A;Experimental source: strain Clip11262
C;Genetics:
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A;Residues: 1-54 +4hLZ>
A;Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50122.1; PID:g415778
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
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AH1648
hypothetical protein lin1729 [imported] - Listeria innocua (strain Clip11262)
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1648
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A;Status: nucleic acid sequence not shown; translation not shown
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                           Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genome: chloroplast
C;Superfamily: rice chloroplast ribosomal protein L32
C;Keywords: chloroplast
                                                      2.4e+02;
                              Score 31; DB 2;
Pred. No. 2.4e+02
                                                                                        5; Mismatches
                           44.9%;
                                                                                                                                              1 ALYKKWKNKLLKS 13
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27 AIVEKWSMELLQA 39
                                                                                     5; Conservative
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                           Query Match
Best Local Similarity
Matches 5; Conserva
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Best Local Similarity
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Best Local Similarity
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A;Status: nucleic acid sequence not shown
                A;Accession: S15538
A;Status: not compar
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Matches
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M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Totle: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Accession: C71028
A;Accession: C71028
A;Actaus: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-62 < KAM>
A;Residues: 1-62 < KAM>
A;Residues: 1-62 < KAM>
A;Residues: 1-62 < KAM>
A;Residues: 1-62 < KAM>
A;Acoss-references: UNIPROT:P62005; GB:AP000006; NID:G3236133; PIDN:BAA30627.1; PID:G325A;A;Coss-references: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank A;Gene: PHS041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 19
$15538
homeotic protein Hox A6 - human (fragment)
NyAlternate names: homeotic protein Hox 1B
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Aug-2004
C;Accession: 51538
R;Boncinelli, E; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc Genome 31, 745-756, 1989
A;Title: Organization of human class I homeobox genes.
A;Reference number: S15036; MUID:90215256; PMID:2576652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-66 <WHA>.
A,Croser-references: UNIPROT:Q54594; EMBL:U11993; NID:g533663; PIDN:AAA99609.1; PID:g1235
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
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A;Reference number: $60784; MUID:95198537; PMID:7891551
A;Accession: $60790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
S61085
M protein precursor - Streptococcus pyogenes (serotype M75) (fragment)
C;Species: Streptococcus pyogenes
A;Variety: serotype M75
C;Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession. S61085; 860790
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emml gene sequences and A;Reference number: S61072
A;Accession: S61085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
44.9%; Score 31; DB 2; I
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1;
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Matches 5; Conservative
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28 ARYKAWKSE 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KKWKNK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 3-62 < WHW>
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+-transporting two-sector ATPase (EC 3.6.3.14) protein 8 - Chinese hamster mitochondrior
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A;Genetic code: SGC1
C;Superfamily: H+-transporting ATP synthase protein 8
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M protein precursor - Streptococcus pyogenes (serotype M48) (fragment)
C;Species: Streptococcus pyogenes
A;Variaty: serotype M48
A;Variaty: serotype M48
C;Variaty: serotype M48
C;Accession: S61080; S60819
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
submitted to the RMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emml gene sequences and the A;Reference number: S61072
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A, Residues: 1-70 < WHA>
A, Residues: 1-70 < WHA>
A, Residues: 1-70 < WHA>
A, Cross-references: UNISON: Q54563; EMBL: UNI961; NID: 9533599; PIDN: AAA99577.1; PID: 912358
R, Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A, Fittle: Non-congruent relationships between variation in emm gene sequences and the poputalistics: Non-congruent relationships P5198537; PMID: 7891551
A, Reference number: S60784; MUID: 95198537; PMID: 7891551
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R;Breen, G.A.M.; Miller, D.L.; Holmans, P.L.; Welch, G.
Biol. Chem. 261, 11680-11685, 1986
A;Title: Mitochondrial DNA of two independent oligomycin-resistant Chinese hamster ovary A;Reference number: A25188; MUID:86304297; PMID:3017940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-67 <BRE>
A;Cross-references: UNIPROT:P14414; GB:M14311; NID:g336719; PIDN:AAA68615.1; PID:g336720
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C;Species: mitochondrion Cricetulus griseus (Chinese hamster)
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                    A/Molecule type: DNA
A/Residues: 1-66 <BON>
A/Coses-references: UNIPROT:P31267
C/Genetics: GDB:HOXA6
A/Cose-references: GDB:120648; OMIM:142951
A/Map position: 7p15.3-7p15.3
C/Superfamily: homeobox homeobox; nucleus; transcription regulation F;2-58/Domain: homeobox homology <HOX>
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                        Length 66
                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 2;
Pred. No. 3e+02;
1; Mismatches
not compared with conceptual translation
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Best Local Similarity 63.6%;
Matches 7; Conservative
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hes 7; Conservative
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Length 57;

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Score 30; DB 2; Ler
Pred. No. 3.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.5%;
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                          Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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| ALIEKWKKE 13
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                                                                                                                                        4 KKWKNKL 10
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22 QKWKDKI 28
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A; Residues: 1-61 < KUR>
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A. Molecule type: protein
A. Molecule type: Drotein
A. Residues: 1-21 cBEN
A. Molecule type: Drotein
A. Residues: 1-21 cBEN
C. Comment: This proteinase inhibitor homolog has very low toxicity. Its physiological fu
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(297813

hypothetical protein RC0907 [imported] - Rickettsia conorii (strain Malish 7)

(5,Species: Rickettsia conorii

(5,Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

(7,Accession: C97813

R.Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rc

(7,Accession: C97813

A,Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A,Reference number: A97700; MUID:21442074; PMID:11557893

A,Accession: C97813

A,Accession: Preliminary

A,Residues: 1-57 «KUR»

A,Residues: 1-57 «KUR»

A,Residues: 1-57 «KUR»

A,Grosse-references: UNIPROT:Q92H64; GB:AE006914; PIDN:AAL03445.1; PID:g15620014; GSPDB:C

G,Genetics:

A,Gene: RC0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venom basic proteinase inhibitor K - eastern green mamba
N;Alternate names: dendrotoxin delta-DaTX
N;Alternate names: dendrotoxin delta-DaTX
C;Species Dendrosapis angusticeps (eastern green mamba)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A91691; C32508; A01213
R;Joubert, P.J; Taljaard, N.
Hoppe-Seyler's Z. Physiol. Chem. 361, 661-674, 1980
A;Title: The amino acid sequences of two proteinase inhibitor homologues from Dendroaspi
A;Reference number: A91691; MUID:81045446; PMID:7429422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R,Benishin, C.G.; Sorensen, R.G.; Brown, W.E.; Krueger, B.K.; Blaustein, M.P.
Mol. Pharmacol. 34, 125-1159, 1988
A;Title: Four polypeptide components of green mamba venom selectively block certain potal A;Reference number: 893137; MUID:88318591; PMID:2457792
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                                                                                                     A.Gene: emm48
C.Superfamily: M5 protein
E;1-19/Domain: aignal sequence (fragment) #status predicted <SIG>
F;20-70/Product: M protein (fragment) #status predicted <MAT>
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                                                                                                                                                                                                                                                   Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 43.5%; Score 30; DB 1; Length 57; Best Local Similarity 55.6%; Pred. No. 3.7e+02; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                Query Match

44.9%; Score 31; DB 2; I
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: A91691
A,Molecule type: protein
A,Residues: 1-57 <0005
A,Cross-references: UNIPROT:P00982
                                                    A;Cross-references: EMBL:U11961
C;Genetics:
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A; Molecule type: DNA
                          A;Residues:
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Rivolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; File: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A; Reference number: A96900; MUID:21359325, PMID:21359325
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A,Residues: 1-61 - ESB>
A,Cross-references: UNIPROT:P51708; GB:U24159; EMBL:U06847; NID:g1046235; PIDN:AAB09191.1
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994
R,Esposito, D.; Fitzmaurice, W.P.; Benjamin, R.C.; Goodman, S.D.; Waldman, A.S.; Scocca,
Nucleic Acids Res. 24, 2360-2368, 1996
A;Fitle: The complete nucleotide sequence of bacteriophage HP1 DNA.
A;Fitle: The complete nucleotide sequence of Pacteriophage HP1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q97EJ1; GB:AE001437; PIDN:AAK81059.1; PID:g15026186; GSPDB:GP
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: phage: HPI
C;Date: 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: 372338; 869512
R;Esposito, D.; Scocca, J.J.
Mol. Microbiol. 13, 685-695, 1994
A;Title: Identification of an HPI phage protein required for site-specific excision. A;Reference number: S72329; MuID:95089704; PMID:7997180
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
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                                                                                                                                                                                                                                                                                                                                                           C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97283
Gaps
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Pred. No. 4e+02;
0; Mismatches 2; Indels
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Indels
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                                                                                                                                                                                                                                                                                                                          ribosomal protein S14 [imported] - Clostridium acetobutylicum
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C,Superfamily: Escherichia coli ribosomal protein S14
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Pred. No. 4e+02;
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C)Accession: PC2248
R;Sakai, N.; Tuni, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.; Yanagihara, I.; Isegawa, Biochem. Biophys. Res. Commun. 198, 485-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 199, 481-491, 19
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Nucleic Acids Res. 23, 2305-2313, 1995
A;Title: Characterization of a glucocorticoid responsive element and identification of ar A;Reference number: S56756; MUID:95334387; PMID:7610060
A;Accession: S56756
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C;Date: 15-Jan-1999 #sequence_revision 15-Jan-1999 #text_change 09-Jul-2004 C;Accession: S78743  
R;Grivell, L.A.; de Haan, M.; Maat, M.J.  
abmitted to the Protein Sequence Database, March 1992 A;Reference number: $19412  
A;Reference number: $19412  
A;Status: S78743  
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-65 <GRI>A;Cross-references: UNIPROT:Q96VG5; EMBL:X59720; MIPS:YCR102w-a C;Genetics:
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C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
C;Accession: S56756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 20-Feb_1995 #sequence_revision 20-Feb-1995 #text_change 17-Sep-1997
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Pred. No. 1.9e+02;
1; Mismatches 0; Indels
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Pred. No. 4.2e+02;
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4; Conservative
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Matches 5; Conservative
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KWDSKLL 14
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Best Local Similarity
Matches 4; Conserv
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A; Molecule type: mRNA
A; Residues: 1-20 <SAK>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02.Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G96517
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., J., J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: F70442
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:O67567; GB:AE000749; NID:g2983975; PIDN:AAC07537.1; PID:g298
A;Experimental source: strain VF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300; MUID:9819666; PMID:9537320
A,Accession: F70442
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                                                                                                                                                                                                                                                                                     ribosomal protein S14 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70442
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Pred. No. 4e+02;
2; Mismatches 1; Indels
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A,Gene: rpsN C,Superfamily: Bscherichia coli ribosomal protein S14

Genetics:

Nature 392, 353-358, 1998

A; Molecule type: DNA A; Residues: 1-62 < AQF>

Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative

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RESULT

protein YCR099c - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae

43.5%;

Best Local Similarity 62.9 Matches 5, Conservative

Query Match

A; Molecule type: DNA A; Residues: 1-63 <STO> A, Status: preliminary

|| |:||: 51 ALSKRWKS 58

RESULT 28 S78743

1 ALYKKWKN 8

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;Molecule type: DNA
;Residues: 1-33 <EVA>
;Cross-references: UNIPROT:Q28428; UNIPROT:Q28429; EMBL:Z27227; NID:g415950; PIDN:CAA817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cispecies: Mycoplasma fermentans
Cibate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
Cibacession: JN0652
RiHu, W.S.; Wang, R.Y.H.; Shih, J.W.K.; Lo, S.C.
AjTitle: Identification of a putative infC-rpmI-rplT operon flanked by long inverted rept
A;Reference number: JN0652; MUID:93252283; PMID:8486291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Accession: B72248
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                   Species: Gorilla gorilla (gorilla)
Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
Residues: 34-57 <EVX>
Cross-references: EMBL:Z27226; NID:g415948; PIDN:CAA81740.1; PID:g415949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: insulin
C;Keywords: disulfide bond; hormone
F;1-33/Domain: relaxin chain 1B (fragment) #status predicted <RXBl>
F;34-57/Domain: relaxin chain 1A (fragment) #status predicted <RXAl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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A;Residues: 1-66 <HUM>
A;Residues: 1-66 <HUM>
A;Cross-references: UNIPROT:Q9XX56; GB:M95046
A;Note: the authors translated codon TGA for residue 47 as Trp
C;Genetics:
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 66;
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Pred. No. 5.4e+02;
3; Mismatches 1; Indels
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Pred. No. 6.3e+02;
2; Mismatches 0.
                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, November 1993
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Best Local Similarity 66.7%;
Matches 4; Conservative
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                                                                                                                            relaxin - gorilla (fragments)
                                                                                                                                                                                                          Accession: S42778; S42777
                                                                                                                                                                                                                                                                                           A;Reference number: S42776
A;Accession: S42778
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2 KWKDDVIK 9
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Best Local Similarity
Matches 4; Conserv
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                                                                             RESULT 33
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A; Residues: 1-48 <DU2>
A; Cross-recences: 0.48 <U2>
A; Cross-recences: 0.48 <U2>
B; Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A; Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge
A; Reference number: $42283; MUID:83241725; PMID:6864790
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                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Readdudes: 1-48 < DUNA
A; Cross-references: UNIPROT: P03794
B; Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 149, 303.330, 1981
A; Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the A; Title: Nucleotide sequence, MUID: 82078034; PMID: 7310871
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Reference number: S14125; MUID:91176556; PMID:2078869
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gene 1.8 protein - phage T7
C'Species: phage T7
C'Bate: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C'Accession: B43003; B43005; S42297; A04419
R.Junn, J.J.; Thomnson K
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C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S14125; S38590
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C;Superfamily: rice chloroplast ribosomal protein L32
C;Keywords: chloroplast; plastid
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;Residues: 1-48 <DUW>
;Coss-references: EMBL:V01146; NID:g431187; PIDN:CAA24398.1; PID:g15577
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submitted to the Nucleic Acid Sequence Database, September 1982
A;Reference number: A94615
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42.0%; Score 29; DB 2; I
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1;
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Pred. No. 4
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irr. Genet. 18, 457-464, 1990
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C,Superfamily: phage T7 gene 1.8 protein
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50.0%;
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Best Local Similarity
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A;Residues: 1-50 <SIE>
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A;Residues: 1-50 <GOC>
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, E. Nature 413, 523-527, 2001.

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: Q8ZBR3; GB: AL590842; PIDN: CAC92574.1; PID: g15981271; GSPDB:GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ype I restriction enzyme S protein, truncated homolog UU097 [imported] - Ureaplasma urea;
Species: Ureaplasma urealyticum
Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000;
Accession: D82933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30503.1; GSPDB:GN001; Experimental source: serovar 3; biovar 1
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                    C.Species: Yersinia pestis
C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C.Accession: AB0406
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                hypothetical protein YPO3344 [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 6.6e+02;
3; Mismatches 1; Indels
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Pred. No. 6.5e+02;
3; Mismatches 2; Indels
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50.0%;
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55.6%;
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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50 YEYYRNKLL 58
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50 FKKIKNKFIE
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                                                         52 YEKWK 56
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-68 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-69 <GLA>
        3 YKKWK 7
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A,Residues: 1-67 «KUR»
A,Crose-references: UNIPROT:097IM2, GB:AE001437, PIDN:AAK79585.1, PID:g15024575, GSPDB:G
A,Experimental source: Clostridium acetobutylicum ATCC824
Nature 399, 323-329, 1999
Ajīlie: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97099
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                                                                                                                                                                                             A;Cross-references: UNIPROT:09X1J1; GB:AE001798; GB:AE000512; NID:g4982033; PIDN:AAD3654
A;Experimental source: strain MSB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
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C;Species: Rickettsia conorii
C;Species: Bo-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97862
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2039-2099, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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inn 0%; Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                           A,Gene: TM1482
C,Superfamily: Escherichia coli ribosomal protein L30
                                                                                                                                                                                                                                                                                                                                                            Query Match 42.0%; Score 29; DB 2; I Best Local Similarity 70.0%; Pred. No. 6.4e+02; Matches 7; Conservative 1; Mismatches 2;
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Best Local Similarity
Matches 4; Conserv
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Matches 6; Conserv
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                                                                                                          A; Status: preliminary A; Molecule type: DNA A; Residues: 1-67 <ARN>
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A; Residues: 1-67 < KUR>
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A;Cross-references: UNIPROT: Q28780; EMBL: 227246; NID: 9416107; PIDN: CAA81759.1; PID: 941610
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C;Species: Papio sp. (baboon)
C;Date: 06-Jan-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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R;Evans, B.B.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: protein
A,Residues: 1-22 «NIS»
A,Cresidues: 1-22 «NIPROT:P80214
C,Keywords: antibiotic; bacteriocin
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Matches 6; Conserv
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C;Superfamily: insulin
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A; Residues: 1-73 < KUR>
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17 LFKKW 21
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A; Residues: 1-24 < EVA>
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A, Status: preliminary
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A; Status: preliminary
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A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Accession: C72562
A,Status: preliminary
A,Molecule type: DNA
A,Residus: 1-69 <ARN>
A,Residus: 1-69 <ARN>
A,Residus: 1-69 <ARN>
A,Residus: 1-69 <ARN>
Crosser-references: UNIPROT:Q9X1A6; GB:AE001791; GB:AE000512; NID:g4981929; PIDN:AAD3645
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein RC0684 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Accession: D97785
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; RC Science 293, 2093-2099, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T31142
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatians. A;Reference number: 220992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;cross_references: UNIPROT:Q92HT7; GB:AE006914; PIDN:AAL03222.1; PID:g15619774; GSPDB:C;Genetics:
A;Gene: RC0684
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Pred. No. 6.68+02;
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40.0%; Pred. No. 6.7e+02;
uismatches 1; Indels
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Pred. No. 6.6e+02;
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Best Local Similarity 40.0.
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50 LARQWRSRLL 59
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54 YERFKNELEK 63
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: DNA
A;Residues: 1-69 <KUR>
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A;Genome: plasmid pNL1
A;Note: orf165
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 02-Aug-2002
C;Accession: F90221
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Jong, I.; Jeffrise, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
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C;Species: Lactobacillus plantarum
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
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A;Reference number: A45913
F90221
1SU ribosomal protein L37AE (rpl37AE) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 42.0%; Score 29; DB 2; I Similarity 54.5%; Pred. No. 6.9e+02; 6; Conservative 1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28; DB 2; 1
Pred. No. 3.1e+02;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: rat ribosomal protein L37a
```

C;Keywords: disulfide bond; hormone  $P;1-24/{\rm Domain}:$  relaxin chain B' (fragment) #status predicted <RXA>

0; Gaps Query Match 40.6%; Score 28; DB 2; Length 24; Best Local Similarity 50.0%; Pred. No. 3.3e+02; Matches 4; Conservative 2; Mismatches 2; Indels

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S KWKNKLLK 12 ||| ::| 2 KWKEDVIK 9

δ g

Search completed: May 16, 2005, 08:42:31 Job time : 12.2069 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 16, 2005, 08:21:21; Search time 54:8017 Seconds (without alignments) 121.475 Million cell updates/sec

US-09-648-816B-9 69

1 ALYKKWKNKLLKS 13 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

145419 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|           |        | Description  | OS0694 borrelia bu | Q9emw7 amsacta moo | Q64130 mus sp. int |            | Q71xv1 listeria mo | Q9rq45 buchnera ap | Q8sg59 ogcodes sp. |        | Q71hq0 lactobacill | Q9azp4 bacteriopha | Q8rn73 streptococc |        | Q9mi16 drosophila |        |        | Q7mkn7 vibrio vuln | Q9a016 streptococc | Q7cn57 streptococc | P87316 schizosacch | Q7p7z9 fusobacteri |        |        | _      | _      | Q707zl kluyveromyc | Q92gm8 rickettsia |        | O50596 clostridium | Q9uc64 homo sapien | Q7y3h6 enterobacte | Q91dt0 dengue viru |
|-----------|--------|--------------|--------------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|-------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------------------|-------------------|--------|--------------------|--------------------|--------------------|--------------------|
| SUMMAKIES |        | ជ            | 050694             | Q9EMW7             | Q64130             | PBPO PARSC | Q71X <u>V</u> 1    | Q9RQ45             | Q8SG59             | QSTUKI | Q71HQ0             | Q9AZP4             | Q8RN73             | Q9Y0X4 | Q9M116            | QBF1C8 | 08F2Z2 | Q7MKN7             | Q9A016             | Q7CN57             | ATPE SCHPO         | Q7P7 <u>Z</u> 9    | Q9G8W3 | QBRJLS | Q98RD7 | Q9AZ27 | Q707Z1             | Q92GM8            | QBCKAS | 050596             | Q9UC64             | Ф7ҮЗН6             | Q91DT0             |
|           |        | 8            | 7                  | ~                  | 7                  | H          | ~                  | ~                  | 7                  | 7      | 7                  | ~                  | ~                  | ~      | ~                 | ~      | ~      | ~                  | 7                  | 0                  | ч                  | 7                  | ~      | 7      | N      | ~      | 0                  | ~                 | 0      | ~                  | ~                  | ~                  | 7                  |
|           |        | Match Length | 34                 | 62                 | 74                 | 45         | 63                 | 99                 | 73                 | 74     | 31                 | 54                 | 26                 | 72     | 27                | 36     | 55     | 26                 | 59                 | 59                 | 63                 | 70                 | 72     | 74     | 55     | 37     | 20                 | 20                | 20     | 21                 | 54                 | 28                 | 9                  |
| ٠         | Query  | Match        | 53.6               | 53.6               | 53.6               | 52.2       | 52.2               | 52.2               | 52.2               | 52.2   | 50.7               | 50.7               | 50.7               | 50.7   | 49.3              | 49.3   | 49.3   | 49.3               | 49.3               | 49.3               | 49.3               | 49.3               | 49.3   | 49.3   | 48.6   | 47.8   | 47.8               | 47.8              | 47.8   | 47.8               | 47.8               | 47.8               | 47.8               |
|           |        | Score        | 37                 | 37                 | 37                 | 36         | 36                 | 36                 | 36                 | 36     |                    | 35                 | 35                 | 35     | 34                | 34     | 34     | 34                 | 34                 | 34                 | 34                 | 34                 | 34     | 34     | 33.5   | 33     | 33                 | 33                | 33     | 33                 | 33                 | 33                 | 33                 |
|           | Result | No.          | -                  | 8                  | m                  | 4          | S                  | 9                  | 7                  | 80     | 6                  | 10                 | 11                 | 12     | 13                | 14     | 15     | 16                 | 17                 | 18                 | 19                 | 20                 | 21     | 22     | 23     | 24     | 25                 | 56                | 27     | 28                 | 58                 | 30                 | 31                 |

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AMV082. Name=AMV082; Amsacta moorei entomopoxvirus (AmEPV). Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;

Q9EMW7 PRELIMINARY; PRT; 62 AA.
Q9EMW7;
Q0LWAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-GT-2002 (TrEMBLrel. 22, Last annotation update)

OS CE DIT ACC

RESULT 2 Q9EMW7

| Q81d78 bacillus ce |        | •      | Q7v0i2 prochloroco | Q81gt8 bacillus ce |        | Q821y9 chlamydophi |        |        | Q6gfcl staphylococ | O77966 homo sapien | Q96bh6 homo sapien | Q98q95 zea mays (m | Q8xlc3 clostridium |
|--------------------|--------|--------|--------------------|--------------------|--------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 081078             | 092974 | Q7R5D8 | Q7V0I2             | Q81GT8             | Q6MCQ8 | Q821Y9             | Q8NVR7 | Q6G7Z7 | Q6GFC1             | 996220             | 9не 96             | 560560             | Q8XLC3             |
| ~                  | 7      | ~      | 7                  | ~                  | 7      | 7                  | ~      | ~      | 7                  | ~                  | ~                  | 7                  | 7                  |
| 25                 | 63     | 65     | 69                 | 72                 | 63     | 31                 | 32     | 32     | 32                 | 34                 | 38                 | 43                 | 57                 |
| 47.8               | 8./F   | 47.8   | 47.8               | 47.8               | 47.1   | 46.4               | 46.4   | 46.4   | 46.4               | 46.4               | 46.4               | 46.4               | 46.4               |
| 33                 | 33     | 33     | 33                 | 33                 | 32.5   | 32                 | 32     | 32     | 32                 | 32                 | 32                 | 32                 | 32                 |
|                    |        |        |                    |                    |        |                    |        |        |                    |                    |                    |                    |                    |

## ALIGNMENTS

|                      |         |             |                       |                   |              |                                                |                 | Borrelia.                               |                 |        |                    |                          |               | R.A.,                                                           | м.ж.,          |               | зh J.,                                                          | , D.                                                          | Donald L.A.,   | , Horst K.,   |                                                  |                                     |                |                           |                             |                      |              |                   |                         |             |                   | ed daba      |               |               |
|----------------------|---------|-------------|-----------------------|-------------------|--------------|------------------------------------------------|-----------------|-----------------------------------------|-----------------|--------|--------------------|--------------------------|---------------|-----------------------------------------------------------------|----------------|---------------|-----------------------------------------------------------------|---------------------------------------------------------------|----------------|---------------|--------------------------------------------------|-------------------------------------|----------------|---------------------------|-----------------------------|----------------------|--------------|-------------------|-------------------------|-------------|-------------------|--------------|---------------|---------------|
|                      |         |             | late)                 | pagre)            |              |                                                |                 | Spirochaetaceae, I                      |                 |        |                    |                          | 1/37551;      | G., Clayton                                                     | L.J., Hickey I | schmann R.D., | t., Quackenbus                                                  | N., Adams M.                                                  | latthey L., Mc | , Cotton M.D. | C.;                                              | te, Borrelia                        |                |                           | •                           |                      |              | mid.              | ; CRC64;                | Length 34;  | -                 |              |               |               |
| 3.4 AB               | 5       | ਰੇ          | Last sequence update) | amocacion update) |              | spirochete                                     |                 |                                         |                 |        |                    |                          | DOI=10.1038   | ., Sutton G                                                     | ., Dodson F    | F., Fleis     | rlavage A.F                                                     | R., Palmer                                                    | ack T.R., w    | ., Fujii c.   | , Venter J.                                      | e spirochaete,                      |                |                           |                             |                      |              | protein; Plasmid. | FD687CA065B19056 CRC64; | 37; DB 2;   | ~ .               | Billaccines  |               |               |
| t-<br>t-             |         |             | Last                  | , המפר            |              | ne disease                                     |                 | Spirochaet                              |                 |        |                    |                          | -9403685;     | Huang W.M                                                       | stchum K.A     | A., Tomb J    | 1 J.D., Ke                                                      | van Vugt                                                      | ?., Utterb     | rland S.A     | Mith H.O.                                        | me diseas                           |                |                           | 1,                          |                      |              | netical pro       | fW; FD687               |             | Pre               |              |               |               |
| . VARITMINARY:       |         |             | (TremBLrel.           | nrotein BB        |              | Borrelia burgdorferi (Lyme disease spirochete) | -3.             | Bacteria; Spirochaetes; Spirochaetales; | .39;            |        | M N.A.             | STRAIN=ATCC 35210 / B31; | 5943; PubMed= | Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., | White O., Ke   | Dougherty B.A | Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J., | Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D., | , Weidman J.F  | Bowman C., Ga | Roberts K.M., Hatch B., Smith H.O., Venter J.C.; | "Genomic sequence of a Lyme disease |                | Nature 390:580-586(1997). | EMBL; AE000784; AAC66012.1; | E70239.              |              |                   | 34 AA; 4081 MW;         | 53.6%;      | Similarity 70.0%; | COMBETABLIAG | YKKWKNKLLK 12 | YKKIKNELIK 19 |
| LT 1<br>94<br>050694 | 050694; | 01-JUN-1998 | 01-JUN-1998           | UI-JUN-2003       | OrderedLocus | Borrelia bur                                   | Plasmid lp28-3. | Bacteria; Sr                            | NCBI TaxID=139; | ا<br>آ | SEQUENCE FROM N.A. | STRAIN=ATCC              | MEDLINE=9806  | Fraser C.M.,                                                    | Lathigra R.,   | Gwinn M.L.,   | Richardson L                                                    | Salzberg S.I                                                  | Gocayne J.D.   | Artiach P.,   | Roberts K.M.                                     | "Genomic seç                        | burgdorferi."; | Nature 390:5              | EMBL; AE0007                | PIR; E70239; E70239. | TIGR; BBH39; | Complete pro      | SEQUENCE 3              | Query Match | Best Local Simi   | '.'          | 3 YKK         | 10 YKK        |
| RESULT<br>050694     | S S     | TO          | 5 6                   | 3 6               | 3 8          | SO                                             | 8               | 8                                       | ŏ               | Z.     | RP                 | Z<br>C                   | 2             | Ş                                                               | Ş              | æ             | æ                                                               | æ                                                             | æ              | æ             | æ                                                | RŢ                                  | RŢ             | Z                         | DR                          | ద                    | DR.          | 3                 | SO                      | ğ           | a a               | D.           | ઠે            | g             |

SARARASSO

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SEQUENCE FROM N.A.

PubMed=15115801; DOI=10.1093/nar/gkh562;

PubMed=15115801; DOI=10.1093/nar/gkh562;

Nelson K.E.; Rasko D.A., Angiuoli E.F., Gill S.R., Paulsen I.T.,

Rolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,

Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,

Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,

Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,

Porberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,

Bayles D.O.; Luchansky J.B., Fraser C.M.;

"Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides in the venom of scorpions from southern Africa.";

Eur. J. Biochem. 26:4799-4810(2002).

-!-PUNCTION: Induces a leak current in voltage-clamped dorsal root ganglion cells of rate by forming pores. Degranulates human granulocytes and has a weak hemolytic activity against human red blood cells. Has antibacterial activity against Gram-negative bacteria but is less active against Gram-positive bacteria. Has antibugal activity.
-!-SUBUNIT: Monomer and homodimer.
-!- SUBUNIT: Monomer and homodimer.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- TASSUE SPECIFICITY: MW=5030.3; METHOD=MALDI; RANGE=1-45;
                                                                                                                                                                                                                                                                                                                                               MEDLINE=22241537; PubMed=12354111;
Moerman L.F.A., Bosteels S., Noppe W., Willems J., Clynen E.,
Schoofs L., Thevissen K., Tytgat J., Van Bldere J., van der Walt J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /erdonck F.;
Antibacterial and antifungal properties of alpha-helical, cationic
                                                                                         Verdonck F., Bosteels S., Desmet J., Moerman L.F.A., Noppe W., Willems J., Tytgat J., van der Walt J.; "Artgat J., van der Walt J.;" "A novel class off pore-forming peptides in the venom of Parabuthus schlechteri Purcell (Sorpions: Buthidae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibiotic; Direct protein sequencing; Fungicide; Hemolysis; Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes (serotype 4b / strain F2365).
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 1; Length 45;
Pred. No. 1.9e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                          FUNCTION, CIRCULAR DICHROISM ANALYSIS, AND SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
4995 MW; 3EEFF71425FA14FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last Sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             core genome components of this species."; Nucleic Acids Res. 32:2386-2395(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome; Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
OrderedLocusNames=LMOf2365_2094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE017329; AAT04864.1;
                                                                                                                                                                                                                           Cimbebasia 16:247-260(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 63.6
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LYKKWKNKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LKKAWKSKLAK 17
SEQUENCE, FUNCTION, SI
AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=265669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 AA;
                                                               TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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      E STATE OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stocking C.;
"Sequential mutations in the interleukin-3 (IL3)/granulocyte-
"Sequential mutations in the interleukin-3 (IL3)/granulocyte-
macrophage colony-stimulating factor/IL5 receptor beta-subunit genes
are necessary for the complete conversion to growth autonomy mediated
by a truncated beta C subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parabuthus schlechteri (Scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Parabuthus.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                    "Complete genomic sequence of the Ammacta moorei entomopoxvirus: analysis and comparison with other poxviruses."; Virology 274:120-139(2000).
EMBL; AF550284; AAGC3788 1; - SEQUENCE 62 AA; 7572 MW; 09621AA92644C023 CRC64;
                                                                                                                                                        Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                         SEQUENCE FROM N.A.
MEDLINE=20396580; PubMed=10936094; DOI=10.1006/viro.2000.0449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=95257920; PubMed=7739524;
Hannemann J., Hara T., Kawai M., Miyajima A., Ostertag W.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.6%; Score 37; DB 2; Length 74; 62.5%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  699F717B446FF992 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Interleukin-3 receptor beta subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                               53.6%; Score 37; DB 2; L
62.5%; Pred. No. 1.8e+02;
tive 2; Mismatches 1;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Parabutopoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0004872; F:receptor activity; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MO1. Cell, Biol. 15:2402-2412(1995).
EMBL; S78451; AAB34209.1; -..
PIR; IS7554; IS7554.
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
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67 YRKWKEKI 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=10095;
                       NCBI_TaxID=28321;
                                                                                                                                                                                          Moyer R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PBPO PARSC
P83312;
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NON TER
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Q64130

RESULT 3 Q64130

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RESULT 4
PBPO PARSC
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DT 28-FEB-DT 28-FEB-DT 08-JUL-DS PATADUI OS PATADUI OS PATADUI OS PATADUI OS PATADUI OS NUBLITARN [1]

Matches

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Gaps

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GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA
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71.4%;
                                                                                                                                        y Match 52.2%;
Local Similarity 54.5%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanosarcina acetivorans
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                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                        2 LYKKWKNKLLK 12
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61 LYHEWKSNALK 71
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Predicted protein.
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SEQUENCE
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Matches
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MEDLINE=22077634; PubMed=12082129;
Castro L.R., Austin A.D., Dowton M.;
"Contrasting rates of mitochondrial molecular evolution in parasitic Diptera and Hymenoptera."
Mol. Biol. Evol. 19:1100-1113 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

BENDLINE-2022990; PubMed=10555290; Clark Ma., Moran N.A., Baumann P.; "Sequence evolution in bacterial endosymbionts having extreme base
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
NCBI_TaxID=9;
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-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SIMILARITY: Belongs to the complex I subunit 3 family.
EMBL; AF484025; AAL88680.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:000137; F:NADH debydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
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                                     Score 36; DB 2; Length 63;
Pred. No. 2.6e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 2; Length 66;
Pred. No. 2.7e+02;
0; Mismatches 1; Indels
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    7504 MW; A31E13B6C0BD3050 CRC64;
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Last annotation update)
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NADH dehydrogenase subunit 3 (Pragment)
                                                                                                                                                                                                                                                                                                        Created)
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Ferredoxin-NADP reductase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           compositions.";
Mol. Biol. Bvol. 16:1586-1598(1999).
EMBL, AR130815; AAF13809.1; -.
HSSP: P28861; IFDR.
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                                          52.2%;
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85.7%;
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                     Query Match
Best Local Similarity 53.0.
Ti Conservative
                                                                                                                       1 ALYKKWKNKLLKS 13
                                                                                                                                                             23 ALLAKWKPTILRS 35
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nes 6, Conservative
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Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                        Buchnera aphidicola.
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63 AA;
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  SEQUENCE
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Q9RQ45;
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Q8SG59,
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Q9RQ45
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STRAINE-21929760; PubMed=11932238; DOI=10.1101/gr.223902;

A Galagan J.B., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A PitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A zimmer A., Barber R.D., Cann I., Graham D.B., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Knettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C.,

Rerry J.G., Jarrell K.P., Jing H., Macario A.J.L., Paulsen I.T.,

Prichett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

A Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DNA polymerase III subunit gamma/tau (EC 2.7.7.7) (Fragment).
Lactobacillus delbrueckii (subsp. lactis).
Bacteria; Firmicutes; Lactobacillales; Lactobacillus.
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Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                                                Score 36; DB 2; Length 73;
Pred. No. 3e+02;
2; Mismatches 3; Indels
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73 AA, 8669 MW, F4FA4DB259451D52 CRC64,
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Interpro; IPR000440; Oxidored q4.
Pfam; PF00507; Oxidored q4; 1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
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EMBL; AE010662; AAM03520.1; -.
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50.7%;
85.7%;
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Matches 7; Conservative
                                                                                   6; Conservative
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                                                                                                                                                4 KKWKNKL 10
                                                                                                                                                                                                             22 KOMWKONKL 28
                   Query Match
Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
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Q9Y0X4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage bIL309.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
VCBI_TaxID=151537;
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                   STRAIN-ATCC 4797;
Langenheim J.F., Ulrich R.L.;
Langenheim J.F., Ulrich R.L.;
Langenheim J.F., Ulrich R.L.;
Langenheim J.F., Ulrich R.L.;
Langenheim J.F., Ulrich R.L.;
BMBL, AR496645;
AA007238 1.; -.
GO, GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
GO, GO:0016740; F:transferase activity; IEA.
Nucleotidyltransferase; Transferase.
31 31 31
SEQÜENCE 31 AA; 3618 MW; 8040108F13440A20 CRC64;
                                                                                                                                                                                                                                                                                                                              50.7%; Score 35; DB 2; Length 31; 71.4%; Pred. No. 1.9e+02; tive 2; Mismatches 0; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceàe;
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Pimtanothai N., Orataiwun P., Nunthapisud P.;
Submitted (FBL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF485834; AAL87710.1; -.
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity
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FROM N.A.
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Q8RN73
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TISSUE-Venom gland;
MEDLINE-2012476; PubMed=10868911; DOI=10.1080/152165400306214;
Zeng X.C., Li W.X., Peng F., Zhu Z.H.;
"Cloning and characterization of a novel cDNA sequence encoding the precursor of a novel wenom peptide (BmKDpp) related to a bradykinin-potentiating peptide from Chinese scorpion Buthus martensii Karsch.";
IUBMB Life 49:207-21012000).
                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthopoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Mesobuthus.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7220;
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Score 35; DB 2; Length 56;
Pred. No. 3.4e+02;
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Wenxin L., Shunyi Z.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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TISSNEE-Venom gland;
Zeng X.-C., Li W.-X., Zu S.-Y.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TW-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b (Fragment).
Name=mt:Cyt-b; Synonyms=cytb;
Drosophia erecta (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
BmK3 (Erradykinin-potentiating peptide).
Name=bpp1; Synonyms=bpp;
                                                                                                                                                                                                                                                                                                           72 AA.
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SEOUENCE 72 AA; 8327 MW; (
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Score 34; DB 2; Length 55; Pred. No. 4.8e+02; 6; Mismatches 1; Indels

CB125F86B70E93F5 CRC64;

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STRAIN=56601 / Serogroup Icterchaemorrhagiae / Serovar lai;
MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                       "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing."; Nature 422:888-893(2003).
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Best Local Similarity 41.7%;
Matches 5; Conservative
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PubMed=12927135; DOI=10.1016/S1055-7903(03)00070-8;
Kastanis P., Eliopoulos E., Goulielmos G.N., Tsakas S., Loukas M.;
"Macroevolutionary relationships of species of Drosophila melanogaster
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MEDLINE=22589143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.,
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
[13] TaxID=173;
[1]
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"Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
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Pred. No. 3.2e+02;
1; Mismatches 0; Indels
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Pred. No. 2.4e+02;
1; Mismatches 3; Indels
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28:518-528(2003)
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Mol. Phylogenet. Evol. 28:518-E
EMBL; AF164585; AAF81380.1; -.
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01-MAR-2003 (TrEMBLrel. 23, C:
01-MAR-2003 (TrEMBLrel. 23, Li
01-MAR-2003 (TrEMBLrel. 23, Li
Hypothetical protein.
OrderedLocusNames=LA2619;
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83.3%;
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Leptospira interrogans.
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Matches 7; Conservative
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26 KXWKNR 31
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PubMed=14656965; DOI=10.1101/gr.1295503;
Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
"Comparative genome analysis of Vibrio vulnificus, a marine
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Vibrionaceae, Vibrio.
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Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
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EMBL, AP005337; BAC94506.1;
Complete protecome; Hypothetical protein.
SEQUENCE 56 AA; 6413 MW; F3A331E55157D270 CRC64;
                                                                                                                                                                                  01-MAR-2004 (TrEMBLrel. 26, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein VV1742.
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PRELIMINARY;
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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SECATE S., SUVOTOV A.N., KENTON S., Lai H.S., Lin S.P.,
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Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
"Complete genome sequence of an MI strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S. A. 98:4658-4663(2001).
EMBL; AR006544; ARX33881.1; -
Complete protecome; Hypothetical protein.
SEQUENCE S9 AA; 7070 MW; 25B521C3EAC45A0C CRC64;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Putative ATP synthase epsilon chain, mitochondrial (BC 3.6.3.14).
Name-atpl5; ORFNames=SPBC31F10.15c;
Schizosaccharomyces pombe (Fission yeast).
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Pred. No. 5.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                              49.3%; Score 34; DB 2; Length 59; 77.8%; Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=spyM18_1274;
Streptococcus pyogenes (Serotype M18).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 AA; 7070 MW; 25B521C3EAC45A0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical phage protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
EMBL; AE010050; AAL97880.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 AA
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                               Local Similarity 77.8
hes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 LYOKIKNKL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LYKKWKNKL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LYKKWKNKL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 LYOKIKNKL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
  NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MGAS8232
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P87316;
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ATPE SCHPO
ATPE SCHPO
AC P87316,
DT 15-UUL-
DT 25-OCT-
DE PUTALIA
GN Name=at
GN Name=at
GN SAMIZOS
OC EUKARYVO
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OCCUST
AC Q7CNS
AC Q7CNS
DT 05-JUI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                           STACIALE FROM N.A.

REC STRAIN-972,

REDINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

REDINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

REDINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

REDINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RECOKS K., Beat N., Hayles J., Baker S., Basham D., Bownan S.,

ROJIOS M., Connor R., Cronin A., Davis P., Feltwell T., Fraser C.M.,

Rentles S., Gobbe A., Hamiln M., Harris D., Hidalgo J., Hodgeon G.,

R. Gentles S., Gobbe A., Hamiln M., Harris D., Hidalgo J., Hodgeon G.,

R. Gentles S., Mungall K., Murphy L., Nibhett D., Odell C.,

R. Mooney P., Moule S., Mungall K., Murphy L., Nibhett D., Odell C.,

R. Mooney P., Moule S., Saunders R., Squares S., Stevens K.,

R. Stelton J., Simmonds M., Squares R., Squares S., Stevens K.,

R. Stelton J., Simmonds M., Squares D., Seeger K., Sharp S.,

R. Richerford K., Rutter S., Saunders D., Seeger K., Milbert B.,

R. Adviser K., O'Neil S., Tivey A., Walsh S.V., Marren T., Whitehead S.,

R. Ander K., Taylor R.G., Tivey A., Walsh S.V., Marren T., Whitehead S.,

R. Adviser K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

R. Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

R. Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

R. Berzym K., Cruzado L., Jimenez J., Sanchez M., Garzon A., Thode G.,

R. Lucas M., Rochet M., Gaillardin C., Tanlada V.A., Garzon A., Thode G.,

R. Dominguez A., Revuelta J.L., Moreno S., Amertrong J., Forsburg S.L.,

R. Mature 415:871-880 (2002).

R. Mature 415:871-880 (2002).

R. Nature 415:871-880 (2002).

R. Nature 415:871-880 (2002).

R. Nature 415:871-880 (2002).

R. Complex (By similarity).

C. C. COMPLEX (By similarity).

C. C. C. Complex (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBDATT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(1), beta(3), gamma(1), delta(1), epsilon(1). CF(0) seems to have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L) (By similarity).
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-!- SIMILARITY: Belongs to the eukaryotic ATPase epsilon family, not
to be confused with the bacterial/chloroplast ATPase epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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InterPro; IPR006721; ATP synth E.
Pfam; PF04627; ATP-synt Eps; I.
ATP synthesis; Cf(1); Hydrogen ion transport; Hydrolase;
Hypothetical protein; Mitochondrion.
SEQUENCE 67 AA; 7741 MW; 167ECBA30FC3BA48 CRC64;
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Schizosaccharomyces
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                                                                                                                     SEQUENCE FROM N.A.
                               NCBI_TaxID=4896;
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STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
MOSZER I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                         MEDLINE=11950559; PubMed=11953379;
DOI=10.1128/IAI.70.5.2419-2433.2002;
Nesper J., Kraiss A., Schild S., Blass J., Klose K.E., Bockemuhl J.,
                                                                                                                                                                                             "Comparative and genetic analyses of the putative Vibrio cholerae lipopolysaccharide core oligosaccharide biosynthesis (wav) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma pulmonis.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2107;
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                                                    Vibrio cholerae.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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Pred. No. 5.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                          Score 34; DB 2; Length 74; Pred. No. 6.4e+02; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome, Hypothetical protein.
SEQUENCE 55 AA; 7069 MW; FE0197BADCF9E677 CRC64;
                                                                                                                                                                                                                                                                                                   74 AA; 8845 MW; 2BDCD57E37F6FCE1 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) WavE (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001 (TIEMBLrel. 18, Last sequence update)
01-UTM-2003 (TIEMBLIE1. 24, Last annotation update)
Hypothetical protein MYPU 0720.
OrderedLocusNames=MYPU_0720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001 (TrEMBLrel. 18, Created)
                                                                                                                                                                                                                             Infect. Immun. 70:2419-2433 (2002).
EMBL; AF443847; AAL77348.1; -.
InterPro; IPR011122; WavE.
Pfan; PF07507; WavE; 1.
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                                                                                                                                                                                                                                                                                                                             49.3%;
50.0%;
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PIR; H90520; H90520.
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Similarity 61.5%;
8; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MypuList; MYPU 0720; -.
                                                                                                                                                                                                                                                                                                                                                                                                        56 YKKWTGLMIK 65
                                                                                                                                                                                                                                                                                                                                                                               3 YKKWKNKLLK 12
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Best Local Similarity
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=666;
                                                                                                                                                                                                                          cluster.";
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                    Reidl J.,
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Q9AZ27
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                                                                                                                          Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                Query Match
49.3%; Score 34; DB 2; Length 70;
Best Local Similarity 85.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.

Burger G., Lang B.F., Maier U.G., McFadden G.I., Gray M.
Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF288090; AAG17734.1; -..
GO; GO:0005739; C:mitochondrion; IEA.
Mitochondrion.
                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 70 AA; 8487 MW; CE9F137BA9BAD9B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Cryptophyta, Cryptomonadaceae, Rhodomonas
NCBI_TaxID=52970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 AA; 8959 MW; 221456EB5D4B7179 CRC64;
                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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Pred. No. 6.2e+02;
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                                        70 AA
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                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                            Ol-MAR-2004 (TrEMBLrel. 26, Li
01-MAR-2004 (TrEMBLrel. 26, Li
Hypothetical protein.
Name-ENV2029:
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54.5%;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.5'
                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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60 IIKKFRNKFLK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYKKWKNKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 LAKKWKN 32
                                                                                                                                                                                                                                                                                                                                                                                                                      2 LYKKWKN 8
                                                                                                                                                                    NCBI_TaxID=209882;
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                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrion.
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                                       Q7P7Z9
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QBRJL5
ID QBRJL
AC QBRJL
DT 01-JU
             RESULT 20
Q7P7Z9
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Q9G8W3
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Gaps

ä Gaps ., ,

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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.B., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                              MEDLINE=21442074; PubMed=11557893; DOI=10.1126/science.1061471; Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                       'Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
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                            Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
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Pred. No. 6.3e+02;
2; Mismatches 3; Indels
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SEOUENCE 50 AA; 6188 MW; B9909690BFA398F3 CRC64;
                                                                                                                                                                                                                                                                                                           50 AA; 5897 MW; A76789F7A87F3509 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 AA.
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J. Bacteriol. 184:4601-4611(2002).
EMBL; AE013991; AAM87419.1;
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DOI=10.1128/JB.184.16.4601-4611.2002;
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EMBL; AB008660; AAL03633.1; -.
PIR; G97836; G97836.
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Best Local Similarity 50.0%;
Matches 5; Conservative
                OrderedLocusNames=RC1095;
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                                                                                                                                       STRAIN=Malish 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=155148;
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Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI TaxID=28985;
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PubMed=14745027; DOI=10.1073/pnas.0304170101;
Butler G., Kenny C., Fagan A., Kurischko C., Gaillardin C.,
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Pred. No. 4.7e+02;
3; Mismatches 0; Indels
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Pred. No. 6.3e+02;
2; Mismatches 4; Indels
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J. Mol. Biol. 311:657-679(2001).
EMBL; AP35538; AAX2862.1; -.
InterPro; IPRO10444; Lambda Kil.
Fin Pro6301; Lambda Kil.
SFOIIENCE 37 AA; 4456 MW; 5346C9C7AD3092F6 CRC64;
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Last sequence update)
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Cwc25 protein (Fragment).
                                                 Last sequence update)
Last annotation update)
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Froc. Natl. Acad. Sci. U.S.A. 101:1632-1637(2004).
Embl.; AJ617304; CAE84414.1; -.
NON TER 50 50
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37 AA
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Best Local Similarity 57.1%;
Matches 4; Conservative
                                                (TrEMBLrel. 17, (TrEMBLrel. 26,
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Best Local Similarity 50.0
Matches 6; Conservative
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PRELIMINARY;
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31 YRKWRSK 37
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01-DEC-2001 (
01-JUN-2003 (
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01-JUN-2001
01-MAR-2004
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                                                                                                     Name=kil;
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                 Q9AZ27;
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Q707Z1
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Thiemer C.A., Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                        MEDLINE-97250136; PubMed-9096222; DOI=10.1006/jmbi.1996.0867; Monod C., Repoila F., Kutateladze M., Tetart F., Krisch H.M.; "The genome of the pseudo T-even bacteriophages, a diverse group that resembles T4.";
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Bertrand C., Petrov V., Nolan J., Letarov A., Desplats C., Chin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOI=10.1128/JB.184.10.2789-2804.2002;
Desplats C., Dez C., Tetart F., Eleaume H., Krisch H.M.;
"Snapshot of the genome of the pseudo-T-even bacteriophage RB49.";
J. Bacteriol. 184:2789-2804(2002).
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Tetart F., Desplats C., Kutateladze M., Monod C., Ackermann H.-W.,
Krisch H.M.;
                                                                             Enterobacteria phage RB49.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
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Ang D., Alchardson A., Mayer M.P., Keppel F., Krisch H.,
Ang Octopoulos C.;
Georgopoulos C.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desplats C., Dez C., Tetart F., Bleaume H., Krisch H.M., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-2000) to the BMBL/GenBank/DDBJ databases.
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Zhao L., Tetart F., Krisch H.M., Arisaka F.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Letarov A.V., Krisch h.M., Tetart P.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
(TrEMBLrel. 25, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=21972795; PubMed=11976309;

    Mol. Biol- 267:237-249(1997).

                                      Hypothetical protein. ORFNames=RB49ORF263c;
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Submitted (JUL-2001)
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"Gene arrangement in the upstream region of Clostridium botulinum type "Gene arrangement in the upstream region of Clostridium butyricum BL6340 progenitor toxin genes is different from that of other types.";

FEMS Microbiol. Lett. 158:215-221(1998).

EMBL; AB004778; BAA24886.1;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment).
                                                                                                                                                                                                Kubota T., Yonekura N., Hariya Y., Isogai E., Isogai H., Amano K.,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                         Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 6.8e+02;
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Pred. No. 6.5e+02;
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                                                                                                                                                                                                                                                                                                                                                          51 AA; 5998 MW; 834EB4A69DD1157F CRC64;
  01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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MEDLINE=95372366; PubMed=7644496;
Gupta X., Hassel T., Singh J.P.;
Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR00143; C-X-C/Interlkn 8.
InterPro; IPR001811; Chemokine ILB.
InterPro; IPR00189; CXC_chmkine_smll.
Pfam; PF00048; ILB; 1.
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                                                                                                                                                           STRAIN=type A Kyoto-F;
MEDLINE=98126542; PubMed=9465394;
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PRINTS; PRO0433; SMALLCYTKCXC.
SMART; SM00199; SCY; 1.
SEQUENCE 54 AA; 6033 MW; C
                                                                                                                                                                                                                                                                                                                                                                                                   47.88;
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Best Local Similarity
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                                                                               Clostridium.
NCBI_TaxID=1491;
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Q9UC64

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AC 09UC6
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DR GO; G
DR GO; G
DR GO; C
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DR PRINT
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**Q7**X3H6

RESULT 30 0773H6 ID 07 AC 07 DT 01

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Glaser P., Frangel L., Buchrieser C., Rusnick C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Butian K.-D., Fahih H., Gamcz-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Comparative genomics of Listeria species.";
         "Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
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dlardia_lamblia_Arcc_50803.
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBI_TaxID=184922;
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Pred. No. 7.9e+02;
1; Mismatches 5; Indels
                                                                                                                                                                      Score 33; DB 2; Length 62;
Pred. No. 7.8e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria
                                                             Nature 423:87-91(2003).
EMBL, AE017006; AAP09460.1; -.
CCMplete proteome; Hypothetical protein.
SEQUENCE 62 AA; 7549 MW; 3C8CCS82A544EFDI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 AA; 7418 MW; B7A15C4291E86115 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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53.8%;
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Overbeek R., Kyrpides N.C.;
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Best Local Similarity 53.0.
7; Conservative
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                                                                                                                                                                                          Best Local Similarity 55.6
Matches 5; Conservative
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28 LYSQWENHL 36
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Q929V4
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Am. J. Trop. Med. Hyg. 52:241-246(1995).
EMBL; S75632; AAB13855.1.
Pfam; PF00948; Flavi_NS1; 1.
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MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Maur M., Goltsman B., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
                                                                                                                                                                            Gaps
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Flavivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95208980; PubMed=7694966;
Guzman M.G., Deubel V., Pelegrino J.L., Rosario D., Marrero M.,
Sariol C., Kouri G.;
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                                                                                                                             Score 33; DB 2; Length 58; Pred. No. 7.3e+02; Mismatches 1; Indels
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Pred. No. 7.6e+02;
0; Mismatches 1; Indels
                      EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                      BDDAAC685C1A457E CRC64;
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ProDom; PD001496; Flavi_NS1; 1.
Karam J.D., Krisch H.M.;
Submitted (JUL-2003) to the J
EMBL; AX34333; AA015470.1;
Hypothetical protein.
SEQUENCE 58 AA; 6858 MW;
                                                                                                                                 47.8%;
62.5%;
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60 AA; 6431 MW;
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nes 6; Conservative
                                                                                                                                                      Best_Local Similarity 62.9
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyprotein (Fragment)
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9 YKIWKNQV 16
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01-DEC-2001
01-MAR-2002
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Gaps

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SEQUENCE FROM N.A.

Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
Rattei T., Mewes H.-w., Wagner M.;
"Genome sequence of an amoeba symbiont and its use for reconstructing
the evolutionary history of chlamydiae.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX908798; CAR-2364.1.; ...
Complete proteome; Hypothetical protein.
SEQUENCE 63 AA; 7680 MW; C17E99528180C856 CRC64;
                                                                           MEDLINE=22668415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kaparal V., Bhattacharyya A., Reznik G., Mithailova N., Lapidus A., Grechkin Y., Bhattacharyya A., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeck R., Xyrgides N.C.; Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32.5; DB 2; Length 63;
Pred. No. 9.5e+02;
                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2; Length 72;
Pred. No. 9e+02;
3; Mismatches 1; Indels
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=226900;
                                                                                                                                                                                                                                  Nature 423:87-91(2003).
EMBL; AE017001; AAP08084.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 72 AA; 8030 MW; DEF6B66451ACA507 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=pc0917;
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Last annotation update)
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50.0%;
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57.1%;
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Best Local Similarity 57.11
Best Local 8; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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24 IYROWKEK 31
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Q821Y9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947; Rocap G., Larimer P.W., Lamerdin O.E., Malfatti S., Chain P., Rocap G., Larimer P.W., Lamerdin O.E., Malfatti S., Chain P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolomen A., Webb B.A., Zinser E.R., Chisholm S.W.; "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
                                                       Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                       Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.
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Pred. No. 8.6e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                    47.8%; Score 33; DB 2; Length 65; 33.3%; Pred. No. 8.2e+02;
                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                      preliminary data.
EMBL; AACB01000006; EAA42442.1; -.
SEQUENCE 65 AA; 7800 MW; 978634866F1F1980 CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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OrderedLocusNames=BC1097;
Bacillus cereus (strain ATCC 14579 / DSM 31).
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EMBL; BX572093; CAE19734.1; -.
GO; GO:0006790; P:sulfur metabolism; IEA.
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Interpro; IPR010033; Thi S.
Pfam; PF02597; This; 1.
IGRPAMS; TIGR01683; this; 1.
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hes 5; Conservative
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KKWDSEILK 55
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Matches 4; Conserv
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SEQUENCE 69 AA;
     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prochlorococcus.
NCBI_TaxID=59919;
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01-JUN-2003 (
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PubMed=1521334; DOI=10.1073/pnas.0402521101;
PubMed=1521334; DOI=10.1073/pnas.0402521101;
Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Holden M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
James K.D., Lennard S., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
                  PubMed=1521324; DDI=10.1073/pnas.0402521101;
Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Holden M.T.G., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Spratt B.G., Parkhill J.;
Spratt B.G., Parkhill J.;
evidence for the rapid evolution of virulence and drug resistance.";
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
Proc. Natl. Acad. 861. U.S.A. 101:9786-9791 (2004).
EMBL; BX571856; CAG41013.1; -
Complete protecome; Hypothetical protein.
SEQUENCE 32 AA; 3996 MW; 20A616AF92F2ADDA CRC64;
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Pred. No. 6e+02;
0; Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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EMBL; BX571857; CAG43665.1;
Complete proteome.
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ORFNames=SAR2027a;
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                               GPIC):
                              Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T., Heidelberg J.F., Holtzapple E.K., Khouri H.M., Federova N.B., Carty H.A., Umayam L.A., Haft D.H., Peterson J.D., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M., Fraser C.M.; "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baba I., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Magai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramateu K., Ramamoto K., Hiramateu K., Renome and virulence determinants of high virulence community-
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                         MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
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                                                                                                                                                                                                                                                                                                                                                                 46.4%; Score 32; DB 2; Length 31; 100.0%; Pred. No. 5.8e+02;
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EMBL, APO04828; BAB95742.1; -.
Complete protecome; Hypothetical protein.
SEQUENCE 32 AA; 3996 WW; 20A616AF92F2ADDA CRC64;
                                                                                                                                                                                                                                                                                                                       31 AA; 3740 MW; 9D85868E6E2949A5 CRC64;
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Last annotation update)
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Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus (strain MSSA476).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxIb=282459;
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                                                                                                                                                                                                                              Nucleic Acids Res. 31:2134-2147(2003).
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01-OCT-2002 (TrEMBLrel. 22, I
Hypothetical protein MH377 orderedLocusNames=WM1877;
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OrderedLocusNames=SAS1859;
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Matches 5; Conserv
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A pitchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garrica A.M., Gay L.J., Hulyk S.W.,
A Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 6.3e+02;
1; Mismatches 3; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015586; AAH15586.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 AA; 4086 MW; 14BFE472AA5E10C1 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II antigen (Fragment).
Name=HLA-DRB6;
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Last annotation update)
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Immunogenetics 48:16-21(1998).
EMBL; U33547; AAC26400.1; -.
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                                                                                              Homo sapiens (Human)
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                                                                                                                                                                                 NCBI_TaxID=9606;
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SEQUENCE
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1096BH6
AC 096BH AC 096BH DT 01-MA DT 
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Score 32; DB 2; Length 38;

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Query Match

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MEDLINE=99403018; PubMed=10471724;
Rabinowicz P.D., Braun E.L., Wolfe A.D., Bowen B., Grotewold E.;
Majze R2R3 Myb genes Sequence analysis reveals amplification in the
Gaps
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MEDLINE=2164373; PubMed=11792842; DOI=10.1073/pnas.022493799;
MEDLINE=2164373; PubMed=11792842; DOI=10.1073/pnas.022493799;
Shimizu T., Ohtani K., Harkawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003189; BAB80825.1; -.
                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
R2R3MYB-domain protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein CPE1119.
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Pred. No. 7.9e+02;
3; Mismatches 3;
1,
                                                                                                                                                                           . 43 AA
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2; Mismatches
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR009057; Homeodomain like
InterPro; IPR001005; Myb_DNA_binding.
PROSITE; PS50090; MYB_3; 1.
                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
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EMBL; AF099430; AAF04705.1; -.
HSSP; P06876; 1GV2.
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Best Local Similarity 45.5%,
Conservative
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Conservative
                                                                                                                                                                         PRELIMINARY;
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24 LHARWRNKWSK 34
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8 HRIWKNKL 15
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SEQUENCE 57 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1502;
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0,
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Query Match 46.4%; Score 32; DB 2; Length 57; Best Local Similarity 58.3%; Pred. No. 1e+03; Matches 7; Conservative 2; Mismatches 3; Indels
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2 LYKKWKNKLLKS 13 : || |||:| | 4 IIKKLKNKILWS 15

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Search completed: May 16, 2005, 08:30:30 Job time : 56.8017 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 74.9483 Seconds (without alignments) 92.887 Million cell updates/sec Run on:

1 KLYKKWKNKLKRSLKRLG 18 US-09-648-816B-10 95 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

1066881

DB seq length: 0 DB seq length: 74 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesem20018:\* genesem20028:\* genesem2003as:\* genesem2003bs:\* genesem20048:\* A\_Geneseq\_16Dec04:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp1980s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |        | Description  | Aay57472 Antimicro | Abg69896 Rabbit pl | Antimic  | Abg69889 Rabbit pl | Aay57501 Antimicro |          | Abg69923 Rabbit pl |          |          | Abg69926 Rabbit pl |          |          | Peptide  |          | Abg69921 Rabbit pl | Ad170276 Peptide a | Ad170278 Peptide a | Abg69990 Rabbit pl | Abg69992 Rabbit pl | Antimic  | Aay57504 Antimicro | Abg69928 Rabbit pl | Abg69927 Rabbit pl | Aay57500 Antimicro | Abg69924 Rabbit pl |
|-----------|--------|--------------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|----------|----------|--------------------|----------|----------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|
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| SUMMARIES |        | OI           | AAY57472           | ABG69896           | AAY57465 | ABG69889           | AAY57501           | AAY57499 | ABG69923           | ABG69925 | AAY57502 | ABG69926           | AAY57496 | ABG69920 | ADL70275 | AAY57497 | ABG69921           | ADL70276           | ADL70278           | ABG69990           | ABG69992           | AAY57503 | AAY57504           | ABG69928           | ABG69927           | AAY57500           | ABG69924           |
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|           |        | Match Length | 18                 | 18                 | 18       | 18                 | 19                 | 19       | 19                 | 19       | 20       | 20                 | 25       | 25       | 33       | 35       | 35                 | 36                 | 39                 | 40                 | 40                 | 18       | 18                 | 18                 | 18                 | 18                 | 18                 |
| æ         | Query  | Match        | 100.0              | 100.0              | 67.4     | 67.4               | 67.4               | 67.4     | 67.4               | 67.4     | 67.4     | 67.4               | 67.4     | 67.4     | 67.4     | 67.4     | 67.4               | 67.4               | 67.4               | 67.4               | 67.4               | 63.2     | 63.2               | 63.2               | 63.2               | 62.1               | 62.1               |
|           |        | Score        | 95                 | 95                 | 64       | 64                 | 64                 | 64       | 64                 | 64       | 64       | 64                 | 64       | 64       | 64       | 64       | 64                 | 64                 | 64                 | 64                 | 64                 | 9        | 9                  | 9                  | 9                  | 59                 | 59                 |
|           | Result | No.          | 1                  | 8                  | m        | 4                  | S                  | 9        | 7                  | 80       | σ        | 10                 | 11       | 12       | 13       | 14       | . 15               | 16                 | 17                 | 18                 | 19                 | 20       | 21                 | 22                 | 23                 | 24                 | 25                 |

| Aay57471 Antimicro Abg6895 Rabbit pl Aay57505 Rabbit pl Adg68929 Rabbit pl Ad170277 Peptide a Aay57470 Antimicro Abg68984 Rabbit pl Aar13930 Cationic Aar13930 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar13936 Cationic Aar21364 Sequence Aab70666 Lupine RC Aab70668 Lupine RC Aab416 Rabbit CA Ad670763 Rabbit CA Aae34418 Rabbit CA Aae34418 Rabbit CA Aae34418 Rabbit CA Aae34419 Rabbit CA Aae34419 Rabbit CA Aae34419 Rabbit CA |
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## ALIGNMENTS

Antimicrobial peptide RP-8 SEQ ID NO:10. AAY57472 standard; peptide; 18 AA. 25-FEB-2000 (first entry) AAY57472; 

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

Oryctolagus cuniculus. Synthetic.

WO9942119-A1.

26-AUG-1999,

99WO-US003350. 17-FEB-1999; (HARB-) HARBOR-UCLA RES & EDUCATION INST.

98US-00025319

18-FEB-1998;

Yeaman MR, Shen AJ;

WPI; 1999-527417/44.

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure; Page 111; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBZBXBXB, BXZXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBXXBB, XBBXZXBB, and their derivatives selected from the group consisting of XBBXBBX, ABBXBBX, BXXBXXB, XBBZXXBB, and XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 anino acida cornelaring a 7-13 amino acida core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions, and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, especializally against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rabbit platelet microbicidal protein, PMP-2, based peptide #8
                                                                                                                              Length 18;
                                                                                                                                                                    0; Indels
                                                                                                                            100.0%; Score 95; DB 2; I 100.0%; Pred. No. 2.5e-06;
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                                                                                                                                                                                                                                                                                                                                                        ABG69896 standard; peptide; 18 AA
                                                                                                                                                                                                                                         KLYKKWKNKLKRSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                               Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeaman MR, Shen AJ;
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                                                                                     Sequence 18 AA;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against activity or for potentiating and fundi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, XBBXZXBB, and BBXZBBXZ; and (b) a second peptide template XBBXXBXB, XBBXZBBX and BBXZBBXZ; and (b) a second peptide template XBBXXBBX, BXXBXB, XBBXXXBB, and consisting of KBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and consisting of KBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and consisting of KBBXBBX, XBBXXBBX, BXXBXXB, XBBXXXBB, and consisting of KBBXBBX, ABBXXBBX, BXXBXXB, ABBXXBB, and consisting of KBBXBBX, BXBBX, BXBXXBB, and consisting of KBBXBBX and Last one non-polar hydrophobic amino acid; Z = at least one non-polar hydrophobic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAYS7463 to AAYS757 represent sequences used in the exemplification of the present invention
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been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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Pred. No. 2.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial peptide RP-1 SEQ ID NO:3.
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                        Sequence 18 AA;
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Sequence 18 AA;

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from perturbations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are [1] an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fundions and full or and increased and containing an antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance the antimicrobial agents that chance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that have potent and broad are based upon natural antimicrobial peptides that have potent and broad create based upon natural antimicrobial peptides that have potent and create based upon natural antimicrobial peptides considered to have undesirable toxicity, immunogenicity, and shortness of duration of resistance. They exhibit lower inherent mammalian cell toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, tretaining activity y and and considered and considered and cons
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                                             Gaps
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    Length 18;
                                             2; Indels
Score 64; DB 2;
Pred. No. 0.051;
                                             2; Mismatches
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                                                                                                                      2 LYKKFKKKLLKSLKRLG 18
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67.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes an antimicrobial peptide (AP) for direct
serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                     Length 18
                                                                                                        2; Indels
                                                                   Score 64; DB 5;
Pred. No. 0.051;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial peptide 19C-RP-1 SEQ ID NO:39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                  AAY57501 standard; peptide; 19 AA
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                                                                                                                                                               2 LYKKFKKKLLKSLKRLG 18
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                                                                 Query Match
Best Local Similarity 76.5'
Matches 13, Conservative
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                                    Sequence 18 AA;
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LYKKFKKKLLKSLKRLG 18

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXXXXB, XBBXXXBX and EBXZBXZ, and (b) a second peptide template XBXX and their derivatives selected from the group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBXXBBX, and consisting of XBBXBBX, XBBXXBB, BXXBXXB, BXBBXXBB, and CABX ABBXXBBX, WBBXXBBX, BXXBXXB, ABBXXBBX, and consisting of XBBZBXBBX, XBBXXBB, BXXBXXB, ABBZXXBB, and consisting of XBBZBXBBX, ABBXXBBX, BXXBXXB, ABBZXXBB, and consisting of XBBZBXBBX, ABBXXBBX, BXXBXXB, BXXBXB, and consisting on on-polar hydropholic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY5757 represent sequences used in the exemplification of the present invention
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                                                                                AAY57499 standard; peptide; 19 AA
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acide containing a 7-13 amino acid core sequence (derived from pwp-1 and pwp-2, platelet microbical protein), and recromers, runcations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13.74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) actimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other specifically against bacteria that enhance the antimicrobial agents of conventional antimicrobials, agents that enhance the antimicrobial conventional antimicrobials, agents to improve efficiency of conventional antimicrobials, agents to improve efficiency of functions of leukocytes, as disinfectants or preservatives for use in thoolay techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short of biology techniques. Antimicrobial peptides of prior art have generally become archivity against pathogens exhibiting multiple antibiotic conservations are based upon natural antimicrobial peptides with the present and broad spectrum activity against pathogens exhibiting multiple antibiotic or resistance. They exhibit lower inherent mammaliance of diviration and an advance of the sension are an advanced or the sension of the sension are an advanced or the sension are an advanced or the sension are sensions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
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                                                                     Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                      Rabbit platelet microbicidal protein, PMP-2, based peptide #35
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Best Local Similarity 76.5
Matches 13; Conservative
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 anino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and retromers, extensions, combinations and fusions; and (2) and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobials peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad appetrum activity against pathogens exhibiting multiple antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradenion, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                    Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                       Rabbit platelet microbicidal protein, PMP-2, based peptide #37
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ABG69925 standard; peptide; 19 AA
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activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZRBXB and its derivatives selected from XZBBZRBXB. BXZXB. XBBXZXBBX and their derivatives selected from the group consisting of XBBXZBBXB. BXZXB. XBBXZXBBX and BBXZBBXZ; and (b) as second opeptide template XBBXZXBB. XBBXZXBBX. ABBXZXBBX. BXZXBBXXBBX. and (b) XBBZXXBBXZBBX; where B at least one positively charged amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides overall effect cellular disruption and rapid apportosis of microbial cells. AAY57463 to AAY57557 represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                 Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                   Antimicrobial peptide OC, 19C-RP-1 SEQ ID NO:40.
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                               AAY57502 standard; peptide; 20
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                                                                                                                                                                                                                                                                                                                                      99WO-US003350.
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                                                                                                25-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 76.5'
Best Local Similarity 76.5'
Conservative
                                                                                                                                                                                                                                    Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                          Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                    17-FEB-1999;
                                                                                                                                                                                                                                                                     WO9942119-A1
                                                                                                                                                                                                                                                                                                       26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeaman MR,
                                                                                                                                                                                                                    Synthetic.
                                                                  AAY57502;
RESULT 9
                   AAY57502
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ABG69926 standard; peptide; 20

RESULT 10

**ABG69926** 

21-OCT-2002 (first entry)

ABG69926;

SXXXX

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Gaps ö

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

Oryctolagus cuniculus

Synthetic

WO9942119-A1

Antimicrobial peptide RP-1+RP-1-10 SEQ ID NO:34.

(first entry)

25-FEB-2000

AAY57496 standard; peptide; 25 AA.

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide corresions containing a 7-13 amino acide core sequence (derived from PWP-1 and PMP-2, platelet microbial protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as active against organisms such as attimicrobial and peptide composition for direct activity or or for potentiating an peptide of 13-7 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial activity of conventional antimicrobials, agents that enhance, potentiate or restore efficacy of conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad are based upon natural antimicrobial peptides that have potent and broad are based upon natural antimicrobial peptides that have potent and broad are based upon natural antimicrobial peptides that have potent and broad are based upon natural antimicrobial peptides of prior art have generally appetite and as agents that manimum activity against pathogens exhibiting multiple antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                       Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                        Rabbit platelet microbicidal protein, PMP-2, based peptide #38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 72; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                            Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeaman MR, Shen AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
                                                                                                                                                             mutant; mutein.
                                                                                                                                                                                                                                                                                         WO200255554-A2
                                                                                                                                                                                                                                                                                                                                              18-JUL-2002.
                                                                                                                                                                                                                                     Synthetic.
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Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure; Page 126; 166pp; English.

(HARB-) HARBOR-UCLA RES & EDUCATION INST

Shen AJ;

Yeaman MR,

WPI; 1999-527417/44.

98US-00025319.

18-FEB-1998;

17-FEB-1999;

26-AUG-1999

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2 LYKKWKNKLKRSLKRLG 18
                                                                               21-OCT-2002 (first entry)
                                            13, Conservative
                    Query Match
Best Local Similarity
Sequence 25 AA;
                                              Matches
                                                                                                                           RESULT 12
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                                                                                         g
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                                                                                                                                                              Gaps
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                                                                                                                                      67.4%; Score 64; DB 5; Length 20; 76.5%; Pred. No. 0.057; ive 2; Mismatches 2; Indels
                                                                                                                                                           2; Indels
                                                                                                                                                                                    18
                                                                                                                                                                                                LYKKWKNKLKRSLKRLG
                                                                                                                                                             13; Conservative
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RESULT 11 AAY57496

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against croganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXENE and its derivatives selected from XZBBZRARE, BXZXZB, XBBXZXBBX and BMZZBBXZ, and (b) a second peptide template XBBXXB, BXXXXBX, XBBXZBBX, and (b) group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXBB, and XBBXXBBBX, where B = at least one positively charged amino acid, x = at least one positively charged amino acid, x = at least one speared by one or more other amino acid, and where B, X and Z may be separated by one or more other camino acids. The peptides can be used to treat bacterial and fungal nections. The peptides also increase the antimicrobial activity of neutrophils. The peptides also increase the antimicrobial activity of apoptosis of microbial effect cellular disruption and rapid apoptosis of microbial activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbit platelet microbicidal protein, PMP-2, based peptide #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.4%; Score 64; DB 2; Length 25; 76.5%; Pred. No. 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG69920 standard; peptide; 25 AA.
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Protide; ar infection.
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                                                                                                                                                                                                                                                                                                                                                                          The invertion features to an antimuticibility comprising a peptide of 5-
150 amino acids containing a 7-13 amino acid core sequence (derived from
PMP-1 and PMP-2. platelet microbiocidal protein), and retromers,
truncations, extensions, combinations, fusions and their derivatives. The
possible structures are fully described in the specification. Also
included are (1) an antimicrobial peptide composition for direct activity
or for potentiating antimicrobial peptide composition for direct activity
or for potentiating antimicrobial agents active against organisms such as
bacteria and fungi comprising a peptide of 13-74 containing an amino acid
core sequence selected from truncations of the peptides described above,
and retromers, extensions, combinations of the peptides described above,
antimicrobial peptides for potentiating antimicrobial activity of
antimicrobial peptides are useful as individual antimicrobial agents
conventional antimicrobials, agents that enhance the antimicrobial agents
conventional antimicrobials, agents that enhance the antimicrobial
conventions of leukocytes, as disinfectants or preservatives for use in
conventional antimicrobial peptides of prior art have generally
conventions and as agents to improve efficiency of molecular
biology techniques. Antimicrobial peptides of prior art have generally
check onsidered to have undesirable toxicity, immunogenicity and short
half-lives due to biodegradation. The peptides that have potent and broad
spectrum activity against pathogens exhibiting multiple antibictic
cresistence. They exhibit lower inherent mammallan cell toxicities and
cresistence are inherent mammallan cell toxicities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                       New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
 preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                                                                                                                                                                                                    invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.4%; Score 64; DB 5; Length 25; 76.5%; Pred. No. 0.07; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL70275 standard; peptide; 33 AA.
                                                                                                                                                                                                                                                                                                                                      Example; Page 70; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LYKKWKNKLKRSLKRLG 18
                                                                                                                    24-AUG-2001; 2001WO-US041877.
                                                                                                                                                  25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide antibiotide PT-1.
                             Oryctolagus cuniculus
                                                                                                                                                                                                              Shen AJ;
                                                                                                                                                                                                                                            WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 AA;
                                                           WO200255554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-2004
                                                                                        18-JUL-2002
                                                                                                                                                                                                              Yeaman MR,
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The present sequence is that of Protide-1 (PT-1), a peptide antibiotide with distinct effector and activator domains. PT-1 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific distinct effectors in the presence of the processe. PT-1 was designed to be cleaved into 2 distinct effectors in the presence of v8 protease. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the absence of v8 protease, but equivalent to or exceeding that of RP-1 in the absence of v8 protease produced by Staphylococcus aureus. Thus, PT-1 was designed to exert optimal antimicrobial activity in the context of infections due to staphylococcal cells elaborating the virulence factor v8 protease. PT-1 was synthesised by Staphylococcus aureus of an example of context-activated procides of the invention that have 2 or more effectors with individual distinct biological functions and one or more effectors upon context activation. The biological function of one or more effectors upon context activation. The proteins and therapy of a broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapa
antibiotide; antimicrobial; interleukin-8; Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                               /note= "Cleaved by V8 protease"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brass EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1; 103pp; English.
                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY57497 standard; peptide; 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 LYKKFKKKLLKSLKRLG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2003; 2003WO-US026405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2002; 2002US-00225562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yount NY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-226740/21.
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                   WO2004017985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33 AA;
                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeaman MR,
                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY57497;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid corre sequence (derived from PMP-1 and PMP-2, platelet microbical protein), and recromers. PMP-1 and PMP-2, platelet microbical protein), and recromers. PMP-1 and PMP-2, platelet microbical protein), and recromers. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as corresponding comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents that enhance the antimicrobial agents that enhance in combination with other specifically against bacteria and fungi, agents in combination with other conventional antimicrobials, agents that enhance the antimicrobial for conventional antimicrobials, agents to improve efficiency of molecular (conventions of leukocytes, as disinfectants or preservatives for use in the foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short to biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of prior art have generally become problems of toxicity immunogenicity, and shortness of defectiveness due to biodegradation, retaining activity in plasma and conversion problems of toxicity, immunogenicity, and shortness of effectiveness due to biodegradation, retaining activity in plasma and conversion problems of toxicity in plasma and antimicrobial peptides and antimicrobial peptides and antimicrobial peptides and antimicrobial peptides of the present sequence is a rabbit pwp based antim
                                                                                                                                              New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 67.4%; Score 64; DB 5; Length 35; Best Local Similarity 76.5%; Pred. No. 0.098; Matches 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protide; antibiotide; antimicrobial; interleukin-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16. .17
/note= "Cleaved by C3 convertase"
                    (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL70276 standard; peptide; 36 AA.
                                                                                                                                                                                                                                         Example; Page 71; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide antibiotide PT-2.
                                                               Shen AJ;
                                                                                                        WPI; 2002-590659/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004017985-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-2004
                                                               Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL70276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rabbit platelet microbicidal protein, PMP-2, based peptide #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.4%; Score 64; DB 2; Length 35; 76.5%; Pred. No. 0.098; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                         (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 126; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69921 standard; peptide; 35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 LYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2001; 2001WO-US041877.
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                                                                                                                                                     99WO-US003350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 76.5¹
Matches 13; Conservative
                    Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                    Shen AJ;
                                                                                                                                                                                                                                                                                                                           WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200255554-A2
                                                               WO9942119-A1
                                                                                                                                                     17-FEB-1999;
                                                                                                                                                                                              18-FEB-1998;
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                                                                                                          26-AUG-1999.
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                                                                                                                                                                                                                                                                                    Yeaman MR,
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG69921;
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Gaps

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The present sequence is that of Protide-2 (PT-2), a peptide antibiotide with distinct effector and activator domains. PT-2 contains a C-terminal cantimicrobial peptide effector (RP-1), an N-terminal chemokine-like peptide effector (interleukin-8 domain) and an activator site specific for C3 convertase, a complement fixing procease. PT-2 is cleaved into 2 distinct effectors in the presence of C3 convertase. In particular, it was designed to exert antimicrobial activity less than that of RP-1 in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert in the presence of C3 convertase. Thus, PT-2 was designed to exert of the innate immune response to antigen exposure. PT-2 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The prove corresponding activator sites that can each initiate or amplify the protein an each in the work of a broad and one or more effectors upon context activation. The provence of the presence of the presence of the provence of the provence of the provence of the presence of the provence of the provence of the provence of the presence of the provence of the provence of the provence of the pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protide; antibiotide; antimicrobial; interleukin-8; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                           Brass EP
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/note= "Cleaved by MMP-9"
                                                                                                                                                                                                                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           Edwards JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               range of pathological conditions.
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                                                                               20-AUG-2003; 2003WO-US026405
                                                                                                                                                               20-AUG-2002; 2002US-00225562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                           Yount NY,
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-226740/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004017985-A1.
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04-MAR-2004
                                                                                                                                                                                                                                                                                                                           Yeaman MR,
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The present sequence is that of Protide-4 (PT-4), a peptide antibiotide with distinct effector and activator domains. PT-4 contains a C-terminal antimicrobial peptide effector (RP-1), an N-terminal chemokina-like antimicrobial peptide effector (RP-1), an N-terminal chemokina-like peptide effector (interleukin-8 domain) and an activator site specific for matrix metalloproteinase MMP-9, which is produced to dissolve the crissue in front of the growing blood vessel tip to allow for its continued tissue invasion. PT-4 was designed to be cleaved into 2 distinct effectors in the presence of MMP-9. In particular, PT-4 exerts artineoplastic and/or antimicrobial activity less than that of RP-1 in the presence of MMP-9, but equivalent to or exceeding that of RP-1 in the presence of MMP-9. Thus, PT-4 exerts optimal antimoplastic and/or antimicrobial activity in the context of new blood vessel formation. PT-4 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one corresponding activator sites that can each initiate or amplify the protides are useful in the disagnosis, prophylaxis and therapy of a broad range of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                        New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit platelet microbicidal protein, PMP-2, based peptide #102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.4%; Score 64; DB 8; Length 39; 76.5%; Pred. No. 0.11; 2; Indels iive 2; Mismatches 2; Indels
                                                     Brass EP;
               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
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                                                                                                                                                                                                       Claim 1; SEQ ID NO 4; 103pp; English
                                                     Yount NY, Edwards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG69990 standard; peptide; 40 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shen AJ;
                                                                                      WPI; 2004-226740/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutant; mutein.
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                                                     Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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Matches
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ABG69990
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-
150 amino acide containing a 7-13 amino acide fore sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The PMP-1 and PMP-2 platelet microbial peptide composition for direct activity or for potentiating antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and funsions; and (2) antimicrobial peptides for potentiating antimicrobial agents, extensions such as absceria and fungi. The entimicrobial peptides are useful as individual antimicrobial agents (antimicrobial peptides are useful as individual antimicrobial agents (antimicrobial peptides are useful as individual antimicrobial peptides are useful as individual antimicrobial peptides of conventional antimicrobials, agents that enhance the antimicrobial for antimicrobial agents that enhance the antimicrobial peptides of foods and cosmetics and as agents to improve efficiency of foods and cosmetics and as agents to improve efficiency of molecular of foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic creststance They exhibit lower inherent mammalian cell toxicity and shortness of defectiveness due to biodegradation, relatining activity in plasma and companients.

The present sequence is a rabbit pMP based antimicrobial peptides
                                                                              New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.4%; Score 64; DB 5; Length 40; 76.5%; Pred. No. 0.11; 2; Indels tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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                                                                                                                                                                                                                                            Example; Page 67; 221pp; English.
                                                                                                                                                                 multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LYKKWKNKLKRSLKRLG 18
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Best Local Similarity 76.5
Matches 13; Conservative
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Synthetic.
WPI; 2002-590659/63
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25-AUG-2000; 2000US-00648816. 24-AUG-2001; 2001WO-US041877

WO200255554-A2.

18-JUL-2002

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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acid a containing a 7-13 amino acid acore sequence (dearload from 150 amino acid a containing a 7-13 amino acid a core sequence (dearload from PWP-1 and PWP-2, platelet microbicial protein), and retromers.

Truncations, extensions, combinations, fusions and their derivatives. The consible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of attimicrobial peptides are useful as individual antimicrobial agents.

Colessor and activity of a sequence sequence sequence sequence are and fungi, agents in combination with other antimicrobial peptides are useful as individual antimicrobial agents.

Conventional antimicrobials, agents that enhance the antimicrobial are conventional antimicrobials, agents to improve efficiency of functions of leukocytes, as disinfectants or preservatives for use in the foods and cosmetics and as agents to improve efficiency of molecular considered to have undesirable toxicity, immunogenicity and short or are based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicity and shortness of testitance or resistance is a rabbit pwp based antimicrobial peptides or effectiveness and event and an administration, retaining activity in plasma and companience is a rabbit pwp antimicrobial peptides.
                                                                                                                                                       New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 67.4%; Score 64; DB 5; Length 40; Local Similarity 76.5%; Pred. No. 0.11; les 13; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial peptide RP-1-2R SEQ ID NO:41.
                   (HARB-) HARBOR-UCLA RES & EDUCATION INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Æ
                                                                                                                                                                                                                                                    Example; Page 67; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY57503 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LYKKWKNKLKRSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09942119-A1.
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                                                                Yeaman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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Matches
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18-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                              ABG69928
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                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                         activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZENENE and its derivatives selected from XENEXZENENE and its derivatives selected from the group consisting of XBENENE, BXZXXXB, XBEXZENEN and BEXZBENZ; and (b) a second peptide template XBENZXENEN, XBENZXENEN, BYENZXENEN, and Capture or SERENCE, where B = at least one positively charged amino acid; at least one non-polar hydrophobic amino acid; at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acid, and where B, X and Z may be separated by one or more other infections. The peptides can be used to treat bacterial and fungal neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. ANYS7463 to ANYS7557 represent sequences
                                                                                                                                                                 present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                           Antimicrobial peptides for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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0
                                                                                                                                                                                                                                                                                                                                                                            63.2%; Score 60; DB 2; Length 18; 75.0%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                   used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrobial peptide RP-1-10F SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                           (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                            Disclosure; Page 59; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY57504 standard; peptide; 18 AA
99WO-US003350
                     98US-00025319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    YKKFKKKLLKSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                       3 YKKWKNKLKRSLKRLG 18
                                                                                                                       against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 75.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-527417/44.
                                                                 Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeaman MR, Shen AJ;
                                                                                     WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                     18-FEB-1998;
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17-FEB-1999;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXENS and its derivatives selected from XZBBZNSARS, BXXZXB, XBBXZNSB and its derivatives as escond peptide template XBBX MAXZB, XBBXZNSB, and (b) group consisting of XBBXBBX; XBBXXBBX, BXXBXXB, XBBZXBB, and XBBZXBBX; where B = at least one positively charged amino acid; x = at least one non-polar hydrosphobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. ANSTAST represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
Antimicrobial peptides for potentiating antimicrobial agents active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.2%; Score 60; DB 2; Length 18; 70.6%; Pred. No. 0.18;
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                                                                                                                  Disclosure, Page 59, 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG69928 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple antibiotic resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYKKFKKKFLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-AUG-2000; 2000US-00648816.
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                                   against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
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Example; Page 72; 221pp; English.

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EVER 150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity of included are (1) an antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-4 containing an amino acid core sequence selected from truncations of the peptides described above, antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, agents that enhance the antimicrobial agents that enhance the antimicrobial supprise against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic are based upon natural antimicrobial peptides of effectiveness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbit platelet microbicidal protein, PMP-2, based peptide #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.2%; Score 60; DB 5; Length 18; 70.6%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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Best Local Similarity 70.6'
Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 23
            8,49,99,99,99,99,99,99,99,99,99,99
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                                                                                                                                                                                                                   overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                      The invention relates to an antimicrobial peptide composition for use
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                  DB 5; Length 18;
                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                 63.2%; Score 60; DB 5; 75.0%; Pred. No. 0.18; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial peptide 13C-RP-1 SEQ ID NO:38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                       AAY57500 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                  3 YKKWKNKLKRSLKRLG 18
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Best Local Similarity 75.0
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus.
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                                                                                                                                                                                                                                                    Sequence 18 AA;
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, XBBXZXBBX and BRXZBBXZ; and (b) a second peptide template XBBXXXB, XBBXXXBB, and selected from the group consisting of XBBXBBX, XBBXXXBX, BXXBXX, XBBXXXBB, and Consisting of XBBXBBX, XBBXXXBX, BXXBXXB, AZBBXXB, and consisting of XBBXBBX, XBBXXXB, BXXBXXB, AZBBXXBB, and consisting of XBBZABBX, XBBXXXB, BXXBXXB, and consisting of XBBZBBX and their derivatives consisting and morpholar hydrophobic amino acid, z at least one morpopholar hydrophobic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAX57463 to AAX57757 represent sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2;
bacterial infection; fungal infection; fungicide; disinfectant;
preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Antimicrobial peptides for potentiating antimicrobial agents active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.1%; Score 59; DB 2; Length 18; 70.6%; Pred. No. 0.25;
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                                                      Disclosure; Page 58; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG69924 standard; peptide; 18 AA
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LYKKFKKKLLKCLKRLG 18
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                  against bacteria and fungi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Conservative
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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EXPRINGE THE STATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TRUNCATIONS, CANDIDATIONS, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or included are (1) an antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide composition for direct activity or retromers, extensions, combinations of the peptides described above, and retromers, extensions, combinations and fungions; and (2) antimicrobial peptides for potentiating antimicrobial activity of leukocytes against organisms such as bacteria and fungi. The artimicrobial peptides are useful as individual antimicrobial agents, agents that enhance, potentiate and fungi. The antimicrobials, agents that enhance the antimicrobial antimicrobials, agents that enhance the antimicrobial or conventions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short and broad spectrum activity against pathogens exhibiting multiple antibiotic are based upon natural antimicrobial peptides that have potent and concerned problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradarion, retaining activity in plasma and overcome problems of toxicity, immunogenicity, in plasma and overcome problems of toxicity, immunogenicity, in plasma and coerum. The present mammalian cell toxicities and eventual antimicrobial peptides that have gotent and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradarion, retaining activity in plasma and overcome problems of toxicity, immunogenicity, and shortness of duration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial, metapeptide, PMP-2; platelet microbicidal protein, antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 5;
Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.1%;
70.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LYKKWKNKLKRSLKRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                against bacteria and fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of elukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficiacy of conventional antimicrobials, agents that enhance the antimicrobial tructions of leukocytes, as disinfectants or preservatives for use in thustions of leukocytes, as disinfectants or preservatives for use in combination with other conventions of leukocytes, as disinfectants of preservatives for use in the considered to have undesirable toxicity, immunogenicity and short been considered to have undesirable toxicity, immunogenicity and short considered to have undesirable toxicity, immunogenicity and short sectivity against pathogens exhibiting multiple antibiocic resistance. They exhibit lower inherent mammalian cell toxicities and expective present sequence is a rabbit pMP based antimicrobial peptide serum. The present sequence is a rabbit PMP based antimicrobial peptide

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                        activity or for potentiating antimicrobial agents active against conganisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBRXB and its derivatives selected from XZBBZBRXBB, BXZXB, BXZXZB, XBBXZXBBX and its derivatives as escond peptide template XBBXZXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBXZXB, XBBXZXBBX and elected from the group consisting of XBBXBBX, XBBXZBBX, BXXBXSB, XBBZXXBB, where B = at least one positively charged amino acid; X = at least one aromatic amino acid; and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
present invention describes an antimicrobial peptide (AP) for direct
                                                                                                                                                                                                                                                                                                                                                                                                                                          neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rabbit platelet microbicidal protein, PMP-2, based peptide #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 56; DB 2; Length 13;
Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13 AA;
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Sequence 13 AA;

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                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for potentiating antimicrobial agents active
                                                                                                                                                                                                                                                      Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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Score 56; DB 5; Length 13; Pred. No. 0.49;
                          1; Indels
                                                                                                                                                                                                                           Antimicrobial peptide RP-1-2R10F SEQ ID NO:43.
                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 59; 166pp; English.
                                                                                                                                               AAY57505 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00025319
                                                                                                                                                                                                                                                                                                                                                                                          99WO-US003350
 58.9%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial peptides for against bacteria and fungi
                                                                                                                                                                                                  25-FEB-2000 (first entry)
            Local Similarity 83.3
es 10; Conservative
                                                    2 LYKKWKNKLKRS 13
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                                                                    2 LYKKWKNKLLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-1999;
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                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                         AAY57505;
Query Match
                           Matches
                                                                                                                      RESULT 28
                                                                                                                                     AAY57505
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against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity

The invention relates to an antimicrobial peptide composition for use

Disclosure, Page 130; 221pp; English.

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New antimicrobial peptide composition for the prevention and treatment infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.

Yeaman MR, Shen AJ; WPI; 2002-590659/63

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selected from XZBBZBXBXB, BXZXB, REAZXZBBX and BBXZBBXZ; and (b) as second peptide template XBBXX and their derivatives selected from the group consisting of XBBXXBBX, XBBXXBBX, XBBXXBBX, XBBXXBBX, and XBBZXXBBX, and XBBZXXBBX; where B = at least one positively charged amino acid; x = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z amy be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of appoptosis of microbial cells. ANYS7463 to AAVS7557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit platelet microbicidal protein, PMP-2, based peptide #41
                                                                                                                                                                                                                                                                               58.9%; Score 56; DB 2; Length 18; 68.8%; Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG69929 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2001; 2001WO-US041877.
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                                                                                                                                                                                                                                                                                                                                                            3 YKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                               YKKFKKKFLKSLKRLG 18
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                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                  Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                         Sequence 18 AA;
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leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New context-activated protide, useful for vascular injury, neoplastic condition, microbial infection, decreased cell death or inflammatory condition.
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/note= "Cleaved by thrombin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YKKWKNKLKRSLKRLG 18
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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBBZBXBXB, BXZXXB, XBBXZXBB, and (B) a second peptide template XBBXXXBX, BXBXXBB, and ESTBBXZBBX, and their derivatives selected from the group consisting of XBBXBBX, XBBXXBB, BXXBXXB, XBBXXBB, and XBBZXXBBX, where B = at least one positively charged amino acid; X = at least one non-polar hydrophobic amino acid; Z = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of meutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AX757463 to AAX5757 represent sequences cused in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                        ö
but equivalent to or exceeding that of RP-1 in the presence of thrombin. Thus, PT-3 exerts optimal antimicrobial activity in the context of thrombin as would be present in the setting of vascular injury or infection. PT-3 is an example of context-activated protides of the invention that have 2 or more effectors with individual distinct biological functions and one or more corresponding activator sites that can each initiate or amplify the biological function of one or more effectors upon context activation. The protides are useful in the diagnosis, prophylaxis and therapy of a broad range of pathological conditions.
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                              Score 54; DB 8; Length 37; Pred. No. 2.5; 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial peptide RP-6 SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 109; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY57470 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                 56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00025319
                                                                                                                                                                                                                                                                                                                                                              2 LYKKWKNKLKRSLKR 16
                                                                                                                                                                                                                                                                                                                                                                                                   22 LYKKFKKKLLKSLKR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          against bacteria and fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                   Local Similarity 73.3
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeaman MR, Shen AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-527417/44
                                                                                                                                                                                                                                           Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acide core sequence (derived from PMP-1 and PMP-2, platelet microbiolal protein), and retromers, PMP-1 and PMP-2, platelet microbiolal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as or for potentiating antimicrobial agents active against organisms such as core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial apptides for potentiating antimicrobial activity of antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial activity of tunctions of leukocytes, as disinfectants or preservatives for use in thoology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short that based upon natural antimicrobial peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                          Gaps
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                             Rabbit platelet microbicidal protein, PMP-2, based peptide #6.
                                                     Length 14;
                                                                                          1; Indels
                                                     2;
                                                     B
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                     Score 51;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 130; 221pp; English.
                                                                                                                                                                                                                                                                ABG69894 standard; peptide; 14 AA
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections caused by organisms,
multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2001; 2001WO-US041877.
                                               Match 53.7%;
Local Similarity 90.0%;
les 9; Conservative
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                                                                                                                                1 KLYKKWKNKL
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                 Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                      ABG69894;
                                                     Query Match
                                                                           Best Loc
Matches
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Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
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                                                                                                                                                                                                           human platelet factor 4 C-13 fragment; amphipathic alpha helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BRIM ) BRISTOL-MYERS SQUIBB CO.
    AAR13936 standard; protein; 23
                                                                                                                                                                                                                                                                                                                                                                                               90US-00484020
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                                                                                                                   (first entry)
                                                                                                                                                                Cationic oligopeptide #7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blake JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-281214/38.
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les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23 AA;
                                                                                                                                                                                                                                                                                                                                                                                               23-FEB-1990;
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19-FEB-1991;
                                                                                                                                                                                                                                                                                               WO9112815-A.
                                                                                           25-MAR-2003
26-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Darveau RP,
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                                                                                                                                                                                                                                                         Synthetic.
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                                                  AAR13936;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compsns. for treating infections sensitive to beta-lactam antibiotics - comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human platelet factor 4 C-13 fragment; amphipathic alpha helix.
                                                                                                                                                                                      Length 14;
                                                                                                                                                                                                                                 1; Indels
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                                                                                                                                                                                      Score 51; DB 5;
Pred. No. 2.6;
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Pred. No. 3.7;
2; Mismatches
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90.0%;
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11; Conservative
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1 KLYKKWKKKL 10
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                           Sequence 14 AA;
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Cosand WL;

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Amphiphilic peptide; anti-microbial; anti-viral; anti-tumour; spermicide; wound healing; sterilant.
                                                                                                                                 Sequence of amphiphilic peptide SEQ ID No. 27 which may be a C- terminal amide and/or may be acetylated at N-terminus.
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                                                  AAR21364 standard; peptide; 18
23
KLYKKLLKKLLKSAKKLG
                                                                                                               (first entry)
                                                                                           (revised)
                                                                                                    (revised)
                                                                                                                                                                                                                    WO9201462-A
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Gaps

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5; Indels

KLYKKWKNKLKRSLKRLG 18 |||||| || :| |:|| KLYKKLLKKLLKSAKKLG 20

RESULT 34 AAR13936

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Gaps

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2; Length 23; Indele

Score 51; DB 2, Pred. No. 4.2; 2; Mismatches

53.7%; 61.1%;

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proliferation of microbes, and for treating microbial infections
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                                                                                                                                                                                        51.6%;
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1 KRLRKFRNKIKEKLKKIG
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(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                   1 KLYKKWKNKLKRSLKRLG
                                                                                                                                                                                                                                                                                                            AAB70666 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                              8; Conservative
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                                                                                                                                                                                                  Similarity
                                                                                                                                                                  Sequence 18 AA;
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Best Local S
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                                                                                                                                                                                                         microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of sperm and hence have application in a spermicide preparation. They also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. AAR20969 and AR20970 were published in Haighten and Ostreah, Bio Chromatography, Vol 2, issue 2, page 80-83, 1987. (Updated on 09-ANN-2003 to and missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
                                                                                                                                Method for inhibiting target cell and virus growth - comprises administering amphiphilic peptide compsns, useful for treating viral and phytopathogenic infections, tumours and burns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO:20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antimicrobial peptides useful as antibiotics for inhibiting growth
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                  peptides of the invention are effective pharmaceuticals having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial; baceericidal; antibiotic; antiviral; microbial growth inhibitor; proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; Burkholderia cepacia; Alcaligenes; Manthomonas.
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                                                                                                                                                                                                                                                                                                                                              2; Length 18;
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Pred. No. 4.6;
2; Mismatches
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                                                                                                                                                                             Claim 4; Page 44; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB70667 standard; peptide; 18
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            90US-00554422
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91US-00725331
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(REGC ) UNIV CALIFORNIA.
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                                                                 (SCRI ) SCRIPPS RES INST
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                                                                                                          WPI; 1992-064700/08
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                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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            19-JUL-1990;
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                                                                   AAB70648 to AAB70675 represent antimicrobial peptides (I), of which AAB70648 to AAB70664, AAB70674 and AAB70657 are derived from the ovine SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic, antimicrobial and antiviral activities, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (I) are useful for inhibiting microbial growth, for inhibiting microbial growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Length 18;
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Pred. No. 6.3;
6; Mismatches
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Claim 1; Page 103; 137pp; English
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The invention relates to a polypeptide comprising at least one protesseresistant or protesse-sensitive sequence, bound to the C-terminal side of the target polypeptide. The polypeptides are useful as antimicrobial agents against Ceratocystis fimbriata, which causes purple blotch in sweet potatoes, or Becherichia coli. They are also used in gene therapy. The present sequence is rabbit rCAP24 peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising at least one protease-resistant or protease-sensitive sequence, bound to the C-terminal side of the target polypeptide, useful as antimicrobial agent against Ceratocystis
                                                                                                                                                                                                         Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide; rabbit; rCAP24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muramoto N, Imaeda T, Hirai M, Shimamura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 11; Page 49; 50pp; English.
AAE34416 standard; peptide; 24 AA.
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26-DEC-2001; 2001JP-00394821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-2002; 2002WO-JP004800
                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus.
                                                                                                                                                           Rabbit rCAP24 peptide
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Best Local Similarity
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                                                                                                        14-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:21.
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                                                                                                                                  Gaps
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                                                                            DB 4; Length 21;
                                                                                                                               4; Indels
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                                                                         51.6%; Score 49; DB 44.4%; Pred. No. 7.3; ive 6; Mismatches
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                                                                                                                                                                                        1 KLYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                       4 KRLRKFRNKIKEKLKKIG 21
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                                                                                                           Similarity 44.4%;
8; Conservative
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Best Local Similarity
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                         Sequence 21 AA;
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                        4 ;
51.6%; Score 49; DB 6; 44.4%; Pred. No. 8.3; iive 6; Mismatches
                                                                                                                         ADK70763 standard; peptide; 24 AA
                                                                                                                                                                                           Rabbit CAP18 peptide fragment 2.
                                             18
                                                                  5
                                             1 KLYKKWKNKLKRSLKRLG
                                                          4 KRLRKFRNKIKEKLKKIG
                                                                                                                                                                     (first entry)
                        8; Conservative
                                                                                                                                                                                                                                                           Oryctolagus cuniculus.
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Gaps

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4; Indels

| :|::||:| ||::| KRLRKFRNKIKEKLKKIG 19

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RESULT 39 AAE34416

1 KLYKKWKNKLKRSLKRLG 18

8; Conservative

Matches

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Query Match
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                                                                                                                                                            The invention relates to a novel polypeptide composition for preventing disease in an organism which comprises one or more types of polypeptide which have an alpha-helix structure and/or thionine component. The composition of the invention demonstrates antibacterial and antifungal activities and may be useful for preventing a disease in an organism, for generating cultivated plants and in providing resistance to plant tissue against fungi such as Pyticularia oryzae (rice blast fungus), Ceratorystis fimbriata and bacteria such as Pseudomonas etc. The composition has high antimicrobial activity at low concentration. The current sequence is that of the rabbit CAPIS peptide fragment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial polypeptide composition for a plant pathogen, comprises one or more types of thionine and/or a polypeptide having an alpha helix structure, as an active ingredient.
                                                                                                 Antimicrobial polypeptide composition for a plant pathogen, comprises one or more types of thionine and/or a polypeptide having an alpha helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-helix; thionine; antibacterial; antifungal; plant; fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria; Pseudomonas; antimicrobial; rabbit; CAP18.
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                                                                                                                                                                                                                                                                                                                    51.6%; Score 49; DB 8 44.4%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbit CAP18-derived peptide fragment 2.
                                                                                                                                           Claim 3; SEQ ID NO 4; 27pp; Japanese.
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                                                                                                                      structure, as an active ingredient.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADK70764 standard; peptide; 24 AA
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                                           (TOYW ) TOYOTA CHUO KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                1 KLYKKWKNKLKRSLKRLG 18
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KRLRKFRNKIKEKLKKIG 21
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15-JAN-2002; 2002JP-0006607
                      15-JAN-2002; 2002JP-0006607
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N-PSDB; ADK70782.
                                                                 WPI; 2004-102620/11.
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                                                                           N-PSDB; ADK70781.
                                                                                                                                                                                                                                                                                                 Sequence 24 AA;
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The invention relates to a novel polypeptide composition for preventing disease in an organism which comprises one or more types of polypeptide which have an alpha-helix structure and/or thionine component. The composition of the invention demonstrates antibacterial and antifungal activities and may be useful for preventing a disease in an organism, for generating cultivated plants and in providing resistance to plant tissue against fungi such as Pyricularia oryzae (rice blast fungus), Ceratocystis finbriate and bacteria anch as Pseudomonas etc. The composition has high antimicrobial activity at low concentration. The
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                                                                                                                                                                                                                                                                                               current sequence is that of the rabbit CAPI8-derived peptide fragment
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Pred. No.
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26-DEC-2001; 2001JP-00394821.
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 AA;
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                                                                                                                                                                                                                                                                                                                                    the invention.
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DB 6; Length 26;

51.6%; Score 49;

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The invention relates to a polypeptide comprising at least one protease-
resistant or protease-sensitive sequence, bound to the C-terminal side of
the target polypeptide. The polypeptides are useful as antimicrobial
agents against Ceratocystis fimbriata, which causes purple blotch in
sweet potatoes, or Escherichia coli. They are also used in gene therapy.
The present sequence is a modified peptide based upon CAP18 derived from
rabbit. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                        New polypeptide comprising at least one protease-resistant or protease-sensitive sequence, bound to the C-terminal side of the target polypeptide, useful as antimicrobial agent against Ceratocystis fimbriata, or Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide; rabbit; rCAP24; CAP18.
                         Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;
rabbit; rCAP24; CAP18.
  Rabbit CAP18 derived peptide, rCAP24-KE.
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                                                                                                                                                                                                                                                           Hirai M,
                                                                                                                                                                                                                                (TOYW ) TOYOTA CHUO KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                 Claim 26; Page 49; 50pp; English
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26-DEC-2001; 2001JP-00394821.
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26-DEC-2001; 2001JP-00394821
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                                                                   Oryctolagus cuniculus
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Best Local Similarity
Matches 8; Conserv
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                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a polypéptide comprising at least one protease-resistent or protease-sensitive sequence, bound to the C-terminal side of the target polypeptide. The polypeptides are useful as antimicrobial agents against Ceratocystis fimbriata, which causes purple blotch in sweet potatoces, or Escherichia coll. They are also used in gene therapy. The present sequence is a modified poptide based upon CAP18 derived from rabbit. This sequence is used in the exemplification of the invention
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               Gaps
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               4; Indels
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  Pred. No. 9;
6; Mismatches
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                                                                                                                                                                                                                   Rabbit CAP18 derived peptide, rCAP24-KD.
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KRLRKFRNKIKEKLKKIG 21
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26-DEC-2001; 2001JP-00394821.
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 44.48;
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KRLRKFRNKIKEKLKKIG
                                       1 KLYKKWKNKLKRSLKRLG
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                                                                                                                                                                                        (first entry)
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              8; Conservative
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                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus
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Best Local Similarity Matches 8; Conserv
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AAE34417
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AAE34419
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Gaps

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Length 26; 4; Indels

DB 6; 9;

Mismatches

rCAP24-RE.

Shimamura T;

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The invention relates to a polypeptide comprising at least one protease-resistant or protease-sensitive sequence, bound to the C-terminal side of the target polypeptide. The polypeptides are useful as antimicrobial agents against Ceratocystis fimbriata, which causes purple blotch in sweet potacoes, or Escherichia coli. They are also used in gene therapy. The present sequence is a modified peptide based upon CAP18 derived from rabbit. This sequence is used in the exemplification of the invention
                                                                                                                                             New polypeptide comprising at least one protesse-resistant or protesse-sensitive sequence, bound to the C-terminal side of the target polypeptide, useful as antimicrobial agent against Ceratocystis fimbriata, or Escherichia coli.
                                                               Hirai M, Shimamura T;
                    (TOYW ) TOYOTA CHUO KENKYUSHO KK.
                                                                                                                                                                                                                                                            Claim 28; Page 50; 50pp; English.
                                                               Muramoto N, Imaeda T,
                                                                                                       WPI; 2003-156762/15
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Gaps ö Query Match 51.6%; Score 49; DB 6; Length 26; Best Local Similarity 44.4%; Pred. No. 9; Matches 8; Conservative 6; Mismatches 4; Indels Sequence 26 AA;

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1 KLYKKWKNKLKRSLKRLG 18 | :|:||:|| ||::| 4 KRLRKFRNKIKEKLKKIG 21

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Sequence 3, Application US/09525269A

Patent No. 6743769

GENERAL INFORMATION:
APPLICANT: Shem, Alexander J.
TITLE OF INVENTION: Metapeptides
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HRS614)
CURRENT APPLICATION NUMBER: US/09/525,269A

CURRENT PILING DATE: 2000-03-13

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 39
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Sequence 3, Appli
Sequence 9, Appli
Sequence 11, Appl
Sequence 12, Appli
Sequence 27, Appl
Sequence 27, Appli
Sequence 4, Appli
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                                                                    May 16, 2005, 08:21:21; Search time 19.2414 Seconds (without alignments) 69.833 Million cell updates/sec
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Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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Sequence
Sequence
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                                                                                                                                                                                                                                       301394
                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-525-269A-10
US-09-525-269A-3
US-09-525-269A-9
US-08-233-203-11
US-08-233-203-12
US-07-725-331-27
US-08-313-61A-7
US-08-313-61A-7
US-08-313-61A-7
US-08-313-61A-7
US-08-313-61A-7
US-08-322-911-7
US-08-322-911-7
US-08-482-191-2
PCT-US91-05047-43
PCT-US96-10227-2
US-08-482-191-3
US-08-760-903-3
US-08-760-903-3
US-08-760-903-3
US-08-77-25-331-18
US-07-725-331-18
US-07-725-331-18
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US91-05047-12
                                                                                                                                                                                                              513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                1 KLYKKWKNKLKRSLKRLG 18
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95
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Match Length
                                                                                                                                                                                                                                                               seq length: 0
seq length: 74
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4.8.4
4.4.4
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Perfect score:
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Maximum DB
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| 228<br>229<br>30                     | 3 45.<br>45.       | нпп                      | 1 2 1     | US-07-725-331-46<br>PCT-US91-05047-46<br>US-07-725-331-3 | Sequence 46, Appl<br>Sequence 46, Appl<br>Sequence 3, Appli |   |
|--------------------------------------|--------------------|--------------------------|-----------|----------------------------------------------------------|-------------------------------------------------------------|---|
| 32 32 4 4 4 4                        | 333<br>455<br>75.  | ოოო                      |           | US-07-725-331-5<br>US-07-725-331-8<br>US-07-725-331-11   | , a, L                                                      |   |
| 14.11                                |                    |                          |           | US-07-725-331-23                                         | Sequence 23, Appl                                           |   |
| nφ                                   | 3 45.              | 3.0                      |           | US-08-295-085-9                                          | 10                                                          |   |
| <b>Γ</b> α                           | 3 45.              | е с<br>-                 |           | US-08-944-133-53                                         | Sequence 53, Appl                                           |   |
|                                      | 45.                | . H                      |           | PCT-US91-05047-3                                         | i 'n                                                        |   |
| 0                                    | 3 45.              | 3                        |           | PCT-US91-05047-5                                         | 'n                                                          |   |
| 41                                   | . 45.              | m r                      |           | PCT-US91-05047-8                                         | Sequence 8, Appli                                           |   |
|                                      | 3 45.              |                          | n w       | PCI-US91-0504/-11<br>PCI-US91-05047-23                   | Sequence 11, Appl<br>Sequence 23, Appl                      |   |
| 4                                    | 3 45.              | 3                        | S         | -US95-10741                                              | Н                                                           |   |
| 45 4                                 | 45.                | -                        | S         | PCT-US95-10741-9                                         | o,                                                          |   |
|                                      |                    |                          |           | ALIGNMENTS                                               |                                                             |   |
| RESILT 1                             |                    |                          |           |                                                          |                                                             |   |
| 525-269                              | A-10               |                          |           |                                                          |                                                             |   |
| ; Sequence 10,                       | , Appli            | , Application US/0952526 | 3/09      | 9525269A                                                 |                                                             |   |
| : GENERAL INFORMATION:               | 6/43/69<br>ORMATIO | Ë                        |           |                                                          |                                                             |   |
| , APPLICANT: Yeaman,                 | Yeaman             | , Michael                | Α,        | • 1                                                      |                                                             |   |
|                                      | Shen,              | Alexander<br>N. Antimic  | יי<br>טיי | J.<br>Obial Dentides and Derived                         | 79                                                          |   |
| , TITLE OF I                         | OF INVENTION:      | N: Metar                 | ept.      | nine santa                                               | Į,                                                          |   |
| ; FILE REFERENCE: 66742-025 (HR5614) | ENCE: 6            | 6742-025                 | (HRS      | 5614)                                                    |                                                             |   |
|                                      | PLICATION DAY      | ON NUMBER: US/0          | מיני      | JS/09/525,269A                                           |                                                             |   |
| PRIOR                                | ICATION            | 5                        | S         | 09/025.319                                               |                                                             |   |
| PRIOR                                | NG DATE            | 6                        | -18       |                                                          |                                                             |   |
| NUMBE                                | SEQ ID NOS         | NOS: 39                  |           | , , , , , , , , , , , , , , , , , , , ,                  |                                                             |   |
| SEO ID NO 1                          | ABL SEQ            | 707                      | 8         | e version 4.0                                            |                                                             |   |
| , LENGTH: 18                         | 80                 |                          |           |                                                          |                                                             |   |
| , TYPE: PRT                          | 10:01              | Concinco Leio            | 9         | Ç                                                        |                                                             |   |
| FEATURE:                             |                    |                          | ובוור     | ט                                                        |                                                             |   |
|                                      | INFORMATION        |                          | Cro.      |                                                          | ·                                                           |   |
| , OTHER INF                          | INFORMATION:       |                          | 2100      | cidal domains from platelet<br>1 and 2 (pMp_1 and pMp_2) | elet microbial                                              |   |
|                                      | A-10               |                          |           | ד מוות פ ונוון                                           | 10011                                                       |   |
| atc                                  | Simi               |                          | 100.0%    | ; Score 95; DB 4;<br>; Pred. No. 5.2e-06;                | 18;                                                         |   |
| Matches 1                            | 18; Con            | Conservative             | 43        | atch                                                     | Indels 0; Gaps (                                            | 0 |
| 20,                                  |                    | KLYKKWKNKLKRSLKRLG       | R166      | 18                                                       |                                                             |   |
| Db 1                                 |                    | KLYKKWKNKLKRSLKRLG       | ar.       | 18                                                       |                                                             |   |
| RESULT 2                             |                    |                          |           |                                                          |                                                             |   |

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COUNTRY:
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                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                    OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial CTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon ; OTHER INFORMATION: microbiocidal domains from platelet microbial ; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-9
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                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFRENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525, 269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025, 319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yearnan, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                        67.4%; Score 64; DB 4; 76.5%; Pred. No. 0.049; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3 LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09525269A
Patent No. 6743769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 9, Application US/09525269A; Patent No. 6743769
                                                                                                                                                                                                                                                                                                                                                                              2 LYKKFKKKLLKSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                    2 LYKKWKNKLKRSLKRLG 18
                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.5
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-525-269A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-525-269A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 9
LENGTH: 13 ·
TYPE: PRT
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                                                                                                                 FEATURE:
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Sequence 11, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: COSANG, Wesley, INFECTIONS COUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
ATREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                             Gaps
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
COTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-8
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                                                                                                                                                 Score 51, DB 4, Length 14;
Pred. No. 1.8,
0, Mismatches 1; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/23,203

FILING DATE:

CLASSIFICATION S14

PRIOR APPLICATION S14

PRIOR APPLICATION NUMBER: US/07/655,321

FILING DATE: 19-FEB-1991

APPLICATION NUMBER: US 07/484,020

FILING DATE: 23-FEB-1990

ATTORNEY/AGENT INFORMATION:

NAME: POOT, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: 0X0063A

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.7%; Score 51; DB 1
61.1%; Pred. No. 2.5;
ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KLYKKWKNKLKRSLKRLG 18
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                                                                                                                                               53.7%;
90.0%;
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TELEFAX: 206/448-4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61...
Best Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                     1 KLYKKWKNKL 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                            1 KLYKKWKKL
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Best Local Similarity
Matches 9; Conserv
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CTHER INFORMATION: May be a C-terminal amide, and/or may OTHER INFORMATION: be acetylated at N-terminus. US-07-725-331-27
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Sequence 27, Application PC/TUS9105047
SEGNERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amalogues Thereof
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Emilnamow
STREET: 180 North Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.6%; Score 50; DB 1; Length 18; 64.7%; Pred. No. 3; ive 2; Mismatches 4; Indel8
    ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
                                                                                                                        ZUDITER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421250-80
SSEE: & Milnamow
1: 180 No. 5294605th Stetson
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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CLASSIFICATION:
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COUNTRY: USA
ZIP: 60601
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                                                                                                             USA
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                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US91-05047-27
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                                                                                                                                                                   APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: ANTIBIOTICS
TITLE OF INVENTION: ANTIBIOTICS
TITLE OF INVENTION: ANTIBIOTICS
CORRESPONDENCES: 12
CORRESPONDENCES: Brist Avenue
STREET: 3005 First Avenue
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Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.7%; Score 51;
61.1%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDAER:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOr. Brian W.
REGISTRATION NUMBER: 32,928
REPERNCE/DOCKET NUMBER: 0N0063A
TELECOMMUNICATION:
TELEPHONE: 206/728-4800
                                                                                      US-08-233-203-12; Sequence 12, Application US/08233203; Patent No. 540898; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KLYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||| || || || || || || || || || || KLYKKLLKKLLKSAKKLG 23
    3 KLYKKLLKKLLKSAKKLG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.1%
Them 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-233-203-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-07-725-331-27
                                                             RESULT 6
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Gaps

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/note= "Xaa is
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             1 KLYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                 | :|::||:|
4 KRLRKFRNKIKEKLKKIG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two bulkers CITY: San Francisco
                            LOCATION: 23
OTHER INFORMATION: /
FRATURE:
NAME/KEY: REGION
LOCATION: 26
OTHER INFORMATION: /
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08313681A

Sequence 7, Application US/08313681A

Sequence 7, Application US/08313681A

APPLICANT: Wright, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hirata, Mishimsa

TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: May be a C-terminal amide, and/or may ; OTHER INFORMATION: be acetylated at N-terminus. PCT-US91-05047-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.6%; Score 50; DB 5; Best Local Similarity 64.7%; Pred. No. 3; Matches 11; Conservative 2; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFREENCE/DOCKET NUMBER: 421250-80
TELECOMUNICATION INFORMATION:
TELEPAX: 312616540
TELEPAX: 312616540
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-226-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KLYKKWKNKLKRSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KLEKKEKKEKKELIKE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: ONE MAINTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-313-681A-7
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Sequence 7, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Hirara, Mishimasa
APPLICANT: Hirara, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                            Query Match 51.6%; Score 49; DB 1; Length 29; Best Local Similarity 44.4%; Pred. No. 6.1; Matches 8; Conservative 6; Mismatches 4; Indels
                                                                                                                                                        ) NAME/KEY: Region

) LOCATION: 27

CTHER INFORMATION: /note= "Xaa is a Gly or Gln"

US-08-313-681A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
                                                                                                        a Gln or Ile
/note= "Xaa is Asp or Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION:
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Gaps

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Query Match 48.4%; Score 46; DB 1; Length 18; Best Local Similarity 58.8%; Pred. No. 9.8; Matches 10; Conservative 3; Mismatches 4; Indels
                     May be a C-terminal amide, may be acetylated at N-terminus.
                                                                                                                                                                                                             2 KLHKKLLKKLKKLLKKL 18
                                                                                                                                                                                   1 KLYKKWKNKLKRSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COBAND, WEBLITLE OF INVENTION: COMITITE OF INVENTION: INFITICE OF INVENTION: ANTIUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
               ; OTHER INFORMATION:
; OTHER INFORMATION:
US-07-725-331-43
  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Patent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Enesaler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
COTY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%; Score 49; DB 3; Length 29; 44.4%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
                                                                                                                                                                                                                                                                     /note= "Xaa is a Gln or Ile'
                                                                                                                                                                                   /note= "Xaa is Asp or Lys'
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE, DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/725,331 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :|::||:| ||::|
4 KRLRKPRNKIKEKLKKIG 21
                 LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 44.4 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
SEQUENCE CHARACTERISTICS
                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                     NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION:
                                                                                                                                                                                                                       NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-07-725-331-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                        US-09-322-911-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Sequence 7, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Weeley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INPECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 1; Length 18; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLUM LIEL.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION NUMBER: US/07/655,321
PRILING DATE: 19-FEB-1991
PRILING DATE: 19-FEB-1990
APPLICATION NUMBER: US/07/484,020
FILING DATE: 23-FEB-1990
ATTONEY/AGENT INFORMATION:
NAME: POOT, BITAN 32,928
REFERENCE/DOCKET NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/448-4775
TELEPHONE: 206/448-4775
                                                                                                                                                                                                                                                                         ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LYKKLLKKLLKSAKKLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
```

```
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dreseller, Goldsmith, Sutker, Shore,
ADDRESSEE: Dreseller, Goldsmith, Sutker, Shore,
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 18;
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/482,191
FILING DATE: PATENTON: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB Pred. No. 9.8; 2; Mismatches
                                                                                                                                  FILING DATE: 07-071-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA: 17-DEC-1993
PRIOR APPLICATION DATA: 08/164,067
PILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 108-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTONNEY, AGGNT INFORMATION:
NAME: CARROLL, PETER G.
REGISTARTION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATTOM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
APPLICATION NUMBER: US 07/554,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 43, Application PC/TUS9105047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LYKKLLKKLLKSAKKLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US91-05047-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-482-191-2
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                                         Sequence 2, Application US/08760903
Patent No. 599381
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILLI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
CORPRESEDENT: STAFFORD.
                                                                                                                                                                                                                                                                                                                                           COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 06-DEC-1996
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: MEDLEN & CARROLL
220 MONTGOMERY STREET, SUITE 2200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 39'-8338
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08482191
Patent No. 6579696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                              CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                    CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS: siz
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                             JS-08-760-903-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: ANDERSON, BYRON
TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILI
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FLING DATE: 06-DEC-1996
ILING DATE: 06-DEC-1996
ATTONREY/AGENT INPORMATION:
NAME: SOUNOFF, CYNTHIA
REGISTRATION NUMBER: 38,314
REGISTRATION NUMBER: 38,314
REGISTRATION NUMBER: 30,916
TELEBHONE: (415) 705-8410
TELEBHONE: (415) 705-8410
TELEBRAX: (415) 39-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
"FMATTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.4%; Score 46; DB 2;
58.8%; Pred. No. 10;
tive 2; Mismatches
                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIF: 94104
                                                                                                                                                                                               Query Match
48.4%; Score 46; DB 98st Local Similarity 58.8%; Pred. No. 9.8; Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/08482191; Patent No. 6579696
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08760903
Patent No. 5998381
                                                                                                                                                                                                                                                                                                                   2 LYKKLLKKLLKSAKKLG 18
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         SEQUENCE CHARACTERISTICS:
1.ENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.8
Matches 10; Conservative
  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS: single
unknown
                                                                                       single
                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US96-10227-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                              TYPE: amino acid STRANDEDNESS: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WILLIAMS, JAMES A.
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: SCHATZ, ROBERT W.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                       May be a C-terminal amide, may be acetylated at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                                                                               48.4%; Score 46; DB 5; 58.8%; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/482,191
APPLICATION NUMBER: US 08/169,701
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 32,837
TELECOMMUNICATION INFORMATION:
                REFERENCE/DOCKET NUMBER: 421250-80 TELECOMMUNICATION INFORMATION: TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALIFORNIA: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9610227
GENERAL INFORMATION:
APPLICANT: WILLIAMS, JAMES A.
REGISTRATION NUMBER: 29,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLYKKWKNKLKRSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLHKKLLKKLKKL 18
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                                                                                                                                                   LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLLGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.89
Matches 10; Conservative
                                                                                TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                   PCT-US91-05047-43
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PCT-US96-10227-2
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48.4%; Score 46; DB 5; Length 19; 58.8%; Pred. No. 10;
                                                                                                     ZIE: 94104
COMPUTER READABLE FORM:
WEDIUM TYPE: Flopy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                      220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                        PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INPORMATION:
NAME: CARROLL, PETER G.
NEGISTRATION NUMBER: 32,837
RESISTRATION NUMBER: 32,837
RESISTRATION NUMBER: 32,837
TELEPHONE: (415) 705-8318
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FERGENCE CHARACTERISTICS:
FERGENCE TARROLL SETTING
SEQUENCE CHARACTERISTICS:
                                        CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.8
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-725-331-18
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                                                               APPLICANT: PUGH, CHARLES
APPLICANT: PRASIK JR., NICHOLAS
APPLICANT: PRASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
CITY: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WILLIAMS, JAMES A.
SHEKHANI, MOHAMMED S.
FIRCA, JOSEPH R.
SCHATZ, ROBERT W.
PUGH, CHARLES
PANASIK JR., NICHOLAS
STAFFORD, DOUGLAS C.
VENTION: PREVENTION AND TREATMENT OF SEPSIS
                                                                                                                                                                                                                                                                                                COUNTRY: CULTER STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-UNN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION NUMBER: US 08/164,067
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/ACENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.4%; Score 46;
illarity 58.8%; Pred. No.
Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application PC/TUS9610227 GENERAL INFORMATION:
WILLIAMS, JAMES A.
SHEKHANI, MOHAWMED S.
FIRCA, JOSEPH R
SCHATZ, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYKKWKNKLKRSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-482-191-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US96-10227-3
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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sequence 18, Application US/07725331

patent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Analogues Thereof
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: E Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
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Gaps

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Sequence 18, Application PC/TUS9105047

Sequence 18, Application PC/TUS9105047

Sequence 18, Application PC/TUS9105047

Sequence 18, Application PC/TUS9105047

APPLICANT: Houghten, Richard

APPLICANT: Blondelle, Sylvie

TITLE OF INVENTION: Ampliphilic Peptide Compositions and

TITLE OF INVENTION: Analogues Thereof

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,

ADDRESSEE: 6 Milnamow

STREET: 180 North Stetson

CITY: Chicago
                                                                                                                                                                                                                       OTHER INFORMATION: May be a C-terminal amide, and/or may OTHER INFORMATION: be acetylated at N-terminus. US-07-725-331-29
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                                                                                                                                                                                                                                                                                                            Query Match
47.4%; Score 45; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 13;
Matches 10; Conservative 2; Mismatches 5; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION DATA:
APPLICATION NUMBER: 907/554,422
APPLICATION NUMBER: 08 07/554,422
APPLICATION NUMBER: 18-10L-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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TELEPAY 312616540
INFORMATION FOR SEQ ID NO: 18: ERWCHT: 18 amino acids TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                       1 KLYKKWKNKLKRSLKRL 17
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              TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                      LENGTH: 18 amino acids
                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
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MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
                                                                                                              TYPE: amino acid STRANDEDNESS:
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USA
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  TELEPHONE:
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be acetylated at N-terminus, Xaa is
Met or methionine sulfoxide.
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APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1; Length 18;
Pred. No. 13;
2; Mismatches 5; Indels
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                                                                             FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER: US 07/554,422
PTILING DATE: 19-JUL-1990
ATTONNEY, AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
PREFERENCE/POCKET NUMBER: 421250-80
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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REGISTRATION NUMBER: 29.381
REFRENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/725,331
                     PatentIn Release #1.24
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PC-DOS/MS-DOS
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Patent No. 5294605
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         INFORMATION: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acid STRANDEDNESS: TOPOLOWY
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Best Local Similarity 58.8
Matches 10; Conservative
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CTHER INFORMATION:
CTHER INFORMATION:
US-07-725-331-18
OPERATING SYSTEM:
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USA
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US-07-725-331-29
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STATE:
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OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial COTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-5
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| Sequence 12, Application US/07725331
| Sequence 12, Application US/07725331
| Patent No. 52944605
| Patent No. 52944605|
| APPLICANT: Houghten, Richard
| APPLICANT: Blondelle, Sylvie
| TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Analogues Thereof
| TUTLE OF INVENTION: Analogues Thereof
| NUMBER OF SEQUENCES: 68
| CORRESPONDENCE ADDRESS: ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow
| STREET: 180 No. 52244605th Stetson
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VOLECULE TYPE: peptide
FRATURE:
OTHER INFORMATION: May be a C-terminal amide, and/or may
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
46.3%; Score 44; DB 4; Length 14;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 0; Indels
FILLE OF INVENTION: Metapeptides
FILE REPERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 14
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIPICATION: 514
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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3126165460
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1 KLYRKFKNKL 10
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                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: BLOOdelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dreseler, Goldsmith, Sutker, Shore,
ADDRESSEE: E Milhamow
STREET: 180 North Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 47.4%; Score 45; DB 5; Length 18; I Similarity 58.8%; Pred. No. 13; 10; Conservative 2; Mismatches 5; Indels
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                                5.
       Pred. No. 13;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLODPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REPRENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 312616540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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                                                                            1 KLYKKWKNKLKRSLKRL 17
                                                                                                                        2 KLLKKLLKKLKKKL 18
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    Best Local Similarity 58.8%;
Matches 10; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OTHER INFORMATION:
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Best Local Similarity
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08233203
Patent No. 540898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: INPECTIONS AND METHODS FOR TREATING
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
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; OTHER INFORMATION: be acetylated at N-terminus, Xaa is ; OTHER INFORMATION: Met or methionine sulfoxide. US-07-725-331-12
                                                                                              Query Match 46.3%; Score 44; DB 1; Length 18; Best Local Similarity 58.8%; Pred. No. 18; Matches 10; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.3%; Score 44; DB 1; Length 18; 58.8%; Pred. No. 18;
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CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
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PRIOR APPLICATION DATA:
APPLICATION UNDRER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELEPHONE: 206/728-4800
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                                                                                                                                                                                  1 KLYKKWKNKLKRSLKRL 17
                                                                                                                                                                                                                            2 KLLKKLXKKLKKL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                          RESULT 26
US-08-233-203-6
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be acetylated at N-terminus, Xaa is
Met or methionine sulfoxide.
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Patent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
STREET: 180 No. 5294605th Stetson
                                      APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Milnamow
ADDRESSEE: & Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.3%; Score 44; DB 5; Length 18; 58.8%; Pred. No. 18; 5; Indels tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
Sequence 12, Application PC/TUS9105047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gamson, Edward P. REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 42.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 3126165418
TELEPAX: 3126165460
INFORMATION FOR SEQ ID NO: 12: SEGUENCE CHARACTERISTICS: LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLYKKWKNKLKRSLKRL 17
                                                                                                                                                                                                                          STREET: 180 North Stetson
CITY: Chicago
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KLLKKLXKKLKKLLKKL
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
PCT-US91-05047-12
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STREET: 10.
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US-07-725-331-46
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RESULT 27

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: C-terminal amide, acetylated at ; OTHER INFORMATION: N-terminus. PCT-US91-05047-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow STREET: 180 No. 5294605th Stetson
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
45.3%; Score 43; DB 5;
Best Local Similarity 58.8%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEPHONE: 3126165460
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KLYKKWKNKLKRSLKRL 17
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INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 3126165418
                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-07-725-331-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.3%; Score 43; DB 1; Length 17; 58.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: C-terminal amide, acetylated at OTHER INFORMATION: N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION UNDRER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                   SOFTWARE: Patentin Release #1.24
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLYKKWKNKLKRSLKRL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 180 North Stetson
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acids
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.87
Matches 10, Conservative
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: IL
COUNTRY: USA
                                                                                                                                                                                                        FILING DATE:
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      COUNTRY:
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LENGTH: 18 amino acids
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3126165460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                       60601
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                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                Query Match
Best Local Similarity 58.8%; Pred. No. 24;
Matches 10; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.3%; Score 43; DB 1; Length 18; Best Local Similarity 58.8%; Pred. No. 24; Matches 10; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIPLCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
CLARCTERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                              RESULT 31
US-07-725-331-5
; Sequence 5, Application US/07725331
; Patent No. 5294605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 32
US-07-725-331-8
; Sequence 8, Application US/07725331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLYKKWKNKLKRSLKRL 17
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                                                                                                                                                     2 KLLKKLLKKLKKL 18
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide PEATURE:
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CTHER INFORMATION:
CTHER INFORMATION:
US-07-725-331-5
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US-07-725-331-3
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PRILCANT: Blooders Richard
APPLICANT: Blooders Applied Foreign Compositions and
TITLE OF INVERTION: Analogue Thereof
TITLE OF INVERTION: Analogue Thereof
CONDERS OF SEQUENCES: 68
CONDERS OF SEQUENCES: 68
CONDERS OF CONDESS: 68
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Fatent No. 5582997
GENERAL INPORMATION:
APPLICANT: Blondelle, Sylvie E.
APPLICANT: Perez-Paya, Enrique
APPLICANT: Perez-Paya, Enrique
APPLICANT: Perez-Paya, Enrique
TITLE OF INVENTION: Lysine/Leucine Polypeptides, Mixture
TITLE OF INVENTION: Sets and Libraries Thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEB: Edward P. Gamson
STREET: 135 South LaSalle Street, Suite 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: May be a C-terminal amide, and/or may oTHER INFORMATION: be acetylated at N-terminus. US-07-725-331-23
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Pred. No. 24;
2; Mismatches 5; Indels
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ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENTATION NUMBER: US/08/295,085
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REFERENCE/DOCKET NUMBER: 185017.0B 3418/61275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 781-9548
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.3%; Score 43; DB 1; Best Local Similarity 58.8%; Pred. No. 24; Matches 10; Conservative 2; Mismatches
NAME: Gameon, Edward P.
REGIESTRATION NUMBER: 29,381
REFRENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INPORMATION:
TELEPHONE: 3126165418
TELEPAX: 3126165418
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGRATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGRATION FOR SEQ ID NO: STRANDEDNESS: STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLYKKWKNKLKRSLKRL 17
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Best Local Similarity 58.8%;
Matches 10; Conservative
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LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
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CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
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Fatent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Ampliphilic Peptide Compositions and TITLE Peptide Compositions and TITLE Peptide Compositions and TITLE Peptide Compositions and TITLE Peptide Compositions and TITLE Peptide Compositions and TITLE Peptide Compositions and TITLE Peptide Compositions and TITLE Peptide Compositions and TITLE Peptide Compositions and TITLE Pe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.3%; Score 43; DB 1; Length 18; Best Local Similarity 58.8%; Pred. No. 24; Matches 10; Conservative 2; Mismatches 5; Indels
                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION NATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE: 19-JUL-1990
APTORNEY AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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MOLECULE TYPE: peptide
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CTHER INFORMATION:
CTHER INFORMATION:
US-07-725-331-11
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US-07-725-331-23
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APPLICANT: Yokum, Thomas S.
APPLICANT: Bright, Frederick M.
APPLICANT: Bright, Frederick M.
APPLICANT: Bright, Frederick M.
APPLICANT: Bright, Frederick M.
APPLICANT: Bright, Frederick M.
APPLICANT: Harmer, Robert P.
TITLE OF INVENTION: Short Amphipathic Peptides with
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Against Bacteria and Intracellular Pathogens
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baton Rouge
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Pred. No. 24;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/232,525
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: RUNDER: 33451
REGISTRATION NUMBER: 33451
REPRENCE/ODCKET NUMBER: ALLY File No. 5789542 9301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 504 346-8049
                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,133
FILING DATE: 06-OCT-1997
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,077
FILING DATE: 03-FEB-1997
APPLICATION NUMBER: US/08/681,075
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: LA COUNTRY: USA ZIP: 10821-241

COMPUTER REDABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/019,490
                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09019490 Patent No. 6566334 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McLaughlin, Mark L.
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NAME: Runnels, John H.
REGISTRATION NUMBER: 33451
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Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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                                                                                                                                                                                                          Sequence 9, Application US/08295085; Patent No. 5582997; GENERAL INPOMENTION:
APPLICANT: Blondelle, Sylvie E. APPLICANT: Perez-Paya, Enrique APPLICANT: Perez-Paya, Enrique APPLICANT: Perez-Paya, Enrique APPLICANT: Perez-Paya, Enrique APPLICANT: Perez-Paya, Enrique APPLICANT: Perez-Paya, Enrique APPLICANT: Perez-Paya, Enrique APPLICANT: Perez-Paya, Enrique APPLICANT: Lorgine Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICANT: Lorgine APPLICAN
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Pred. No. 24;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,085
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 1 IMS017.0B 3418/61275
TELEFORMUICATION INFORMATION:
TELEFORMUICATION INFORMATION:
TELEFORMUICATION INFORMATION:
TELEFORMUICATION 19:
FELEFORMUICATION 19:
FELEFORMUICATION 19:
FELEFORMUICATION: 9:
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Patent No. 5789542
GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L
TITLE OF INVENTION: Amphipathic Peptides
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
CITY: Baron Rouge
                                               KLLKKLLKKLKKLLKKL 18
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KLYKKWKNKLKRSLKRL 17
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Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-295-085-9
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ZIP: 70821-2471
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
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                                                                                                                                                           RESULT 36
US-08-295-085-9
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                                           CTHER INFORMATION: May be a C-terminal amide, and/or may OTHER INFORMATION: be acetylated at N-terminus. PCT-US91-05047-3
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be acetylated at N-terminus, Xaa is
Met or methionine sulfoxide.
                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEB: Dreasler, Goldsmith, Sutker, Shore,
ADDRESSEB: Aninamow
STREET: 180 North Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.3%; Score 43; DB 5; Length 18; 58.8%; Pred. No. 24; 2; Mismatches 5; Indels
                                                                                                                               Length 18,
                                                                                                                                  DB 5;
                                                                                                                                                      Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEACHTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION DATA:
APPLICATION NUMBER: DC7/US91/05047
PILING DATE: 19-UL-1990
APPLICATION NUMBER: 29.381
REGISTATION NUMBER: 29.381
                                                                                                                                  45.3%; Score 43; 58.8%; Pred. No.
                                                                                                                                                                                                                        1 KLYKKWKNKLKRSLKRL 17
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                  Query Match
Best Local Similarity 58.89
.....hes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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Matches 10; Conservative
  MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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OTHER INFORMATION:
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GENERAL INFORMATION:
APPLICANT: HOUGHLEN, Richard
APPLICANT: BLOORelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
STREET: 180 North Stetson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                             MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Blondelle, Sylvie E.
AUTHORS: Houghten, Richard A.
TITLE: Design of Model Amphipathic Peptides Having
TITLE: Potent Antimicrobial Activities
JOURNAL: Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                      RELEVANT RESIDUES IN SEQ ID NO: 10: FROM 1 TO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 45.3%; Score 43; DB 1 Similarity 58.8%; Pred. No. 24; 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
                                      TELEPHONE: (504) 387-3221
TELEFAX: (504) 346-8049
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH 18 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gamson, Edward P. REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 42.
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (504) 387-3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLYKKWKNKLKRSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KLLKKLLKKLKKL 18
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Chicago
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TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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1992
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Best Local Similarity
Matches 10; Conserva
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
ITILE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is Met or methionine sulfoxide.
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ZIP: 60601
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION DATA:
APPLICATION NUMBER: 18-ULUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
FILING DATE: 19910717
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 411250-80
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                 ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KLYKKWKNKLKRSLKRL 17
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
PCT-US91-05047-11
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PCT-US91-05047-23
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COUNTRY:
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; Sequence 11, Application PC/TUS9105047
; GENERAL INFORMATION:
APPLICANT: Houghten, Richard
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is Met or methionine sulfoxide.
                 PCT-US91-05047-8
Sequence 8, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.3%; Score 43; DB 5; Length 18; 58.8%; Pred. No. 24; tive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                       ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312616540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FRIDAMENTONES: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KLYKKWKNKLKRSLKRL 17
                                                                                                                                                                                                                                                                ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
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CTHER INFORMATION:
CTHER INFORMATION:
PCT-US91-05047-8
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Matches 10; Conserva
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                                                                                                                                                                                                                                                                                                                                          STATE:
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RESULT 45
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Sets and Libraries Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 5; Length 18; Pred. No. 24; Mismatches 5; Indels
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Pred. No. 24;
2; Mismatches 5; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10741
FILING DATE:
CURSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENEAL:
APPLICANT:
TITLE OF INVENTION: Lysine/Lect.
TITLE OF INVENTION: Sets and Libraries TITLE OF INVENTION: Sets and Libraries TITLE OF ORRESS: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward P. Gamson
CORRESPET: 135 South LaSalle Street, Suite 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: IMS017.0B 3418/61275
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 781-9470
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION: 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US95-10741-1; Sequence 1, Application PC/TUS9510741; GENERAL INFORMATION:
                                                                                                       TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLYKKWKNKLKRSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KLLKKLLKKLKKLLKKL 18
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Best Local Similarity 58.8%;
Matches 10; Conservative ;
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58.8%;
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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MOLECULE TYPE: peptide
PCT-US95-10741-1
                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 135 South
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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                                                             Lysine/Leucine Polypeptides, Mixture
Sets and Libraries Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/COCKET WUMBER: 19,381
TELECHONES/CACION INFORMATION:
TELECHONE: (312) 781-9470
TELECHONE: (312) 781-9470
TELEFAX: (312) 781-948
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 18 aming acids
                        GENERAL
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Sets and Librarian
TITLE OF INVENTION: Sets and Librarian
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward P. Gamson
ADDRESSEE: Edward P. Gamson
ADDRESSEE: The Street Suite 1625
                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 5;
Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: May 16, 2005, 08:40:42
Job time : 20.2414 secs
Sequence 9, Application PC/TUS9510741 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KLLKKLLKKLKKLLKKL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
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                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide PCT-US95-10741-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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Sequence 1, Application US/10131433; Publication No. US20030054422A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
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68, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                            May 16, 2005, 08:38:44; Search time 67.6552 Seconds (without alignments) 88.876 Million cell updates/sec
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(cgn2_6/ptodata/I/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/I/pubpaa/US07_NEW_PUB.pep:*

(cgn2_6/ptodata/I/pubpaa/US06_PUBGOMB.pep:*

(cgn2_6/ptodata/I/pubpaa/US06_PUBGOMB.pep:*

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(cgn2_6/ptodata/I/pubpaa/US09_PUBGOMB.pep:*

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(cgn2_6/ptodata/I/pubpaa/US09_PUBGOMB.pep:*

(cgn2_6/ptodata/I/pubpaa/US108_PUBGOMB.pep:*

(cgn2_6/ptodata/I/pubpaa/US60_NEW_PUB.pep:*

(cgn2_6/ptodata/I/pubpaa/US60_PUBCOMB.pep:*

(cgn2_6/ptodata/I/pubpaa/US
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-131-433-1
US-10-060-102-5
US-10-721-839-5
US-10-344-709C-15
US-10-344-709C-15
US-10-109-171-55
US-10-109-171-11
US-10-424-599-196493
US-10-424-599-17429
US-10-424-599-17429
US-10-109-171-68
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                                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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95
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Match 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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Sequence 158393, Application US/10424599

Fublication No. US20040031072A1

Sequence 158393, Application US/2041031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

NUMBER OF SEQ ID NOS: 285684
                                                                                Sequence 126, Applemente 126, Applemente 243915, Sequence 243585, Sequence 177506, Sequence 177506, Sequence 12056, Sequence 220565, Sequence 28, Applemente 143572, Sequence 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 205, Applemente 
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Sequence 37, Appl
Sequence 37, Appl
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Sequence 204139,
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Pred. No. 6;
1; Mismatches 0; Indels
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US-10-424-599-158393
5 US-10-414-342-10
US-09-864-761-47529
US-09-864-201-47529
US-09-864-201-47529
US-09-864-201-201
US-09-864-761-201
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S US-10-424-599-205
S US-10-609-865-989-205
S US-10-801-897-205
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69.2%;
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51 RIYKKFKNKIKRS 63
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Glycine max
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TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALIA.
TITLE OF INVENTION: CATHELLICIDINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/10344709C

Sequence 15, Application US/2040170642A1

Sequence 16, Application US/2040170642A1

GENERAL INFORMATION:

TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof

TITLE OF INVENTION: Gerived antimicrobial peptide or a derivative thereof

TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof

TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof

CURRENT APPLICATION NUMBER: US/10/344,709C

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: A 1416/2000

PRIOR APPLICATION NUMBER: A 1416/2000

PRIOR PILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 37
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// Sequence 55, Application US/09820053A

// Publication No. US20030083243A1

// GENERAL INFORMATION:
// APPLICANT: Owen, Donald R.
// TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
// TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
// CURRENT PEPLICANTON NUMBER: US/09/820,053A
// CURRENT PEPLICANTON NUMBER: 2011-03-28
// NUMBER OF SEQ ID NOS: 165
        FILE REPERENCE: IOWA:035US

FILE REPERENCE: IOWA:035US

CURRENT APPLICATION NUMBER: US/10/721,839

CURRENT FILING DATE: 2003-11-25

PRIOR PELING DATE: 2002-02-22

PRIOR FILING DATE: 2002-02-22

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOPTWARE: PATENTIN VET: 2.1

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLYKKWKNKLKRSLKRLG 18
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4 KRLRKFRNKIKEKLKKIG 21
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Best Local Similarity 44.44
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Ovis aries US-10-721-839-5
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Sequence 5, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAUNY
APPLICANT: ROLLER, RICHARD
APPLICANT: TROKER, RICHARD
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: CATHELICIDINS
FILE REFERENCE: IOWA-03292
FILE REFERENCE: IOWA-03293
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR PILICATION NUMBER: 60/265,270
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR APPLICATION NUMBER: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
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PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
                                     APPLICANT: UNILEVER, PLC
TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
FILE REFERENCE: Lipopolysaccharide Immunoassay
CURRENT APPLICATION NUMBER: US/10/131,433
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/09/545,180
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.6%; Score 49; DB 14; Length 32; llarity 44.4%; Pred. No. 13; Conservative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 37;
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Pred. No. 15;
6; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KLYKKWKNKLKRSLKRLG 18
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KRLRKFRNKIKEKLKKIG 21
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APPLICANT: STAPLETON, JACK
APPLICANT: STINSKI, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
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ORGANISM: Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
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ORGANISM: Lapine
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                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 32
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LENGTH: 37
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FEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD_RES
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                        1 KLYKKWKNKLKRSLKRL 17
                                                              5 KLAKKAKAKLKKALKAL 21
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (21);
; OTHER INFORMATION: AMIDATION
US-10-109-171-11
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52 WKXQLKKKLKKMG 64
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NAME/KEY: unsure
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Sequence 55, Application US/20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
TITLE OF PLICANT: Owen, DONALS BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT APPLICATION NUMBER: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 55
LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 49.5%; Score 47; DB 14; Length 23; Best Local Similarity 52.9%; Pred. No. 18; Matches 9; Conservative 4; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09820053A
Publication No. US20030083243A1
GENERAL INPORMATION:
APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELKO27
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 11
LENGTH: 21
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NAME/KEY: MOD RES
DOCATION: (21)
CTHER INFORMATION: AMIDATION
US-09-820-053A-11
                                                                                                                              OTHER INFORMATION: SYNTHETIC SEQUENCE US-09-820-053A-55
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3 KLFKKFAKKLAKKLKKL 19
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KLFKKFAKKLAKKLKKL 19
                                                                TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 23
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Best Local Similarity
Matches 11; Conserv
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US-09-820-053A-11
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US-10-109-171-55
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Sequence 196493, Application US/10424599
; Sequence 196493, Application No. US20040031072A1
; Publication No. US20040031072A1
; Publication No. US20040031072A1
; APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILLE REPRENCE: 38-21(5223)B
CURRENT FILLING DATE: 2003-04-28
UNMBER OF SEQ ID NOS: 285684
SEQ ID NO 196493
LENGTH: 65
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Sequence 11, Application US/10109171
Publication 0. US20030109452A1
GENERAL INFORMATION:
APPLICANT: Owen, Donald R.
APPLICANT: Owen, Donald R.
APPLICANT: Owen, BHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE FILE REFERENCE: HELAC28
CURRENT APPLICATION NUMBER: US/10/109,171
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 21
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US-10-424-599-196493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 14;
Pred. No. 23;
2; Mismatches 4
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Pred. No. 63;
4; Mismatches 2
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OTHER INFORMATION: unsure at all Xaa locations
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Sequence 10, Application US/10414342

Publication No. US2004005908A1

GENERAL INFORMATION:
APPLICANT: McLaughlin, Mark L.
APPLICANT: Enright, Frederick M.
APPLICANT: Enright, Frederick M.
APPLICANT: Hammer, Robert P.
TITLE OF INVENTION: Short Amphipathic Peptides with
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Against Bacteria and Intracellular Pathogens
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,342
FILING DATE:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/796,123
FILING DATE: 06-FEB-1997
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                            47.4%; Score 45; 56.2%; Pred. No. 3
CURRENT APPLICATION NUMBER: US/10/109,171
                                                                                                                                 TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
OTHER INFORMATION: SYNTHETIC SEQUENCE
NAME/KEY: MOD RES
LOCATION: (20)
OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: NUMBER: 33451
REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: 9619
TELECOMMUNICATION INFORMATION:
TELEPRA: (504) 387-3221
TELEPRA: (504) 346-8049
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
BLONDELLE, Sylvie E.
AUTHORS: Houghten, Richard A.
                  CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 68
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLYKKWKNKLKRSLKR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KLFKKALKKLKKALKK 18
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ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.2³
Matches 9; Conservative
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                                                      Sequence 177429, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: Law Construct Thomas J

APPLICANT: Cavorar Thomas J

APPLICANT: Cavorar Thomas J

APPLICANT: Cavorar Winua

APPLICANT: Cavoraywei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 177429
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APPLICANT: Owen, Donald R.
TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE FILE REFERENCE: HELKO28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 30;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_131234C.1.pep
US-10-424-599-177429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15;
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; Sequence 68, Application US/09820053A
; Publication No. US20030083243A1
; Publication No. US20030083243A1
; GENERAL INFORMATION:
    APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELXO27
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT APPLICATION NUMBER: US/09/820,053A
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45.5;
Pred. No. 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 68, Application US/10109171
Publication No. US20030109452A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KLYKKWKNKLKRS-LKRLG 18
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Best Local Similarity 56.2%;
Matches 9; Conservative
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Best Local Similarity 68.4%;
Matches 13; Conservative
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KLFKKALKKLKKALKK 18
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; OTHER INFORMATION: AMIDATION
US-09-820-053A-68
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                 JS-10-424-599-177429
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LENGTH: 20
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC022205.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
US-09-864-761-47529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 16;
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APPLICANT: Reactive Surfaces, Ltd.
TITLE OF INVENTION: Antifungal Paints and Coatings
FILE REPERENCE: RACT-00400
CURRENT APPLICATION NUMBER: US/10/884,355A
CURRENT FILING DATE: 2004-07-02
PRIOR PILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
44.2%; Score 42; DB 9;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches
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                                                                                              , DB ,
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APPLICANT: Zhelev, NIKolai
TITLE OF INVENTION: Transport Vectors
FILE REFERENCE: CCI-010
CURRENT APPLICATION NUMBER: US/09/854,204
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/438,460
PRIOR PILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-13
PRIOR FILING DATE: 1999-11-13
PRIOR PILING DATE: 1999-11-13
PRIOR PILING DATE: 1999-02-04
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-06-22
PRIOR PLING DATE: 1999-06-22
PRIOR PLING DATE: 1999-06-22
PRIOR PLING DATE: 1999-06-22
PRIOR PLING DATE: 1999-06-22
PRIOR PLING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTING DATE: 1999-11-11
                                                                                                                                      5; Mismatches
                                                                                                     45.3%; Score 43; 43.8%; Pred. No.
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; Sequence 126, Application US/10884355A
; Publication No. US20050058689A1
                                                                                                                                                                                                                                                                                          Sequence 64, Application US/09854204
Patent No. US200200098266A1
GENERAL INFORMATION:
APPLICANT: Fischer, Peter Martin
                                                                                                                                                                        1 KLYKKWKNKLKRSLKR 16
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KLIKKWRKKQQRNWRK 21
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                                                                                                                   Best Local Similarity 43.8
Matches 7; Conservative
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US-09-854-204-64
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                                                                                                       Query Match
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 Design of Model Amphipathic Peptides Having
Potent Antimicrobial Activities
                                                               PAGES: 12688-12694
DATE: 1992
RELEVANT RESIDUES IN SEQ ID NO: 10: FROM 1 TO 18
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence I
                                   Biochemistry
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                 TITLE: PC
JOURNAL:
VOLUME:
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NO 243585
LENGTH: 59
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Pred. No. 2e+02;
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OTHER INFORMATION: EXPRESSED IN BOND MARKOW, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.55
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Pred. No. 1.8e+02;
2; Mismatches 6; Indels
                                                                                        PRIOR APPLICATION UNUBER: 2011-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-01-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 47200
PRIOR PILING DATE: 2001-01-29
NUMBER: ADDICATION NUMBER: US SOFTWARE: AND MADER: US SOFTWARE: AND MADER: US SOFTWARE: AND MADER: U
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                                                                         FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
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; Sequence 243585, Application US/10424599
; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: MAP TO AC004869.1 OTHER INFORMATION: EXPRESSED IN PLAC
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Best Local Similarity 46.7%;
Matches 7; Conservative
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
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| Sequence 47200, Application US/09664761
| Patent No. US20020048763A1
| Patent No. US20020048763A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David R. APPLICANT: Chen, Wensheng TTLLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY TILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILLE REFERENCE: Apomica-X-1
| CURRENT FILLING DATE: 2001-05-23 |
| PRIOR PELICATION NUMBER: US 60/180, 312 |
| PRIOR FILLING DATE: 2000-06-26 |
| PRIOR APPLICATION NUMBER: US 09/632,366 |
| PRIOR FILLING DATE: 2000-06-03 |
| PRIOR FILLING DATE: 2000-06-03 |
| PRIOR FILLING DATE: 2000-06-03 |
| PRIOR FILLING DATE: 2000-09-04 |
| PRIOR FILLING DATE: 2000-09-05 |
| PRIOR FILLING DATE: 2000-09-05 |
| PRIOR FILLING DATE: 2000-09-07 |
| PRIOR FILLING DATE: 2000-09-07 |
| PRIOR FILLING DATE: 2000-09-07 |
| PRIOR FILLING DATE: 2000-09-27 |
| PRIOR PILLING DATE: PCT/USO1/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 264915, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REPRENCE: 38-21(5223)8

CURRENT APPLICANT: APPLICANT: 2003-04-28

FILLE REPRENCE: 38-21(5223)8

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 264915
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44.2%; Score 42; DB 15; Length 51;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                              DB 17; Length 45;
                                                                                                                                                                                                                                                                                                                                       6; Indels
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US-10-424-599-264915
                                                                                                                                                                                                                                                              Query Match

44.2%; Score 42; DB 17;
Best Local Similarity 47.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 3; Mismatches 6
                                                                                                                                              ) ORGANISM: Scorpion Parabutoporin
US-10-884-355A-126
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                                                                                                                                                                                                                                                                                                                                                                                                                2 LYKKWKNKLKRSLKRLG 18
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7 LKKAWKSKLAKKLRAKG 23
SOFTWARE: Patentin version 3.3
SEQ ID NO 126
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
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us-09-648-816b-10.rapb

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APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TILLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 145431

LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: Ear Rosa Thomas J
APPLICANT: Ear Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Willia
APPLICANT: Cao Willia
APPLICANT: Cao Willia
APPLICANT: Cao Willia
APPLICANT: Cao Willia
APPLICANT: Cao Willia
APPLICANT: Cao Willia
APPLICANT: Cao Willia
APPLICANT: Cao Willia
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILER PEFRENCE: 30-21(5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 220565
LENGTH: 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT3847_41200C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT4530_46151C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 16;
Pred. No. 3e+02;
0; Mismatches 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                         Sequence 145431, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 220565, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LYKKWKNKLKRSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 WKNKLKRSLKRLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserva
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                                           JS-10-437-963-145431
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US-10-319-786-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                APPLICANT: Lar Rosa Thomas J
APPLICANT: Experiment To a void K
APPLICANT: About Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37256, Application US/10767701

Sequence 37256, Application WS/10767701

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

LENGTH: 63
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25;
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  6; Indels
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US-10-767-701-37256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: PAT_MRT3847_92610C.1.pep
US-10-424-599-277506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 15;
Pred. No. 1.2e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(63)
OTHER INFORMATION: ungure at all Xaa locations
3; Mismatches
                                                                                                                                                                                                 Sequence 277506, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                        27 KKKKKKKNKIKKKKKKKG 44
                                           1 KLYKKWKNKLKRSLKRLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.2%;
ilarity 66.7%;
Conservative
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KWKKKRMRRLKR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWKKKRMRRLKR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
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  Matches
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US-09-864408A-118
Sequence 118, Application US/09864408A
Publication NO. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: NO. US20040009474A1el Human Polynucleotides and Polypeptides Encocyping Reference: 2402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 68
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                                                                                                                                                                                                                                                                            Length 62;
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                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_41246C.1.pep
US-10-424-599-220615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_10065C.1.pep
US-10-424-599-143572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 15; L
Pred. No. 4.1e+02;
5; Mismatches 2;
                                                                                                                                                                                                                                                                            Query Match
42.1%; Score 40; DB 15; L
Best Local Similarity 41.2%; Pred. No. 3.8e+02;
Matches 7; Conservative 5; Mismatches 5;
                                                                       FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(62)
OTHER INFORMATION: unsure at all Xaa locations
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 118
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 143572, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                1 KLYKKWKNKLKRSLKRL 17
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46 KLYRDWQNRIIPREKQL 62
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Best Local Similarity 46.2%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                  ORGANISM: Glycine max
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                                                                                                                                                                             FEATURE:
     LENGTH:
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                  APPLICANT: Little, Roger G
TITLE OF INVENTION: Biologically Active Peptides from
Functional Domains of Bactericidal/Permeability-Increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 220615, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
BAPPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihna
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (52323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 220615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.1%; Score 40; DB 15; Length 21; Best Local Similarity 53.3%; Pred. No. 1.4e+02; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NDBER: US/10/319,786
FILING DATE: 13-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                                    Protein and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 93,1133-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/473,344
FILING DATE: 7-UNN-1995
APPLICATION NUMBER: US 08/306,473
FILING DATE: 15-SEP-1995
APPLICATION NUMBER: US 08/209,762
FILING DATE: 11-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
OTHER INFORMATION: "BPI.47"
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KLYKKWKNKLKRSLK 15
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7 RFLKKWKAAAKRFLK 21
                                                                                                                         NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                      ZIP: 60606
GENERAL INFORMATION:
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Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROFEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1...18 OTHER INFORMATION: N-terminal acetylated and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.1%; Score 39; DB 11;
42.9%; Pred. No. 1.7e+02;
tive 5; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 10036-2811

COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPREATING SYSTEM: DOS
SOFFWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA: US/09/865,989
FILING DATE: 25-MAY-2001
CLASSIFICATION: UNROWN-
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-terminal amidated

SEQUENCE DESCRIPTION: SEQ ID NO: 205: US-09-865-989-205
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MOLECULE TYPE: No. US20040029807A9e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 205, Application US/10099574A; Publication No. US20030060604A1; GENERAL INFORMATION:
                                                                                                                                Sequence 205, Application US/09865989 Publication No. US20040029807A9 GENERAL INFORMATION:
                                                                                                                                                                                               APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-493-5556
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    S LFREWLEELKQKLK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LYKKWKNKLKRSLK 15
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5 LFREWLEELKOKLK 18
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                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserva
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US-10-099-574A-205
                                                                                                            US-09-865-989-205
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; LOCATION: (1)..(1); OTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid US-09-864-408A-118
                                                                                                                                                                                                                                                                                                                                                                                                                                    Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS:
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                        Query Match 42.1%; Score 40; DB 11; Length 72; Best Local Similarity 43.8%; Pred. No. 4.4e+02; Matches 7; Conservative 3; Mismatches 6; Indels
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Pred. No. 1.7e+02;
5; Mismatches 3; Indels
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CTHER INFORMATION: N-terminal acetylated and C-terminal amidated sEQUENCE DESCRIPTION: SEQ ID NO: 205: US-09-865-989-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCÉ/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
RAPPLICATION WUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: No. US20030008827Ale
                                                                                                                                                                                                                                                                                                                            Sequence 205, Application US/09865989
Publication No. US20030008827A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
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INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                    Query Match
Best Local Similarity 42.9 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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Gaps

2 LYKKWKNKLKRSLK 15

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ZIP: 10036-2811
COMPUTER READABLE FORM:
                                                                                                                          COUNTRY: USA
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APPLICANT: Surfurer, Klaus
APPLICANT: Butcher, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COTHER: NY
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Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
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Pred. No. 1.7e+02;
5; Mismatches 3; Indels
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C-terminal amidated
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: DISACTION:
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FREESD Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,574A
FILING DATE: 29-SEF-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAUXA A
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 254
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
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LFREWLEELKQKLK 18
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                 ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS: si
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SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS.
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: «Unknown>
FILING DATE: «Unknown>
ATTORNEY/AGET INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 66141 PENNIE
TELEFAX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 15;
Pred. No. 1.7e+02;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES
TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-
TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMI
                        STREET: 1155 Avenue of the Americas
                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,836B
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TOPOLOGY: linear
MOLECULE TYPE: No. US20030203842Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1155 Avenue of the Americas
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Publication No. US20030208059A1
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                                                                                                                                                                                                                                                                                                      FILING DATE: 28-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 18 amino acids
                                                                                                             ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.1%;
42.9%;
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1...18 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:::| :||: ||
5 LFREWLEELKOKLK 18
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Best Local Similarity 42.9°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
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APPLICATION NUMBER: US/09/453,840
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SOFTWARE: PastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/801,897
FILING DATE: 15-Mar-2004
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
APPLICATION NUMBER: US/09/865,989
PILING DATE: 25-May-2001
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17-DEC-1999
                                                                                                                                                                                                                                       TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                   TELEFAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                           STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1...18
OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LYKKWKNKLKRSLK 15
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5 LFREWLEELKOKLK 18
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REGISTRATION NUMBER: 3(
                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                   Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 42.9
Matches 6; Conservative
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MEDIUM TYPE: Diskette
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ZIP: 10036-2811
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US-10-801-897-205
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Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 15; Length 18;
Pred. No. 1.7e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal acetylated and C-terminal amidated
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,599
FILING DATE: 29-CTT-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/40,136
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZi, LAUKA A
REGISTRATION NUMBER: 30,742
REBRENCE/DOCKET NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ. 1D NO: 205:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/802,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: No. US20030208059Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 205, Application US/10802080 Publication No. US20040181034A1 GENERAL INFORMATION:
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
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LFREWLEELKOKLK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036-2811
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CTHER INFORMATION:
CTHER INFORMATION:
US-10-283-599-205
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STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Other
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US-10-802-080-205
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Gaps
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Publication No. US20040198662A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Isabelle
APPLICANT: Grante, Isabelle
APPLICANT: Metz, Gunther, Tabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
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42.9%; Pred. No. 1.7e+02;
ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-terminal acetylated and
FILING DATE: 01-DEC-1999
APPLICATION NUMBER: 08/940,095
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminal amidated SEQUENCE DESCRIPTION: SEQ ID NO: 205:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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Gaps

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40.0%; Pred. No. 2e+02;
tive 6; Mismatches 3; Indels
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MEDIUM TYPE: Diskette

MEDIUM TYPE: Diskette

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: PEATSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/865,989

FILING DATE: 25-May-2001

CLASSIFICATION AUMBER: 09/465,719

FILING DATE: 17-DEC-1999

ATTORNEY/AGENT INFORMATION:

NAME: COLUMENT, LABOR AND AUMBER: 09/465,719

REGISTRATION NUMBER: 30,742

REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                N-terminal acetylated and C-terminal amidated
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Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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; MOLECULE TYPE: No. USCO30008827Ale
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-865-989-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:::| :||:||
5 LFREWLEELKQKLK 18
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                                                                                                                                                                   ; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-937-767-205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                   MOLECULE TYPE: None
FEATURE:
           amino acid
                                                            linear
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                               NAME/KEY: Other
                                  STRANDEDNESS:
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TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 16; Length 18;
Pred. No. 1.7e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal acetylated and C-terminal amidated
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REGISTRATION NUMBER: 30,742
REFERENCE JOCKET NUMBER: 009196-0005-999
TELECOMMUNICATION INFORMATION:
           009196-0006-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10.36-2811
ZIP: 10.36-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: EN Compatible
COMPUTER: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN COMPACE: EN
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: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 205, Application US/10937767; Publication No. US20050080013A1; GENERAL INFORMATION:
APPLICANT: Daselux, Jean-Louis APPLICANT: Sekul, Renate APPLICANT: Buttner, Klaus APPLICANT: Cornut, Isabelle APPLICANT: Metz, Gunther; TITLE OF INVENTION: AND THEIR USE TG
REFERENCE/DOCKET NUMBER: 0091
TELECPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELERAX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 205: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.1%;
42.9%;
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5 LFREWLEELKOKLK 18
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Best Local Similarity 42.9
Matches 6; Conservative
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Pennie & STREET: 1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                                           COCATION: 1...18
CTHER INFORMATION:
CTHER INFORMATION:
US-10-801-897-205
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: None
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Other
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US-10-937-767-205
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STATE:
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APPLICAMT: COINUL, IBEACEAL
APPLICAMT: COINUL, ABOLIPOPROTEIN A-1 AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
MUMBER OF SEQUENCES: 254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenie of the Americas
CITY: NAY
COUNTRY: USA
ZIP: 10034-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: TBM Compatible
OPERATING SYSTEM: DOS
COMPUTER: TBM Compatible
OPERATING SYSTEM: DATE:
APPLICATION NUMBER: US/10/099,574A
FILING DATE: 29-SEP-1997
CLASSIFICATION NUMBER: 099196-0005-999
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAUYA A
REGISTRATION NUMBER: 009196-0005-999
TELEPHONE: 650-493-4556
TELECOMMUNICATION NUMBER: 0931-5556
TELECOMMUNICATION NUMBER: 009186-0005-999
TELEPHONE: 650-493-4556
TELECOMMUNICATION NUMBER: 009186-0005-999
TELEPHONE: 650-493-4556
TELERACTING SOURCE CHARACTERISTICS:
LENGTH: 22 amino acids
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Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROPEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPDEMIC DISORDERS
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: No. US20030060604Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/10099836B; Publication No. US20030203842A1; GENERAL INFORMATION: APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
Cornut, Isabelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:::| |:| :||:
5 LFREWLNELLEALKQ 19
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Best Local Similarity 40.09
Matches 6; Conservative
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STRANDEDNESS: 81
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US-10-099-836B-37
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  APPLICANT:
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                                                                                                                                                                                                                                      APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.1%; Score 39; DB 11; Length 22; 40.0%; Pred. No. 2e+02; trive 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEO VERSION 2.0
CURRY APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: No. US20040029807A9e

SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-865-989-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/10099574A
Publication No. US20030060604A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
                                                                                                                                                                           Sequence 37, Application US/09865989
Publication No. US20040029807A9
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650-493-4935
TELEX: 650-493-5556
TELEX: 66141 PENNIE
INPORMATION-POR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 258
                       2 LYKKWKNKLKRSLKR 16
                                              |:::| |:| :||:
5 LFREWLNELLEALKQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LYKKWKNKLKRSLKR 16
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LFREWLNELLEALKQ 19
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 39
US-10-099-574A-37
                                                                                                                               RESULT 38
US-09-865-989-37
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Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPEDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                          41.1%; Score 39; DB 15; Length 22; 40.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATIBLE
SOFTWARE: FRASTER: DOS
SOFTWARE: FRASTER: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/802, DRIOR APPLICATION DATA:
APPLICATION NUMBER: US/99453,840
FILING DATE: 01-DEC-1999
APPLICATION NUMBER: 08/940,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 Avenue of the Americas CITY: New York
                            009196-0007-999
                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pennie & Edmonds LLP
                      REFERENCE/DOCKET NUMBER: 009196-0007
TELECOMOUNICATION INFORMATION:
TELERAX: 650-493-4935
TELERAX: 66141 PENNIE.
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. US20030208059Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/10802080 Publication No. US20040181034A1 GENERAL INFORMATION: APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 650-493-4935
TELEPA: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 22 amino acids
      REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sekul, Renate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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5 LFREWLNELLEALKQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                   2 LYKKWKNKLKRSLKR 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-802-080-37
                                                                                                                                                                                                                                                                                       US-10-283-599-37
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APPLICANT: Sekul, Renate
APPLICANT: Sekul, Renate
APPLICANT: Cornut, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: GENE THERAPY APPROACHES TO
TITLE OF INVENTION: USB TO TREAT DYSLIPIDEMIC DISORDERS.
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie F 73
STRPF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 15; Length 22;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                          NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PESTEED 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,836B
FILING DATE: 28-Aug-2002
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: No. US20030203842Ale SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: Pennie & Edmonds LLP
F: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOSSOPERATING SYSTEM: DOSSOPTWARE: FASTSEQ VERSION 2.0 CURRENT APPLICATION NUMBER: US/10/283,599 FILING DATE: 29-OCT-2002 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/10283599
Publication No. US20030208059A1
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,136
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                   FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.1%;
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LFREWINELLEALKQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-099-836B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NO COUNTRY:
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COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:::| |:|
5 LFREWLNELLEALKQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: None US-10-937-767-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: 811
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Setul. Senate
APPLICANT: Setul, Renate
APPLICANT: Setul, Renate
APPLICANT: Setul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                       ö
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                                                                                           Score 39; DB 16; Length 22;
Pred. No. 2e+02;
6; Mismatches 3; Indels
                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               009196-0006-999
; MOLECULE TYPE: None
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-802-080-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOOFWARE: FastESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/801,897
FILING DATE: 15-Mar-2004
CLASSIFICATION: DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
APPLICATION NUMBER: 09/465,719
FILING DATE: 25-May-2001
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTONNEY, AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-000(
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFHONE: 660-493-556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: Amino acide
                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/10801897; Publication No. US20040198662A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFIGURATION COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                               41.1%;
40.0%;
                                                                                                                                                                                                |:::| |:| :||:
5 LFREWLNELLEALKQ 19
                                                                                                                                                                           2 LYKKWKNKLKRSLKR 16
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                                                                                           Query Match
Best Local Similarity 40.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
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Septional in November 2017, 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 2018 | 20
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 204139
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Glycine max
; FATURE: ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_26364C.1.pep
US-10-424-599-204139

Query Match
Best Local Similarity 43.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps

Qy 2 LYKKWKNKLKRSLKRL 17
: | | | | | | |
Db 11 IMESWKSKLCKNLVRL 26
```

Search completed: May 16, 2005, 09:23:43 Job time : 68.6552 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 15.5172 Seconds (without alignments) 111.611 Million cell updates/sec Run on:

US-09-648-816B-10 95 1 KLYKKWKNKLKRSLKRLG 18 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

22893

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | de             |        |    | SUMMARIES |                    |
|---------------|-------|----------------|--------|----|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB |           | Description        |
| -             | 41.5  | 43.7           | 55     | 7  | H90520    | hypothetical prote |
| 7             | 41    | 43.2           | 25     | 7  | S38425    | ribosomal protein  |
| ٣             | 41    | 43.2           | 25     | 7  | T49214    | ribosomal protein  |
| 4             | 41    | 43.2           | 69     | 7  | C72262    | O                  |
| S             | 39    | 41.1           | 22     | 7  | C64330.   | ribosomal protein  |
| 9             | 39    | 41.1           | 57     | 7  | C97937    | Ø                  |
| 7             |       | 40.0           | 25     | Н  | JC4278    |                    |
| ω.            | 38    | 40.0           | 25     | Н  | R6BY4B    |                    |
| σ             | 38    | 40.0           | 25     | ~  | JQ1617    |                    |
| 10            |       | 40.0           | 25     | 7  | JC4685    | ribosomal protein  |
| 11            | 38    | 40.0           | 74     | 7  | I57554    | •~                 |
| 12            | 37    | 38.9           | 25     | 7  | T38719    | ribosomal protein  |
| 13            | 37    | 38.9           | 61     | 7  | E97043    | hypothetical prote |
| 14            | 36    | 37.9           | 34     | 7  | E70239    | hypothetical prote |
| 15            |       | •              | 45     | 7  | T52272    | R2R3-MYB transcrip |
| 16            |       | 36.8           | 49     | 7  | T07304    | hypothetical prote |
| 17            |       | 36.8           | 63     | ~  | C81442    | 50s ribosomal prot |
| 18            | 35    | 36.8           | 70     | 7  | B90351    | conserved hypothet |
| 19            | 34.5  | 36.3           | 39     | 7  | G64522    | hypothetical prote |
| 20            | 34    | 35.8           | 32     | ~  | D70241    | conserved hypothet |
| 21            | 34    | 35.8           | 45     | 7  | T52123    | hypothetical prote |
| . 22          | 34    | 35.8           | 45     | N  | T52282    | R2R3-MYB transcrip |
| 23            | 34    | 35.8           | 48     | Н  | Q1BP87    | gene 1.8 protein - |
| 24            | 34    | 35.8           | 9      | 7  | H75130    | cal                |
|               | 34    | 35.8           | 63     | N  | S07666    | cecropin B - fruit |
| 56            | 34    | . 35.8         | 65     | 7  | A97900    | cal                |
| 27            | 34    | 35.8           | 99     | 7  | T12922    | -                  |
| 28            | 34    | 35.8           | 99     | 0  | 139       | ical               |
| 29            | 34    | 35.8           | 67     | 7  | T40218    | probable ATP synth |

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Gaps ö

Score 41; DB 2; Length 25; Pred. No. 18; 0; Mismatches 4; Indels

Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative C

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| hypothetical prote |        | H+-exporting ATPas | H+-exporting ATPas | plantaricin A - La | hypothetical prote | hypothetical chl p | hypothetical prote | R2R3-MYB transcrip | R2R3-MYB transcrip | hypothetical prote | hypothetical prote | ribosomal protein | cecropin C - fruit | Spl2 protein homol | hypothetical prote |
|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| AB1771             | A05061 | S31269             | A53927             | A45913             | A05058             | C26871             | H81591             | T52125             | T52276             | E95242             | H98106             | F70442            | S23501             | 832026             | D84156             |
| ~                  | N      | ~                  | ~                  | ~                  | 7                  | 4                  | 7                  | 7                  | 7                  | 7                  | ~                  | 7                 | 7                  | ~                  | 0                  |
| 67                 | 69     | 40                 | 43                 | 22                 | 27                 | 35                 | 40                 | 45                 | 45                 | 29                 | 59                 | 62                | 63                 | 64                 | 65                 |
| 35.8               | 35.8   | 35.3               | 35.3               | 34.7               | 34.7               | 34.7               | 34.7               | 34.7               | 34.7               | 34.7               | 34.7               | 34.7              | 34.7               | 34.7               | 34.7               |
| 34                 | 34     | 33.5               | 33.5               | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                | 33                 | 33                 | 33                 |
| 30                 | 31     | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                | 43                 | 44                 | 45                 |

## ALIGNMENTS

| RESULT 1                                                                                                                        |
|---------------------------------------------------------------------------------------------------------------------------------|
| hypothetical protein MYPU_0720 [imported] - Mycoplasma pulmonis (strain UAB CTIP)                                               |
| C;Species: Mycopiasma puimonis<br>C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004                   |
| C;Accession: H90220 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;                    |
| AUCIEIC ACINE REB. 23, 211372133, 2001 AUTILE: THE complete genome sequence of the murine respiratory pathogen Mycoplasma pulmo |
| A.Accession: H90520                                                                                                             |
| A;Status: preliminary A;Molecule type: DNA                                                                                      |
| A;Residues: 1-55 <kur><br/>A;Cross-references: UNIPROT:Q98RD7; GB:AL445566; PID:g14089485; PIDN:CAC13245.1; GSPDB:GN</kur>      |
| A,Experimental source: strain UAB CTIP                                                                                          |
| A;Gene: MYPU 0720<br>A;Genetic code: SGC3                                                                                       |
| 43.78;                                                                                                                          |
| Best Local Similarity 55.6%; Pred. No. 32; Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;                          |
| QY 1 KLYKKWRONKLKRSLKRLG 18                                                                                                     |
| Db 2 KKYKKW-NINKKLKKHG 18                                                                                                       |
| RESULT 2                                                                                                                        |
| S38425                                                                                                                          |
| ribosomal protein GL41 - upland cotton                                                                                          |
| C;Species: Gossypium hirsutum (upland cotton)                                                                                   |
| C. Accession: S38425                                                                                                            |
| R;Turley, R.B.; Ferguson, D.L.; Meredith, W.R.                                                                                  |
| submitted to the EMBL Data Library, October 1993                                                                                |
| A.Kelefence fulloper: 538425<br>b.keression: 638425                                                                             |
| A;Status: preliminary                                                                                                           |
| A; Molecule type: mRNA                                                                                                          |
| A; Kesidues: 1-25 <iuk></iuk>                                                                                                   |
| AfroBs-terencess university industrial and the Cisucefamily: rat ribosomal protein L41                                          |

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transposase, uncharacterized, truncation [imported] - Streptococcus pneumoniae (strain Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P28751; EMBL:X82550; NID:g575383; PIDN:CAA57899.1; PID:g57538; C;Superfamily: rat ribosomal protein L41
C;Keywords: ribosome
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C A;Itle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:P54025, GB:U67480, GB:L77117, NID:g2826265, PIDN:AAB98230.1, GB:dentetics
Genetics
A,Map position: REV232198-232130
C,Superfamily: rat ribosomal protein L41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-22 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribosomal protein L41, cytosolic [similarity] - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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R; Chan, Y.L.; Olvera, J.; Wool, I.G.
Biochem. Biophys. Res. Commun. 214, 810-818, 1995
A; Title: The primary structures of rat ribosomal proteins L4 and A; Reference number: JC4277; MUID: 96024571; PMID: 7575549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 38; DB 1; Length 25; 58.3%; Pred. No. 48; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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Pred. No. 75;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
41.1%; Score 39; DB
Best Local Similarity 56.2%; Pred. No. 31;
Matches 9; Conservative 1; Mismatches
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Best Local Similarity 42.1%;
Matches 8; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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A;Residues: 1-25 <CHA>
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Pypothetical protein - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Datesion: C72262

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A,Experimental source: strain MSB8
C,Genetics:
A,Gene: TM1386
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R; Benes, V.; Wurmbach, B.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5

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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: Z25014
A;Accession: T49214
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 < BENS
A;Cross-references: UNIPROT:P62120; EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.200
A;Experimental source: cultivar Columbia; BAC clone F27K19
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                                                                                                                                                                                          ribosomal protein GL41-like - Arabidopsis thaliana
NiAlternate names: protein F27K19.200
C:Species: Arabidopsis thaliana (mouse-ar cress)
C:Species: Q2-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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Pred. No. 18;
0; Mismatches 4; Indels
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Pred. No. 47;
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C,Superfamily: rat ribosomal protein L41
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ilarity 66.7%;
Conservative
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Best Local Similarity 40.vv
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-69 <ARN>
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||: | | ||| KWRKKRMRRLKR 15

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Tibosomal protein L41.e - human
NyAlternate names: HG12 protein; ribosomal protein YL41
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 17.Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JQ1617; JC5659; $31691
R;Klaudiny, J; von der Kammer, H; Scheit, K.H.
Biochem: Biophys. Res. Commun. 187; 901-906, 1992
A;Title: Characterization by CDNA cloning of the mRNA of a highly basic human protein hom A;Reference number: JQ1617; MUID:92412140; PMID:1326959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: JQ1617
A;Molecule type: mRNA
A;Residues: 1-25 <KLLA
A;Residues: 1-25 <KLLA
A;Cose-references: UNIPROT:P28751; EMBL:Z12962; NID:g36135; PIDN:CAA78306.1; PID:g36136
R;Lee, J.H.; Kim, J.M.; Kim, M.S.; Lee, Y.T.; Marshak, D.R.; Bae, Y.S.
Biochem: Biophys: Res. Commun. 238, 462-467, 1997
A;Title: The highly basic ribosomal protein Lul interacts with the beta subunit of protess
A;Reference number: JC5659; MUID:97446005; PMID:9299532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z12962; NID:g36135; PIDN:CAA78306.1; PID:g36136
C;Comment: This protein stimulates phosphorylation of the beta chain of DNA topoisomerase
C;Superfamily: rat ribosomal protein L41
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C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4685
R;Starkey, C.R.; Menon, R.P.; Prabhu, S.; Levy, L.S.
B;Scham: Biophys. Res. Commun. 220, 648-652, 1996
A;Title: Primary sequence and evolutionary conservation of ribosomal protein genes from the Reference number: JC4685; MuID:96183078; PMID:8607819
A;Accession: JC4685.
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48;
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Pred. No. 48;
1; Mismatches
   Pred. No. 48;
1; Mismatches
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Pred. No. 4
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A,Gene: rpL41
C,Superfamily: rat ribosomal protein L41
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Best Local Similarity 58.3%;
Matches 7; Conservative
58.3%;
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Best Local Similarity 58.3%;
Matches 7; Conservative
                                 7; Conservative
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                                                                                                                                                            4 KWRKKRTRRLKR 15
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Best Local Similarity
Matches 7; Conserv
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A; Molecule type: mRNA
A; Residues: 1-25 < LEE>
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A; Residues: 1-25 <STA>
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                                                                                                                                                                                   ribosomal protein L41.e, cytosolic - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D1290; protein YDL133c-a; protein YDL184c; ribosomal protein C;Species Saccharomyces cerevisiae
C;Species Saccharomyces cerevisiae
C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 09-Jul-2004
C;Accession: S22246; S22247; S11264; SS8733; S67739; S78073
Curr. Genet. 17, Hashimoto, T.; Otaka, E.
Curr. Genet. 17, 185-190, 1990
A;Title: Yeast ribosomal proteins: XI. Molecular analysis of two genes encoding YL41, an A;Reference number: S22246; MUID:90254826; PMID:2187623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: S11264
A,Molecule type: protein
A,Residues: 1-25 <OTA->
R;Verhasselt, P.; Voet, M.; Volckaert, G.
R;Verhasselt, P.; Voet, M.; Volckaert, G.
A;Title: New open reading frames, one of which is similar to the nifV gene of Azotobacte
A,Reference number: S58730; MUID:96021607; PMID:8533471
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S22246
A;Molecule type: DNA
A;Residues: 1-25 <SUZ>
A;Crose-references: UNIPROT:P05746; EMBL:X16066; GSPDB:GN00004; MIPS:YDL133c-a; NID:g481
A;Genetics: RPL47B
A;Accession: S22247
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Experimental source: strain S288C
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Mol. Gen. Genet. 195, 544-546, 1984
A;Title: Yeast ribosomal proteins. VIII. Isolation of two proteins and sequence characte
A;Reference number: S11249
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A;Residues: 1-25 <SUM>
A;Cross-references: EMBL:X16065; GSPDB:GN00004; MIPS:YDL184c; NID:g4817; PIDN:CAA34201.
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A;Genetics: RPL47A
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994
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F;1-25/Product: ribosomal protein L41.e #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: 558733
A;Status: nucleic acid sequence not shown; translation not shown
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R; Volckaert, G.; Verhasselt, P.; Voet, M. submitted to the Protein Sequence Database, July 1996 A; Reference number: S67735 A; Accession: S67739

Molecule type: DNA Residues: 1-25 <VOL>

A; Molecule type: DNA A; Residues: 1-25 <VER>

(Genetics: RPL47A !/Saluz, H.P.; Woelfl, S.; Hanemann, V. ubmitted to the Protein Sequence Database, July 1996 i/Reference number: S67677

;Genetics: RPL47B ;Genetics: <RPL47B> senetics: RRPL47B> ;Cross-references: MIPS:YDL133c-a ;Cross-references: MIPS:YDL133c-a; SGD:S0002293

A; Molecule type: DNA A; Residues: 1-25 <SAL> Accession: S78073

C;Genetics: <RPL47A> A;Gene: SGD:RPL47A; YL41A; MIPS:YDL184c A;Cross-references: MIPS:YDL184c; SGD:S0002343

A;Map position: 4L

Superfamily: rat ribosomal protein L41

A; Map position: 4L

DB 1; Length 25; 40.0%; Score 38; Query Match

RESULT 11

157554

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C; Species: Clostridium acetobutylicum
C; Species: Clostridium acetobutylicum
C; Dale: 14-Sep-2001 #text_change 09-Jul-2004
C; Accession: B97043
R; Nolling, J.; Bernett, G.N.; Koonin, B.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4023-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A; Accession: B97043
A; Stetus: preliminary
A; Molecule type: DNA
A; Residues: 1-61 < KUR>
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A,Experimental source: Clostridium acetobutylicum ATCC824
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A;Authors: Smith, H.O.; Venter, J.C.
A;Attle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
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A;Description: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.
A;Reference number: 225968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein BBH39 - Lyme disease spirochete plasmid H/1p28-3
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R2R3-MYB transcription factor [imported] - Arabidopsis thaliana (fragment) C;5pecies: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004 C;Accession: T52272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 2; I
Pred. No. 1.5e+02;
3; Mismatches 4;
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A;Molecule type: mENA
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Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-34 < KLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: CAC1164
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Matches
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-74 <RES>
A;Cross-references: UNIPROT:Q64130; GB:S78451; NID:g998544; PIDN:AAB34209.1; PID:g998545
C;Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
interleukin-3 receptor beta subunit - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 157554
R;Hannemann, J: Hara, T:; Kawai, M.; Miyajima, A.; Ostertag, W.; Stocking, C.
Mol. Cell. Biol. 15, 2402-2412, 1995
A;Title: Sequential mutations in the interleukin-3 (IL3)/granulocyte-macrophage colony-semediated by a truncated beta C subunit.
A;Reference number: 157554; MUID:95257920; PMID:7739524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z21797
A;Accession: T38731
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-25 <GEN>
A;Cross-references: EMBL: Z99167; PIDN:CAB40152.1; GSPDB:GN00066; SPDB:SPAC3G6.13c
A;Experimental source: strain 972h-; cosmid c3G6
R;Bothe, G.; Pohl, T.; McDougall, R.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: UNIPROT: Q9Y710, EMBL: Z69369; PIDN: CAB40187.1; GSPDB: GN00066 A, Experimentel source: etrain 972h-; cosmid G3F10 R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38719; T38731; T39176
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Reference number: Z21807
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T38719.
ribosomal protein L41 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%; Score 38; DB 2; Length 74; 50.0%; Pred. No. 1.3e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SPAC31F10.18c; SPAC3G6.13c; SPAC3F10.18c; SPAC8F11.01c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T38719
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-25 < MUR>
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58.3%; Pred. No. 66;
iive 1; Mismatches
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A;Introns: 24/2
C;Superfamily: rat ribosomal protein L41
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
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RTYRKWKEKI 74
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Matches
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A;Cross-references: UNIPROT:Q97X77; GB:AE006641; NID:g13815131; PIDN:AAK42065.1; GSPDB:G:
C;Genetics:
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: 664522.
G;Accession: 664522.
G;Accession: 664522.
G;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A.
A;Reference number: A64520; WulD:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conserved hypothetical protein BBI13 - Lyme disease spirochete plasmid I/lp28-4
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 113-Reb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: D70241
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Spon, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; WillD:98065943; PMID:9403685
A;Accession: D70241
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36.3%; Score 34.5; DB 2; Length 39;
Best Local Similarity 40.9%; Pred. No. 2.3e+02;
Matches 9; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 2; I
Pred. No. 3.4e+02;
6; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.8%;
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Matches 5, Conservative
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A; Residues: 1-70 < KUR>
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Cispecies: chloroplast Chlorella vulgaris
Cipate: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
CiAccession: T07304
RiWaksaugi, T.: Nagai, T.: Kapoor, M.: Sugita, M.; Ito, M.; Ito, S.: Tsudzuki, J.: Nakas Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlc A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession. C81442
A;Reference unaber: A81250; MUD:20150912; PMID:10688204
A;Reference number: A81250; MUD:20150912; PMID:10688204
A;Meeidues: 1-63 *ABA
A;Meeidues: 1-63 *ABA
A;Meeidues: 1-63 *ABA
A;Residues: 1-63 *ABA
A;Cossereference: UNIPROT:09PIQ1; GB:AL119074; GB:AL11168; NID:g6967505; PIDN:CAB7271
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C81442
508 ribosomal protein L35 Cj0244 [imported] - Campylobacter jejuni (strain NCTC 11168)
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C; Genetics:
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               A;Cross-references: UNIPROT:Q9SAL6; EMBL:Z97049; PIDN:CAB09729.1 & Experimental source: ecotype Landsberg erecta; whole plants C;Genetics: A;Genetics: A;Gene: MYB15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 2; Length 49;
Pred. No. 2.4e+02;
1; Mismatches 5; Indels
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                                                                                                                                            Score 35; DB 2; Length 45;
Pred. No. 2.2e+02;
                                                                                                                                                                                          4; Indels
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A;Gene: rpm1; C;0244
C;Superfamily: Bscherichia coli ribosomal protein L35
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57.1%;
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50.0%;
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                                                                                                                                                                 Best Local Similarity 50.0
Matches 6; Conservative
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RWMNYLKPDIKR 13
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KRFKVGKNKIKR 23
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nes 7; Conserva
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C; Keywords: chloroplast
A;Residues: 1-45 <ROM>
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R;Dunn, J.J.; Studier, F.W.
J. Mol. Biol. 148, 303-330, 1981
A;Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the beg
A;Reference number: A92866; MUID:82078034; PMID:7310871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribunn, J.J.; Studier, F.W.
J. Mol. Blol. 166, 477-735, 1983
A.fitle: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 gerl
A.Reference number: S42283; MUID:83241725; PMID:6864790
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submitted to the EMBL Data Library, July 1999
A;Reference number: A75001
A;Reference number: A75001
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A,Experimental source: strain Orsay
C;Species: phage T7
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C;Accession: B43003; B43005; $42297; A04419
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C,Species: Drosophila melanogaster
C,Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Pyrococcus abyssi
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Accession: H75130
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                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-48 <DU2>
A;Cross-references: GB:V01127; NID:g15498; PIDN:CAA24341.1; PID:g15513
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                                                                                 R; Dunn,\ J.J.; Thompson, K. submitted to the Nucleic Acid Sequence Database, September 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lypothetical protein PAB7213 - Pyrococcus abyssi (strain Orsay)
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Pred. No. 3.3e+02;
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Pred. No. 4e+02;
5; Mismatches
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C,Superfamily: phage T7 gene 1.8 protein
                                                                                                                                                                     A;Accession: B43003
A;Molecule type: DNA
A;Residues: 1-48 <DUN>
A;Cross-references: UNIPROT:P03794
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Best Local Similarity 37.5%;
Matches 6; Conservative
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ilarity 55.6%;
Conservative
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41 YGEYRRLKRELLGIG
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                                                                                                                                           A; Reference number: A94615
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-60 <KAW>
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A; Residues: 1-48 < DUW>
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                    A;Cross-references: UNIPROT:050867; GB:AE000789; NID:92690079; PIDN:AAC66183.1; PID:9269
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid
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A.Molecule type: mRNA
A.Residues: 1-45 < ROM>
A.Croest-references: UNIPROT:Q9LY95; UNIPROT:O65720; EMBL:295764; PIDN:CAB09196.1
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein MYB40 [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52123
R;Romero, I.; Fuertes, A.; Benito, M.J.; Malpica, J.; Leyva, A.; Paz-Ares, J.
A;Description: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.
A;Reference number: Z25968
A;Accession: T52123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R2R3-WYB transcription factor [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52282
R;Romero, I.; Fuertes, A.; Benito, M.J.; Malpica, J.; Leyva, A.; Paz-Ares, J.
B;Bomero, I.; Fuertes, Data Library, May 1997
A;Description: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.
A;Reference number: Z25968
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A;Experimental source: ecotype Landsberg erecta; whole plants
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Pred. No. 3.1e+02;
2; Mismatches 4; Indel8
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Pred. No. 3.1e+02;
2; Mismatches 5; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-45 <ROM>
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50.0%;
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50.0%;
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RWINYLRPDLKRGG 15
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Matches 7; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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RWTNYLRPDLKR 13
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C;Genetics:

RESULT 23 Q1BP87

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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Kochingstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Ee, K., Levine, A.; Liu, H.; Masuda, S.; Maucel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaio, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekfguchi, J.; Sekowaka, A.; Seror, T.; Winters: Schleich, S.; Schroeter, R.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters: P.; Winters, P.; Winters, Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Accession: E69926
A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Listeria monocytogenes
Cispecies: Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cispecies: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Date: Da
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ATP synthase epsilon chain, mitochondrial - fission yeast (Schizosaccharomyces E
C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:299114; GB:AL009126; NID:g2634230; PIDN:CAB13901.1; PID:e1185481; A;Experimental source: strain 168 C;Genetics: A;Gene: yosK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein lmo2567 [imported] - Listeria monocytogenes (strain EGD-e)
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40.0%; Pred. No. 4.4e+02;
tive 3; Mismatches 6;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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N.Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl,
submitted to the EMBL Data Library, August 1997
A; Reference number: Z21913
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KDWDEWKRRYSRKLK 54
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nes 6; Conservative
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A; Residues: 1-66 < KUN>
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A; Residues: 1-66 <GLA>
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Best Local S:
Matches 6
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A;Crose: references: UNIPROT:Q8CZ83; GB:AE007317; PIDN:AAK99029.1; PID:g15457771; GSPDB:G
C;Genetics:
A;Gene: spr0225
                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P14956; EMBL:X16972; NID:g7712; PIDN:CAA34845.1; PID:g134545
C;Genetics:
                                                                                                                               A,Title: The cecropin locus in Drosophila, a compact gene cluster involved in the respon
A,Reference number: S07664, MUID:90107946, PMID:2104802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agronomy Streptococcus pneumoniae (strain R6)
hypothetical protein spr0225 [imported] - Streptococcus pneumoniae (strain R6)
c;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-OCt-2001 #sequenc_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: A97900
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E. R; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; P.; Sun, P.M.; Winkler, M.E.
J; Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Status preliminary
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Pred. No. 4.3e+02;
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                                                     R;Kylsten, P.; Samakovlis, C.; Hultmark,
EMBO J. 9, 217-224, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: FlyBase:FBgn0000278
A;Introns: 33/3
C;Superfamily: cecropin
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38.5%;
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Best Local Similarity 38.9
Matches 7; Conservative
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nes 5; Conservative
                                                                                                                                                                                                             A;Accession: S07666
A;Molecule type: DNA
A;Residues: 1-63 <KYL>
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                    Accession: S07666
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H--exporting ATPase (EC 3.6.3.6) chain PMP1 - yeast (Saccharomyces cerevisiae)
NyAlternate names: plasma membrane proteolipid PMP1; protein YCR024c-a
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S31269; S22591
R;Navarre, C.; Ghislain, M.; Leterme, S.; Ferroud, C.; Dufour, J.P.; Goffeau, A.
J. Biol. Chem. 267, 6425-6428, 1992
A;Tille: Purification and complete sequence of a small proteolipid associated with the p.
A;Reference number: S31269; MUID:92210627; PMID:1532582
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J. Biol. Chem. 269, 21262-21268, 1994
A;Title: Two distinct genes encode small isoproteolipids affecting plasma membrane H(+)-1
A;Reference number: A53927; MUID:94342298; PMID:8063750
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submitted to the EMBL Data Library, December 1994
A;Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 and ]
A;Reference number: S50428
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A;Residues: 1-43 <DIE>
A;Cross-references: EMBL:U18530; NID:g602367; PIDN:AAB64509.1; PID:g1906389; MIPS:YEL0170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Cross-references: UNIPROT: P32903; EMBL: M77845; NID: 9172196; PIDN: AAA34883.1; PID: 91721
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F;3-40/Product: H+-transporting ATPase chain PMP1 #status experimental <MAT>
F;7-23/Domain: transmembrane #status predicted <TWM>
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                                                                                         Length 69;
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C;Superfamily: rice chloroplast ribosomal protein L32 C;Keywords: chloroplast
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Pred. No. 3.2e+02;
6; Mismatches 2;
                                                                                      Score 34; DB 2;
Pred. No. 4.6e+02;
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A,Cross-references: SGD:S0000619; MIPS:YCR024c-a
A,Map position: 3R
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nilarity 54.5%;
Conservative 1
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ilarity 40.0%;
Conservative
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les 6; Conserv
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A; Residues: 1-43 <NAV>
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A; Residues: 1-40 <NAV>
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Matches 6
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Matches
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A;Molecule type: DNA
A;Residues: 1-67 <MOO>
A;Residues: 1-67 <MOO>
A;Cross-references: UNIPROT:P87316; EMBL:Z97204; PIDN:CAB10091.1; GSPDB:GN00067; SPDB:SF
A;Expensional source: strain 972h-; cosmid c31F10
C;Genetics:
A;Gene: SPDB:SPBC31F10.15c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riglamer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, S.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Dr.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A; Congarative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q927S6; GB:ALS92022; PIDN:CAC97938.1; PID:g16415248; GSPDB:C
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2712
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Kolbyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi
Nature 322, 572-574, 1986
A;Title: Chloroplast gene organization deduced from complete sequence of liverwort March
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C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: S01514; A05061
R;Kohchi, T.; Shirai, H.; Fukuzawa, H.; Sano, T.; Komano, T.; Umesono, K.; Inokuchi, J. Mol. Biol. 203, 353-372, 1988
A;Title: Structure and organization of Marchantia polymorpha chloroplast genome. IV. A;Reference number: S01512; MUID:89068688; PMID:3199437
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 4.5e+02;
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                                                                                                                                                                                                                                                                                                                                 Score 34; DB 2; I
Pred. No. 4.5e+02;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                            A,Map position: 2
A,Genome: nuclear
A,Introns: 10/2
C,Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 LYTRWKN 49
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LYKKWKN 8
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A;Molecule type: DNA
A;Residues: 1-69 <KOH>
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-67 <GLA>
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A,Genome: chloroplast
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us-09-648-816b-10.rpr

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34.7%;
ilarity 60.0%;
Conservative 1
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nes 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-40 <REA>
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Matches
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A;Reference number: A00150
A;Reference number: A00150
A;Accession: A05058
A;Accession: A05058
A;Molecule type: DNA
A;Residues: 1.27 AC0NY
A;Cross references: UNIPROT:Q32620; EMBL:X04465; NID:g11640; PID:g11702
B;Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi Nature 325, 572-574, 1986
A;Cross reference number: A38014
A;Contents annotation; gene organization, sites, features
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: chloroplast
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A;Map position: 5L
C;Keywords: hydrolase; transmembrane protein
F;6-43/Product: H+-transporting ATPase chain PMP2 #status experimental <MAT>
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hypothetical protein 27 - liverwort (Marchantia polymorpha) chloroplast
C;Species: chloroplast Marchantia polymorpha
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05058
                                                                                                                                                                                                                                                                                                                              plantaricin A - Lactobacillus plantarum
C;Species: Lactobacillus plantarum
C;Species: Lactobacillus plantarum
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: A45913
R;Nissen-Meyer, J:; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F.
submitted to the Protein Sequence Database, April 1993
A;Reference number: A45913
A;Accession: A45913
A;Status: preliminary
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                                                                                     Score 33.5; DB 2; Length 43;
Pred. No. 3.5e+02;
6; Mismatches 2; Indels
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C26871
hypothetical chl protein - Escherichia coli (fragment)
C;Species: Escherichia coli
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Pred. No. 2.2e+02;
1; Mismatches 0;
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A; Residues: 1.22 «NIS»
A; Crosa-references: UNIPROT: P80214
C; Keywords: antibiotic; bacteriocin
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83.3%;
                                                                                       Query Match
Best Local Similarity 40.0%;
Matches 6; Conservative
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29 IYRKWQAR-QRGLQR 42
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Best Local Similarity 83.3
Matches 5; Conservative
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: C26871
R;Johann, S; Hinton, S.M.
B;Johann, S; Hinton, S.M.
J; Bacteriol 169, 1911-1916, 1987
A;Fitle: Cloning and nucleotide sequence of the chlD locus.
A;Reference number: A26871; MUID:87194564; PMID:3553151
A;Accession: C26877
A;Residues: 1.32 cJOH>
A;Residues: 1.32 cJOH>
A;Cross-references: GB:MIG182; NID:g145541; PIDN:AAA83841.1; PID:g1128946; GB:L34009; NI
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A;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain K12
C; Comment: This is the hypothetical translation of a sequence that was not reported as a
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A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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A;Molecule type: mRNA
A;Residues: 1-45 - ROM>
A;Residues: 1-45 - ROM>
A;Cross-references: UNIPROT:065898; UNIPROT:Q9FR97; EMBL:295778; PIDN:CAB09210.1
A;Accession: T52126
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Date: 21-2125; T52126
R;Romero, I:; Fuertes, A:; Benito, M.J.; Malpica, J.; Leyva, A.; Paz-Ares, J.
submitted to the EMBL Data Library, May 1997
A;Description: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81591
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Pred. No. 3.8e+02;
1; Mismatches 3;
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A;Molecule type: mRNA
A;Residues: 1-45 <RO2>
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22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                        34.7%;
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28 KNWRNSTKKLEKNEG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.0
Matches 6; Conservative
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YPKWKSRKK 22
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A; Molecule type: DNA
A; Residues: 1-63 <TRY>
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A;Gene: spr1883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CiSpecies: Streptococcus pneumoniae
CiSpecies: Streptococcus pneumoniae
CiDate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
CiAccession: E95242
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
Ci, J.D.; Jomayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt. I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                           RZR3-MYB transcription factor [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52276
R;Romero, I.; Fuertes, A.; Benito, M.J.; Malpica, J.; Leyva, A.; Paz-Ares, J.
Bibmitted to the BMBL Data Library, May 1997
A;Bescription: One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
E95242
hypothetical protein SP2071 [imported] - Streptococcus pneumoniae (strain TIGR4)
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C;Species: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                            Gaps
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-45 < RCMA
A;Cross-references: UNIPROT:Q9SAM7; EMBL:Z95740; PIDN:CAB09172.1
C;Genetics: ecotype Landsberg erecta; whole plants
A;Note: AtMYB12
                            Length 45;
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Pred. No. 4.3e+02;
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Pred. No. 5.5e+02;
2; Mismatches 7; Indels
                         Score 33; DB 2; I
Pred. No. 4.3e+02;
4; Mismatches 3;
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50.0%;
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40.0%;
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KNWRNSTKKLEKNEG
                         Query Match
Best Local Similarity 41.7
Matches 5; Conservative
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Matches 6; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-59 < KUR>
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C. Accession: H98106
R. Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es, R. Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es, R.; LeBlanc, D.J.; Lee, L.N.; Lee, L.N.; Minkler, R.S.; Mc.
J. Bacteriol. 183, 5709-5717, 2001
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Residues: Dreliminary
A;Residues: 1-59 «KUR»
A;Residues: 1-59 «KUR»
A;Residues: 1-59 «KUR»
A;Cross-references: UNIPROT:097NF9; UNIPROT:08CY79; GB:AE007317; PIDN:AAL00685.1; PID:915
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A;Experimental source: strain VF5
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
A;Reference number: A70300; MUID:98196666; PMID:9537320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70442
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C;Species: Drosophila melanogaster
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
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34.7%; Score 33; DB 2; Length 62;
Best Local Similarity 55.6%; Pred. No. 5.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels
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Pred. No. 5.5e+02;
2; Mismatches 7; Indels
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hypothetical protein BH4052 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D84156
R;Takani, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Reference number: A83650; MuID:20512582; PMID:11058132
A;Accession: D84156
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S32026
R;Galli, J.; Wieslander, L.
Bubmitted to the EWBL Data Library, January 1993
A;Description: Structure of the smallest salivary gland secretory protein gene in chiron A;Reference number: S32027
A;Accession: S32026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <STO>
A;Cross-references: UNIPROT: O9KSN6; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB077
A;Experimental source: strain C-125
C;Genetics:
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C;Species: Chironomus halophilus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                   Gaps
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A;Moleoule type: DNA
A;Residues: 1-64 «GAL»
A;Cross-references: UNIPROT:QO8763; EMBL:X70776; NID:g11123; PID:g11124
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Pred. No. 5.9e+02;
2; Mismatches 3; Indels
                                                                                                                  34.7%; Score 33; DB 2; Length 63; 38.5%; Pred. No. 5.8e+02; Live 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.7%; Score 33; DB 2; Length 65; 53.8%; Pred. No. 6e+02; tive 3; Mismatches 3; Indels
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Job time : 16.5172 secs
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Best Local Similarity 58.3%;
Matches 7; Conservative ;
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25 WLKKLGKRIERIG 37
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49 KEFTKKLKRVLER 61
                                                                                                                  Query Match
Best Local Similarity 38.5
Matches 5; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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A,Map position: 3
A,Introns: 33/3
C,Superfamily: cecropin
C,Keywords: hemolymph
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A;Gene: BH4052
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D84156
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"Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).
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MEDLINE=20023866; PubMed=10759889;
Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
Hiraoka Y.;
                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical Try-Asp repeats containing protein (Fragment).
Name=SPACI8B11.10;
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STRAIN=968 h90;
Ding D., Tomita Y., Hiraoka Y.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB027768; BAA87072.1; --
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31 AA; 3669 MW; 1523469FBAE7B3B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaces;
Schizosaccharomyces.
NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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Pred. No. 18;
2; Mismatches
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092999
RL41 AGABI
QBDTR7
                                                                                                                                                                                RL41 METJA
RL41 ICTPU
PCG3 PACGO
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091IU7
091IU8
091IU9
091IV0
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1 YEKDINKLKRELEELG 16
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Local Similarity 62.5%;
hes 10; Conservative
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     SEQUENCE FROM N.A.
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SEQUENCE
     Name=env;
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Matches
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Q9USG3
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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06V606
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RL41_HORVU
RL41_ORYSA
RL41_PEA
RL41_TOBAC
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Maximum Match 100%
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1: uniprot_sprot:*
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95
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Match Length DB
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Maximum DB seq length: 74
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STRAIN=13;
MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                 STRAIN=13 / Type A;
MEDLINE-21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Oqasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 77;
7; Mismatches 3; Indels
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Pred. No. 76;
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EMBL; AP003188; BAB80479.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE SO AA. 5894 MW; EA6C276FBCS9D2F5 CRC64;
                                                                                                                                                                                                                                                                                                    71 AA; 8643 MW; 3B61EB6CAD1CA3F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein CPE0773.
OrderedLocusNames=CPE0773;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL, AP003187; BAB80251.1; -.
Complete proteome.
SEQUENCE 71 AA; 8643 MW; 3B61EB6CAD1CA3F9 CF
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Similarity 56.2%;
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Best Local Similarity 41.2.
Local Similarity 41.2.
Conservative
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A.
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     NCBI_TaxID=1502;
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Buonaguro L., Tagliamonte M., Tornesello M., Pilotti E., Casoli C.,
Lazzarin A., Tambusai G., Ciccozzi M., Rezza G., Buonaguro F.M.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY350353; AAR12497.1; -...
                                                                     Buonagaro L., Tagliamonte M., Tornesello M., Pilotti E., Casoli C. Lazazin A., Tambussi G., Ciccozzi M., Rezza G., Buonaguro F.M.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY350369; AAR1213.1; -.

GO, GO:0019031; C:viral envelope; IEA.

InterPro; IPR00710; GP120.

InterPro; IPR007110; Ig-like.

Pfam; PF00516; GP120; Ig-like.
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OrderedLocusNames=CPR0545.
OrderedLocusNames=CPR0545;
Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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Pred. No. 50;
2; Mismatches 4; Indels
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
VCBI_TaxID=11676;
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Pred. No.
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InterPro; IPR007110; Ig-like.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                       47.4%;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KWKNKLKRSLKRLG 18
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KWNNTLQRIAKKLG 62
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les 8; Conserv
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                                                      SEQUENCE FROM N.A.
NCBI_TaxID=11676;
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SEQUENCE
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SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verdonck F.;

"Antibacterial and antifungal properties of alpha-helical, cationic peptides in the venom of scorpions from southern Africa.";

Bur. J. Blochem. 269:4799-4810(2002).

--- FUNCTION: Induces a leak current in voltage-clamped dorsal root ganglion cells of rate by forming pores. Degranulates human granulocytes and has a weak hemolytic activity against human red blood cells. Has antibacterial activity against human red bacteria but is less active against Gram-negative bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=95264411; PubMed=7745725;
Briant L., Wade C.M., Puel J., Brown A.J., Guyader M.;
Hanalysis of envelope sequence variants suggests multiple mechanisms of mother-to-child transmission of human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                          Moerman L.F.A., Bosteels S., Noppe W., Willems J., Clynen E.,
Schoofs L., Thevissen K., Tytgat J., Van Eldere J., van der Walt J.,
                                                                             Parabuthus schlechteri (Scorpion)
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthida, Buthoidea, Buthidae, Parabuthus.
NCBI_TaxID=190110;
                                                                                                                                                                                                                             TISSUB=Venom; verdons; P., Bosteels S., Desmet J., Moerman L.F.A., Noppe W., Willems J., Tytogat J., van der Walt J.; Willems J., Tytogat J., van der Walt J.; Wallems J., Tytogat J., van der Walt J.; Morel class of pore-forming peptides in the venom of Parabuthus schlechteri Purcell (Scorions: Buthidae).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibiotic; Direct protein sequencing; Fungicide; Hemolysis;
Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antifungal activity.
--- SUBUNT: Monomer and homodimer.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUB SPECIFICITY: Expressed by the venom gland.
--- MASS SPECTROMETRY: MW=5030.3; METHOD=MALDI; RANGE=1-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1; Length 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 AA; 4995 MW; 3EEFF71425FA14FA CRC64;
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annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                            28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Envelope glycoprotein, V3 region (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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MEDLINE=22241537; PubMed=12354111;
        (Rel. 41, Created)
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7 LKKAWKSKLAKKLRAKG 23
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                                                                                                                                                                                                              AND MASS SPECTROMETRY.
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Matches
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MEDLINE-98334296; PubMed-9671221;

MEDLINE-98334296; PubMed-9671221;

MESTALD MC. Merzouki A., Arella M., Sadowski I.J.;

The strance moninjection drug users in Vancouver, Canada.";

LAIDS Res. Hum. Retroviruses 14:917-919(1998).

REBL; AFOS8149; AAC15162.1;

RESP; P20871; 1CE4.

RGG; GO:0016021; C:integral to membrane; IEA.

RGG; GO:0019028; C:viral capsald; IEA.

RGG; GO:0019028; C:viral envelope; IEA.

RGG; GO:0019028; C:viral envelope; IEA.

RGG; GO:0019011; C:viral envelope; IEA.

RGG; GO:0019011; C:viral envelope; IEA.

RGG; GO:0019011; C:viral envelope; IEA.

RGG; GO:0019011; C:viral envelope; IEA.

RGG; GO:00110011; C:viral envelope; IEA.
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Briant L., Wade C.M., Puel J., Brown A.J., Guyader M.; "Analysis of envelope sequence variants suggests multiple mechanisms of mother-to-child transmission of human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00516; GP120; 1.
Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                   Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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Pred. No. 1e+02;
4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                     4276762C52C006B5 CRC64;
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                                                              1.";
EMBL; U24718; AAB07144.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Envelope glycoprotein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
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InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                       7814 MW;
                                                                                                                                                                                                                                                                                                                                                                              45.3%;
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tes 7; Conservative
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Matches 7; Conservative
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SEQUENCE
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MEDLINE=214(28) HubMed=12573587; DOI=10.1006/viro.2002.1759; Imlach S., Leen C., Bell J.E., Simmonds P.; Imlach S., Leen C., Bell J.E., Simmonds P.; Impenotypic analysis of peripheral blood gammadelta T lymphocytes and "phenotypic analysis of peripheral blood gammadelta T lymphocytes and virology 305:415-427(2003) virology 305:415-427(2003) virology 305:415-427(2003) EMBL; AY171520; AAN72374.1; -. EMBL; AX171520; AAN72374.1; -. GO, GO:0016021; C:integral to membrane; IEA. GO, GO:0019028; C:viral envelope; IEA. GO, GO:0019031; C:viral envelope; IEA. GO, GO:0005198; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145; Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F., Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C., Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                       AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
Mucleic Acida Res. 29:2145-2153(2001).
EMBL; Al445563; CAC13245.1; --
PIR; H90520; H90520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0T-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein MYPU 0720.
OrderedLocusNames=MYPU 0720;
Mycoplasma pulmonis.
Bacteria, Firmicutes; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.7%; Score 41.5; DB 2; Length 55; 55.6%; Pred. No. 1.4e+02; Live 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 2; Length 74;
Pred. No. 1.6e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mypulist; MYPU 0720; -
Complete proteome; Hypothetical protein.
SEQUENCE 55 AA; 7069 MW; FE0197BADCF9E677 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AA; 8489 MW; 6C73A2E2E6FB0942 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Envelope glycoprotein (Fragment).
                                                                          Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000777; GP120.
InterPro; IPR007110; Ig-like.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.2%;
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les 10; Conservative
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Best Local Similarity 50.00,
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56 EKWNNTLKQIVKKL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KKWKNKLKRSLKRL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=95127302; PubMed=7826703;
PLUTUA Y., Bergetrom T., Norkrans G., Horal P.;
"HIV type I V3 sequence diversity in contact-traced Swedish couples at the time of sexual transmission.";
AIDS Res. Hum. Retroviruses 10:1187-1189 (1994).
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
               EMBL, U24765; AAB07191.1; -...
EMBL, U24765; AAB07191.1; -...
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:005198; F:structural molecule activity; IEA.
InterPro; IPR00077; GP120.
Pfam; PF00516; GP120; I.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane
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                                                                                                                                                                                                                                             Score 42, DB 2; Length 69;
Pred. No. 1.5e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mulder K.E.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; 110934, AAA66504.1; -
HSSP; P20871; 1CE4
                                                                                                                                                                                                            69 AA; 7627 MW; 1ACE2D1B84F2173A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019198; F:structural molecule activity; IEA.
InterPro; IPR000777; GP120.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 AA; 8085 MW; A3878D440AC527A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein, v3 region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Pred. No. 1.5e+02;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 AA.
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01-MAR-2003 (TrEMBLrel. 23, Created)
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 Virol. 69:3778-3788(1995).
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53.8%;
                                                                                                                                                                                                                                                 44.2%;
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Best Local Similarity Succession 7; Conservative
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Best Local Similarity 53.0
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KWENTLKQIVKKL 58
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RN [2]

RN EDGUENCE FROM N.A. (AT3G08520; AT3G11120 AND AT3G56020).

RC STRAIN=CV. Columbia;

RD STGUENCE COlumbia;

RA MEDIINE=21016720; PubMed=11130713; DOI=10.1038/35048706;

RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

RA Balanoubat M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

RA Beimone V., Choisne N., Artiguenave F., Robert C., Brottier P.,

RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,

RA Wincker E., Drzonek H., Weissenbach J., Saurin W., Quetier F.,

RA Wincker E., Drzonek H., Wolland R., Brandt P., Nyakaura G.,

RA Winchelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakaura G.,

RA Wiedelmann R., Rauser G., Loehnert T.-H., Nordank B.,

ROTZI A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Bargues M., Viale D.,

RA Ge Haan M., Marse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,

Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,

RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jonkins J.,

RA Rooney T., Rizzo M., Walte A., Utterback T., Puili C.Y., Shea T.P.,

RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Wanter J.C.,

RA Sasmoto S., Kimura T., Ideaswa K., Kawashima K., Kabamizu R.,

RA Riyokawa C., Kohara M., Matsumoto M., Walter J.,

RA Ratanabe A., Yamada M., Yasuda M., Tabata S.;

RA Hatanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ATIG56045).

SEQUENCE FROM N.A. (ATIG56045).

STRAIN=cv. Columbia;

MEDLINE=21046719; PubMed=11130712; DOI=10.1038/35048500;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

A white O., Alonso J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A ill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Inn X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Ngoney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C. M., Veyberg M., Wysotskaia V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name-RPL41D; OrderedLocusNames=At3g56020; ORFNames=F27K19_200;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=RPL41B; OrderedLocusNames=At3g08520; ORFNames=T8G24.5, T8G24_5;
                                                                                                                                                                                                                                                                                                                                                                                             Name=RPL41A; OrderedLocusNames=At1g56045; ORFNames=T6H22.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=RPL41C; OrderedLocusNames=At3g11120; ORFNames=F9F8.7;
                                                                                                                                          P621<u>7</u>0; P35015;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
605 ribosomal protein L41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000).
                                                                                                        STANDARD;
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RESULT 13

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REA1 ARATH

ID PRIA12D

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                         SEQUENCE FROM N.A. (AT3G08520).

STRAIN=CV. Columbia;

MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;

X waada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Yamada K., Lim W. H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Hayashizaki Y., Johnson-Hopson C., Hsuan V W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tange R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Deltapine 62;
MEDLINE=55062728; PubMed=7972506; DOI=10.1104/pp.105.4.1449;
Turley R.B., Ferguson D.L., Meredith W.R.;
"Isolation and characterization of a cDNA encoding ribosomal protein L41 from cotton (Gossypium hirsutum L.).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Malvales, Malvaceae, Malvoideae, Gossypium.
"Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 302:842-846(2003).
-1- SIMILARITY: Belongs to the ribosomal protein L41e family.
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ID RL41 GOSHI STANDARD; PRT; 25 AA.
AC PG2122; P35015;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DF 60S ribosomal protein L41.
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Pred. No. 76;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007836; Ribosomal L41.
Pfam; PF05162; Ribosomal L41; T.
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                                                                Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; T49214; T49214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY058053;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no usy modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pisum sativum (Garden pea).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
NCBI_TaxID=3888;
                                                                                                                                                                                                                                                                                                                             STRAIN=CV. Japonica / Nipponbare;
STRAIN=CV. Japonica / Nipponbare;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
Zismann V., Pai G., Bowman C.L., Pujii C.Y., VanAken S.E.,
Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Coyza sativa chromosome 3 BAC OSJUBB0091J19 genomic sequence.";
Submitted (FEB-2001) to the FWBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the ribosomal protein L41e family.
                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 25; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 AA; 3428 MW; 9AD629D4293C039E CRC64;
                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P62123; P35015;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
605 ribosomal protein L41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long a modified and this statement is not removed.
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                       25 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC084320; AAK09215.1; -.
InterPro; IPR007836; Ribosomal L41.
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF05162; Ribosomal_L41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 43.2%;
Similarity 66.7%;
8; Conservative
                                                                                                                             60S ribosomal protein L41.
                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KWKNKLKRSLKR 16
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                EL41 ORYSA STANDARD, P61125; P35015; O1-FEB-1994 (Rel. 28, C. 01-FEB-1994 (Rel. 28, L. 25-OCT-2004 (Rel. 45, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                             Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
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ID RL41 PEA
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                       셤
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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibsib.ch).
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Barley L41 ribosomal protein from immature endosperm.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ribosomal protein L41e family.
                    -!- SIMILARITY: Belongs to the ribosomal protein 141e family.
                                                                                                                                                                                                                                                                                                                                                                                                Score 41, DB 1; Length 25, Pred. No. 76; 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1; Length 25;
Pred. No. 76;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                           25 AA; 3428 MW; 9AD629D4293C039E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 AA; 3428 MW; 9AD629D4293C039E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EL41_HORVU STANDARD; PRT; 25 AA. P62124; P35015; 01-FEB-1994 (Rel. 28, Created) 25-FEB-1994 (Rel. 28, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) 60S ribosomal protein L41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        InterPro; IPR007836; Ribosomal L41.
Pfam; PF05162; Ribosomal L41; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007836; Ribosomal L41.
Pfam; PF05162; Ribosomal L41; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=cv. Bomi; TISSUE=Endosperm;
Rasmussen S.K.;
Physiol. 105:1449-1450(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ001160; CAA04564.1; -.
                                                                                                                                                                                                                                            EMBL; X75423; CAA53175.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       43.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare (Barley).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 66...
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KWKKKRMRRLKR 15
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Best Local Similarity
Local 8; Conserve
                                                                                                                                                                                                                                                                   PIR; S38425; S38425.
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                                                                                                                                                                                                                                                                                                                                    Ribosomal protein.
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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RESULT 15
TO 19 HORVU
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 NCBI_TaxID=11676;
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Solanaceae, Nicotiana.
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Zhou X.-R.; Subaitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
subaitted (APR-1995) to the ribosomal protein L41e family.
                                                                                                        Score 41; DB 1; Length 25;
Pred. No. 76;
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Pred. No. 76;
0; Mismatches 4; Indels
                                                                                                                                   4; Indels
                                                                                 25 AA; 3428 MW; 9AD629D4293C039E CRC64;
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entities requires a license agreement (or send an email to license@isb-sib.ch)
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                                 EMBL; L47967; AAA79268.1; -.
InterPro; IPR007836; Ribosomal L41.
Pfam; PP05162; Ribosomal L41; I.
Ribosomal protein.
SEQUENCE 25 AA; 3428 MW; 9AD6291
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InterPro, IPR007836; Ribosomal_L41.
Pfam; PF05162; Ribosomal_L41; I.
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Matches 8; Conservative
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Matches 8; Conservative
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
                                                                                                                                                                                                                                Chang K.S.S., Lin C.I., Chen J.H., Shih C.H., Lin H.C., Lin R.Y.,
Twu S.C., Salminen M.O.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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EMBL; AR7550284, AR757088.1; 09621RA92644C023 CRC64;
MEDLINE=97159690; PubMed=9007206;
Chang K.S., Lin C.I., Chen J.H., Shih C.H., Lin H.C., Lin R.Y.,
Twu S.C., Salminen M.O.;
"HIV type 1 env gene diversity detected in Taiwan.";
AIDS Res. Hum. Retroviruses 13:201-204(1997).
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Pred. No. 1.8e+02;
3; Mismatches 5; Indels
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Pred. No. 1.3e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 AA; 4941 MW; 4A04BFE5B1F68AE4 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Matches 7; Conservative
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MEDILINE=20170331; PubMed=10708058;
Casado C., Urtasun I., Martin-Walther M.V., Garcia S., Rodriguez C., Casado C., Urtasun I., Martin-Walther M.V., Garcia S., Rodriguez C., Gasado C., Urtasun I., Martinez C.;
"Gal Romero J., Lopez-Galindez C.;
"Genetic analysis of HIV-1 samples from Spain.";
J. Acquir. Immune Defic. Syndr. 23:68-74 (2000).
Genetic analysis of HIV-1 samples from Spain.";
GO; GO:0015021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEB.
GO; GO:0005198; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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InterPro; IPR007110; Ig-like.
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Matches 7; Conservative
: | | | | : : | | | | 54 RWNNTLKQIVKRL 66
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MEDLINE=20170331; PubMed=10708058;
MEDLINE=20170331; PubMed=10708058;
MEDLINE=20170331; PubMed=10708058;
Med Romero J., Lopez-Calindez C.;
T. denetic analysis of HIV-1 samples from Spain.";
T. Acquir. Immune Defic. Syndr. 23:68-74 (2000).
MEMBL; AF152023; AF806461.1; -
MEMBL; AF152023; AF806461.1; -
MEMBL; AF152033; AF806461.1; -
MEMBL; AF15203; AF806461.1; -
MEMBL; AF15203; AF106461.1; AF10651.1;                                                                                                                                                                                                                                                                                                                                                      Schuitemaker H.;
"Analysis of the temporal relationship between human immunodeficiency
"Analysis of the temporal relationship between human immunodeficiency
virus type 1 quasispecies in sequential blood samples and various
organs obtained at autopsy.";
J. Virol. 72:488-496(1998).
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AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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MEDLINE=98080419; PubMed=9420250;
van't Wout A.B., Ran L.J., Kuiken C.L., Kootstra N.A., Pals S.T.,
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Pred: No. 2e+02;
3; Mismatches 3; Indels
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EMBL; AF021597; AAC04051.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019038; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IFR000777; GF120.
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   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                        Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          + 1 | | | | | : : |
40 EKWENTLKRVVTKL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 53.8 Matches 7; Conservative
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Matches 7; Conservative
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R MBL, AF152785; AAF08423.1; -.

R MBL, AF152785; AAF08423.1; -.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019018; F:structural molecule activity; IEA.

R GO; GO:0019010; F:golis C:viral capsid; IEA.

R InterPro; IPR00777; GP120.

R InterPro; IPR00710; IGI-like.

R Pfam; PF00516; GP120; 1.

W AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                             Gaps
Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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                                                                                                   Score 41; DB 2; Length 68;
Pred. No. 2e+02;
                                                                                                                                             3; Indels
                                                            68 AA; 7552 MW; AF6FC8ABB0984437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Envelope protein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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                                                                                                                         Pred. No. 2e+0
3; Mismatches
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Viruses; Retroid viruses; Retroviridae; Lentivirus
      EMBL; AF152763; AAF08401.1; -.
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Matches 7; Conservative
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54 KWNNTLKQVVKKL
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Q9X1A6
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Casado C., Urtasun I., Martin-Walther M.V., Garcia S., Rodriguez C.,
del Romero J., Lopez-Galindez C.;
"Genetic analysis of HIV-1 samples from Spain.";
J. Acquir. Immune Defic. Syndr. 23:68-74 (2000).
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AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane
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                                                                                                                              Length 68;
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                                                                                                                                                                                    3; Indels
                                                                  OEAF858A971B4EE3 CRC64;
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Last annotation update)
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
                                                                                                                           Score 41; DB 2;
Pred. No. 2e+02;
3; Mismatches
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Pred. No. 2e+02;
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7700 MW; /
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54 KWNNTLKQIVKKL 66
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                                                                                                                           Query Match
Best Local Similarity 53.8
Matches 7; Conservative
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hes 7; Conservative
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PIR; C72262; C72262.
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                                                                                                                                                                                     Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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Pred. No. 2e+02;
7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                        Score 41; DB 2; Length 68;
Pred. No. 2e+02;
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AE7243AA781F36CF CRC64;
                                                                                                                                                                                                                                                                     68 AA; 7786 MW; AF153B912669D658 CRC64;
  GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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Last annotation update)
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C:integral to membrane; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 AA
                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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                                                                                                      InterPro; IPR000777; GP120.
InterPro; IPR007110; Ig-like.
Pfam; PF00516; GP120; 1.
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40.0%;
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54 YERFKNELEKKAKRI 68
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TISSUE=Venom gland;
MEDLINE=20124706; PubMed=10868911; DOI=10.1080/152165400306214;
Zeng X.C., Li W.X., Peng F., Zhu Z.H.;
"Cloning and characterization of a novel cDNA sequence encoding the precursor of a novel venom peptide (BmKbpp) related to a bradykinin-potentiating peptide from Chinese scorpion Buthus martensii Karsch.";
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MEDLINE=21184690; PubMed=11287558;
DOI=10.1128/JVI.75.9.4091-4102.2001;
MCBreen S., Imlach S., Shirafuji T., Scott G.R., Leen C., Bell J.E.,
                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
BmK3 (Bradykinin-potentiating peptide).
Name=bppl; Synonyms=bpp;
Name=bppl; Synonyms=bpp;
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Bukaryota; Metasca; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthida; Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simmonds P.;
"Infection of the CD45RA+ (naive) subset of peripheral CD8+
"Infection of buman immunodeficiency virus type 1 in vivo.";
J. Virol. 75:4091-4102(2001).
EMBL. AP825790; AAK3B944.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
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Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Venom gland;
Wenxin L., Shunyi Z.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE-Venom gland; Zeng X.-C., Li W.-X., Zu S.-Y.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C256333D801857C6 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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. 24, Last annotation update)
                                                                                                                                          72 AA
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01-DEC-2001 (TEEMBLrel. 19, Last seq
01-JUN-2003 (TEEMBLrel. 24, Last ann
                                                                                                                                          PRT;
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EMBL, AF145953; AAF99564.1; -.
EMBL, AF145952; AAF99563.1; -.
SEQUENCE 72 AA; 8327 MW; C2
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  53 KWNNTLKQIVKKL 65
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Matches 8; Conservative
                                                                                                                                          PRELIMINARY;
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                                                                                  RESULT 30
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                                                                            MEDLINE-95127302; PubMed-7826703;
Furtus Y., Bergetrom T., Norkrans G., Horal P.;
"HIV type 1 V3 sequence diversity in contact-traced Swedish couples at
the time of sexual transmission.";
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Quinones-Mateu M.E., Albright J.L., Torre V., Reinis M., Vandasova J.,
Bruckova M., Arts E.J.;
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AIDS Res. Hum. Retrovivuses 15:85-89(1999).
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:virtal capsid; IEA.
GO; GO:0019028; F:virtal capsid; IEA.
GO; GO:0019031; C:virtal envelope; IEB.
GO; GO:0019031; C:virtal envelope; IEB.
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Pred. No. 2.1e+02;
3; Mismatches 3; Indels
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Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    EMBL; U10932; AA46502.1; -
GN GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000777; GP120.
InterPro; IPR000777; GP120.
InterPro; IPR00110; Ig-like.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein:
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pred. No. 2.1e+02;
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InterPro; IPR007110; Ig-like.
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                                                    SEQUENCE FROM N.A.
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NCBI_TaxID=11676;
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RESULT 29

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SEQUENCE 59 AA;
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"Distinct clustering of HIV type I sequences derived from injection versus noninjection drug users in Vancouver, Canada.";
AIDS Res. Hum. Retroviruses 14:917-919(1998).
EMBL, AF058157; AAC15170.1; --
HSSP; P20871; ICE4.
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Enkaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Agaricaceae; Agaricus.
[1]
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
Pfam; PR00516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
NOW_TER 12 1
NOW_TER 72 AA; 8296 MW; CE9A16A0A277770 CMC.
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                                                                                                                                                                                                                               Length 72;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:001908; F:structural molecule activity; IEA.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBI_TaxID=11676;
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Pred. No. 2.2e+02;
                                                                                                                                                                                                                          Score 41; DB 2; I
Pred. No. 2.1e+02;
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InterPro; IPR007110; Ig-like.
Pfam; PF00516; GP120; 1.
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53 KWNNTLKKIVVKLG 66
                                                                                                                                                                                                 Query Match
Best Local Similarity 53.0
7; Conservative
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01-JUN-2003
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P78569;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Sonnenberg A.S.M., de Groot P.W.J., Schaap P.J., Baars J.J.P., Visser J., van Griensven L.J.L.D.; "Isolation of expressed sequence tags of Agaricus bisporus and their assignment to chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.
Qian Y., Li S., Zhu H., Najar P.Z., Lai H., White J., Roe B.A.,
Perretti J.J.;
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                                                                                                                                Appl. Environ. Microbiol. 62:4542-4547(1996).
-!- SIMILARITY: Belongs to the ribosomal protein L41e family.
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Pred. No. 2.4e+02;
2; Mismatches 6; Indels
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Pred. No. 1.1e+02;
2; Mismatches 4; Indels
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Last annotation update)
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EMBL; AE014961; AANS8942.1; -
InterPro; IPR007793; DivIVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
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InterPro; IPR007836; Ribosomal_L41.
Pfam; PF05162; Ribosomal_L41; I.
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01-007-2003 (TrEMBLrel. 25, Last
Hypothetical protein SWU.1260c.
orderedLocusNames=SMU.1260c;
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Conservative
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les 7; Conservative
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Newfoundiand;
MEDLINE=SI212028 PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
Drebot M.A., Gavrilovokaya I., Mackow E.R., Chen Z., Lindsay R.,
Sanchez A.J., Nichol S.T., Artsob H.;
"Genetic and serotypic characterization of Sin Nombre-like viruses in Canadian Peromyscus maniculatus mice.";
Virus Res. 75:75-86(2001).
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Ontario 95;
MEDLINE=12122028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
Drebot M.A., Gavrilovakaya I., Mackow E.R., Chen Z., Lindsay R.,
Sanchez A.J., Nichol S.T., Artsob H.;
"Genetic and serotypic characterization of Sin Nombre-like viruses in Canadian Peromyscus maniculatus mice.";
                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
NCBI_TaxID=37705;
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VCBI_TaxID=37705;
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Pred. No. 2.8e+02;
4; Mismatches 4; Indels
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Drebot M.D.A. Jr., Artsob H.A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF380926; AAK59323.1; -.
NON TER 67 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Ontario 95;
Drebot M.D.A. Jr., Artsob H.A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF380927; AAK59324.1; -.
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67 AA; 7786 MW; 9874495B87FED423 CRC64;
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0911U9; (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                              67 AA.
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Similarity 50.0%;
8; Conservative
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Conservative
                                                                                                                                                                                                               Glycoprotein Gl (Fragment).
Sin Nombre virus.
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                                                           PRELIMINARY;
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les 8; Conserv
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Matches
RESULT 37
091IU8
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Lazzarin A., Tambussi G., Ciccozzi M., Rezza G., Buonaguro F.M.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX350346; AAR12490.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coat protein; Envelope protein; Glycoprotein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus
NCBI_TaxID=37705;
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Pred. No. 2.8e+02;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 63;
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STRAIN-Quebec 96a;
Drebot M.D.A. Jr., Artsob H.A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF380928; AAK59325.1;
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67 AA; 7804 MW; 82C4488B74F209E3 CRC64;
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Last annotation update)
                                                                                                                       (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO, GO:0019931, C:viral envelope, IEA.
InterPro, IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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53.8%;
                                                                                 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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Sin Nombre virus.
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Matches 8; Conservative
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Best Local Similarity
7; Conserve
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01-DEC-2001
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Length 67; 4; Indels ö

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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Best Local Similarity 53.0
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Best Local Similarity 53.8
Matches 7; Conservative
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NON TER
SEQUENCE
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Furnta Y., Bergetrom T., Norkrans G., Horal P.;
"HIV type I V3 sequence diversity in contact-traced Swedish couples at the time of sexual transmission.";
AIDS Res. Hum. Retroviruses 10:1187-1189 (1994).
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MEDLINE=21212028; PubMed=11311430; DOI=10.1016/S0168-1702(01)00227-1;
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NCBI_TaxID=37705;
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Drebot M.A. Jr., Artsob H.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF380925; AAK59322.1; -.
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Mulder K.E.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Glycoprotein G1 (Fragment).
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1 KLYKKWKNKLKRSLKR 16
                                 25 KLTNRFQENLKKSLKR 40
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Q70447
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                                                                                                                                                                                                                                                             Gaps
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InterPro, IPR008985, ConA like_lec_gl.
InterPro, IPR000777, GP120.
Pfam; PF00516; GP120; GP120.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO00777; GP120.
InterPro; IPRO07110; Ig-like.
Pfam; PPF0516; GP120; 1.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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Pred. No. 2.9e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mulder K.E.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
8007 MW; 784B5ADAD03A7E2A CRC64;
                                                                                                                                                        70 AA; 8084 MW; 95878D4404C6714D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U10943; AAA66513.1; -. GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0019028; C:viral capsid; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:00019031; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                         Score 40; DB 2;
Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Envelope glycoprotein, v3 region (Fragment)
                                                                                                                                                                                                                                                             3; Mismatches
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MEDLINE=95127302; PubMed=7826703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
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53.8%;
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53.8%;
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22 AA; 3089 MW; F948D74DD4EC98CB CRC64;
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                                                                                                                                                                                    25 AA
                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007836; Ribosomal_L41. Pfam; PF05162; Ribosomal_L41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF401598; AAK95170.1; -.
                            41.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.1%;
                                                                                    1 KLYKKWKNKLKRSLKR 16
                                                                                                              4 KWYKKRLRRLKRERKR 19
                                         Best Local Similarity 56.2
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KWKNKLKRSLKR 16
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KWRKKRMRGLKR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                               Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                       Name=RPL41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCG3_PACGO
ID PCG3_PACGO
AC P82416;
                                                                                                                                                                                    RL41 ICTPU Q90YS7;
 SEQUENCE
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                            Query Match
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                                                                                                                                                           RESULT 44
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                                                                                                                                                                                                                                                                                                                                              Gaps
                               MEDLINE-98334296; PubMed-9671221;

Bstable M.C., Merzouki A., Arella M., Sadowski I.J.;

"Distinct clustering of HIV type I sequences derived from injection versus noninjection drug users in Vancouver, Canada.";

AIDS Res. Hum. Retroviruses 14:917-919(1998).

BNBL; APO58151; AAC15164.1; -.
                                                                                                                                                                                                                               Pfam; PF00516; GP120; I.
AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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                                                                                                                                                                                                                                                                                                               Score 40; DB 2; Length 73;
Pred. No. 3e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
                                                                                                                                                                                                                                                                                      73 AA; 8356 MW; 369543B65DD12680 CRC64;
                                                                                                                                         GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0051989; F:structural molecule activity; IEA.
InterPro; IPR0007710; GP120.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L41e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50S ribosomal protein L41e.
Name=rp141e; OrderedLocusNames=MJ0242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
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                                                                                                                                                                                                                                                                                                                  42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67480; AAB98230.1; -. PIR; C64330; C64330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                          | | | | | : | : | 53 KWNNTLKHIVKKL 65
                                                                                                                                                                                                                                                                                                                                                                          5 KWKNKLKRSLKRL 17
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                             SEQUENCE FROM N.A.
    NCBI_TaxID=11676;
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P540<u>2</u>5;
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-! FUNCTION: Interacts with the beta subunit of protein kinase CKII and simulates phosphorylation of DNA topoisomerase II alpha by
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
Formicidae; Ponerinae; Ponerini; Pachycondyla.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ictalurus punctatus (Channel catfish).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
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-!- SIMILARITY: Belongs to the ribosomal protein L41e family
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Pred. No. 1.5e+02;
1; Mismatches 4; Indels
   Length 22;
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Score 39; DB 1; 1
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-0CT-2004 (Rel. 45, Created)
25-0CT-2004 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
60S ribosomal protein L41.
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InterPro; IPR010002; Ponericin.
Pfam; PP07442; Ponericin; 1.
Antibiotic; Direct protein sequencing; Pungicide; Insect immunity.
SEQUENCE 30 AA; 3383 MM; BC0463D0AF140B53 CRC64;
                                                                                                                                                                  41.1%; Score 39; DB 1; Length 30; 50.0%; Pred. No. 1.8e+02; tive 2; Mismatches 6; Indels
      FUNCTION, AND MASS SPECTROMETRY.
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Best Local Similarity 50.0
Matches 8; Conservative
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Search completed: May 16, 2005, 08:30:31 Job time : 76.8793 secs

3 YKKWKNKLKRSLKRLG 18 

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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May 16, 2005, 08:21:21; Search time 54:1293 Seconds (without alignments) 92.887 Million cell updates/sec Run on:

US-09-648-816B-13 65 score: Perfect

1 ALYKRLFKKLKKF 13 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

1066881 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003ss:\* geneseqp2001bs:\* A\_Geneseq\_16Dec04:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| ion                           | Antimicro | Rabbit pl | . Rabbit pl | Antimic  | Rabbit pl | Cationi  | Antimicro | Rabbit pl | Antivir  | Human his | / Cationic | 3 Cationic | -        | Antibacte | Antibacte | Antibacte | Antiviral |          | Apolipopr |          | SFnew pep | 5Fnew    | ~        |          | Anti-athe |
|-------------------------------|-----------|-----------|-------------|----------|-----------|----------|-----------|-----------|----------|-----------|------------|------------|----------|-----------|-----------|-----------|-----------|----------|-----------|----------|-----------|----------|----------|----------|-----------|
| Description                   | Aay57475  | Abg69899  | Abg69991    | Aay57473 | Abg69897  | Aar13929 | Aay57474  | Abg69898  | Aab13952 | Aau08314  | Aar13927   | Aar13928   | Aaw10351 | Aay68001  | Aaw10352  | Aay68002  | Aab13951  | Aau08313 | Abb83730  | Abb83737 | Aae39735  | Aae39742 | Adi41463 | Adi41470 | Adm79444  |
| ID                            | AAY57475  | ABG69899  | ABG69991 .  | AAY57473 | ABG69897  | AAR13929 | AAY57474  | ABG69898  | AAB13952 | AAU08314  | AAR13927   | AAR13928   | AAW10351 | AAY68001  | AAW10352  | AAY68002  | AAB13951  | AAU08313 | ABB83730  | ABB83737 | AAE39735  | AAE39742 | ADI41463 | AD141470 | ADM79444  |
| 08                            | 6         | Ŋ         | ហ           | ~        | Ŋ         | ~        | ~         | S         | ٣        | 4         | ~          | 7          | 7        | m         | 7         | m         | m         | 4        | S         | Ŋ        | 7         | 7        | œ        | œ        | œ         |
| %<br>Query<br>Match Length DB | 13        | 13        | 35          | 13       | 13        | 18       | 13        | 13        | 28       | 29        | 18         | 18         | 18       | . 18      | 19        | 19        | 28        | 29       | 14        | 14       | 14        | 14       | 14       | 14       | 14        |
| %<br>Query<br>Match           | 100.0     | 100.0     | 100.0       | 75.4     | 75.4      | 75.4     | 73.8      | 73.8      | 70.8     | 70.8      | 66.2       | 66.2       | 66.2     | 66.2      | 66.2      | 66.2      | 64.6      | 64.6     | 63.1      | 63.1     | 63.1      | 63.1     | 63.1     | 63.1     | 63.1      |
| Score                         | 65        | 65        | 65          | 49       | 49        | 49       | 48        | 48        | 46       | 46        | 43         | 43         | 43       | 43        | 43        | 43        | 42        | 42       | 41        | 41       | 41        | 41       | 41       | 41       | 41        |
| Result<br>No.                 | 1         | 8         | m           | 4        | Ŋ         | 9        | 7         | 80        | 0,       | 10        | 11         | 12         | 13       | 14        | 15        | 16        | 17        | 18       | 19        | 20       | 21        | 22       | 23       | 24       | 25        |

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| Adm 19437<br>Adm 19437<br>Adm 222864<br>Adm 222864<br>Adm 21380<br>Adm 21380<br>Adm 21372<br>Adm 21972<br>Adm 21972<br>Adm 79419<br>Adm 79419<br>Adm 7943<br>Adm 7944 |  |
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| ADM79437 ADS87808 ADS87801 ADS87801 AAR21380 AAR21380 AAR33719 AAR33719 AAR39724 AAR39724 AAR39724 AAR39739 AAR39739 AAR13953 AAR13953 AAR13953 AAR728969 AAR13939 AAR7085                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |  |
| <b>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |  |
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## ALIGNMENTS

Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis. (HARB-) HARBOR-UCLA RES & EDUCATION INST. Antimicrobial peptide RP-11 SEQ ID NO:13. AAY57475 standard; peptide; 13 AA 99WO-US003350. 98US-00025319 (first entry) Oryctolagus cuniculus. 18-FEB-1998; 17-FEB-1999; WO9942119-A1 25-FEB-2000 26-AUG-1999 Synthetic. AAY57475; RESULT 1

Shen AJ; Yeaman MR, WPI; 1999-527417/44.

Antimicrobial peptides for potentiating antimicrobial agents active against bacteria and fungi.

Disclosure; Page 112; 166pp; English.

The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi. The AP comprises: (a) a peptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXEBA and its derivatives selected from XZBBZBXEBA. BXZXB, BXZXZB, XBBXZXBBA and BBXZBBXZ; and (b) as second peptide template XBBXZXBB, XBBXZXBB, and (b) group consisting of XBBXBBX, SBXXBBX, BXXBXSB, SBBZXXBB, and XBBZXXBBXZBBX; where B = at least one positively charged amino acid; X = at least one aromatic amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of

Gaps

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100.0%; Score 65; DB 5; Length 13; 100.0%; Pred. No. 0.0012; ive 0; Mismatches 0; Indels

Local Similarity

Query Match Matches

Sequence 13 AA;

1 ALYKRLFKKLKKF 13 13; Conservative

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half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide

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considered to have undesirable toxicity, immunogenicity and short

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting multiple antibiotic resistance.
neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                               Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                       Gaps
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                                                                                                                                                                                                                                                           Rabbit platelet microbicidal protein, PMP-2, based peptide #11.
                                                     100.0%; Score 65; DB 2; Length 13.
100.0%; Pred. No. 0.0012; ....marches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 131; 221pp; English.
                                                                                                                                                                                           ABG69899 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2001; 2001WO-US041877.
                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-2000; 2000US-00648816.
                                                                                                                                                                                                                                     (first entry)
                                                                                                              1 ALYKRIFKKIKKF 13
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                                                                                       13; Conservative
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Synthetic.
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                                                                 Query Match
Best Local Similarity
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antimicrobial peptide composition for the prevention and treatment of ections caused by organisms, such as bacteria and fungi, exhibiting
                                                                                                                                                                                                                                                                                                  rabbit;
                                                                                                                                                                                                                    Rabbit platelet microbicidal protein, PMP-2, based peptide #103
                                                                                                                                                                                                                                                          Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance;
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                                                                                                        ABG69991 standard; peptide; 35 AA.
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                                                                                                                                                                                  21-OCT-2002 (first entry)
1 ALYKRLFKKCKKF 13
                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections caused
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against organisms such as bacteria and fungi comprising a peptide of 5-150 anno acids containing a 7-13 amino acid core sequence (derived from PMP-1 and PMP-2, platelet microbiocidal protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial peptide composition for direct activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid and retromers, extensions, combinations and fusions; and (2) antimicrobial activity of

invention relates to an antimicrobial peptide composition for use

leukocytes against organisms such as bacteria and fungi. The antimicrobial peptides are useful as individual antimicrobial agents, specifically against bacteria and fungi, agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of lenkocytes, as dishifectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally

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The present invention describes an antimicrobial peptide (AP) for direct activity or for potentiating antimicrobial agents active against occanisms such as bacteria and fungi. The AP comprises: (a) a posptide containing an amino acid sequence selected from the group consisting essentially of a first peptide template XZBZBXBXB and its derivatives selected from XZBZBXBXB, BXZXXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XZBZXXB, XBBXZXBBX and BBXZBBXZ; and (b) a second peptide template XBBXXXBX, XBBXZBBX, and (b) a second peptide template XBBXXXBX, XBBXZBB, and XBBZXXBBXXBBX; where B = at least one positively charged amino acid; X = at least one anon-polar hydrophobic amino acid; Z = at least one aromatic amino acid, and where B, X and Z may be separated by one or more other amino acids. The peptides can be used to treat bacterial and fungal infections. The peptides also increase the antimicrobial activity of
antimicrobials, agents that enhance, potentiate or restore efficacy of conventional antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agent to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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                                                                                                                                                                                                                                                                                                                                       100.0%; Score 65; DB 5; Length 35; 100.0%; Pred. No. 0.0029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57473 standard; peptide; 13 AA
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Les 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-527417/44.
                                                                                                                                                                                                                                                                                                  Sequence 35 AA;
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The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5. 150 amino acide corts sequence (derived from PMP-1 and PMP-2, platelet microbicoidal protein), and retromers, runcations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also possible structures are fully described in the specification. Also core sequence selected from truncations of the peptides described activity or for potentiating antimicrobial agents active against organisms such as bacteria and fungi comprising a peptide of 13-74 containing an amino acid or for potentiating comprising a peptide of 13-74 containing an amino acid and microbial peptides for potentiating antimicrobial activity of antimicrobial peptides are useful as individual antimicrobial against organisms such as bacteria and fungi. Agents in combination with other antimicrobials, agents that enhance, potentiate or restore efficacy of antimicrobials, agents that enhance the antimicrobial functions of leukocytes, as disinfectants or preservatives for use in foods and cosmetics and as agents to improve efficiency of molecular biology techniques. Antimicrobial peptides of prior art have generally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
neutrophils. The peptides overall effect cellular disruption and rapid apoptosis of microbial cells. AAY57463 to AAX57557 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; platelet microbiocidal protein; PMP-1; PMP-2; bacterial infection; fungal infection; fungicide; disinfectant; preservative; foods; cosmetic; multiple antibiotic resistance; rabbit;
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rabbit platelet microbicidal protein, PMP-2, based peptide #9
                                                                                                                      Length 13;
                                                                                                                                                         1; Indels
                                                                                                                      DB 2;
                                                                                                                                      0.42;
                                                                                                                  75.4%; Score 49; DB 83.3%; Pred. No. 0.42 ive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 131; 221pp; English.
                                                                                                                                                                                                                                                                                                                                      ABG69897 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multiple antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2001; 2001WO-US041877
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                      Local Similarity 83.3
les 10, Conservative
                                                                                                                                                                                               1 ALYKRIFKKIKK 12
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1 ALYKKLFKKLLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infections caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant; mutein.
                                                                               Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                           ABG69897;
                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alpha-helical structure and is believed to act as an ionophore, making holes in bacterial call membranes. The peptide and antibiotic act synergistially. See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprise beta-lactam antibiotic and cationic oligopeptide, useful against
Enterobacteriaceae, Pseudomonas aeruginosa etc.
been considered to have undesirable toxicity, immunogenicity and short half-lives due to biodegradation. The peptides of the present invention are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammalian cell toxicities and overcome problems of toxicity, immunogenicity, and shortness of duration of effectiveness due to biodegradation, retaining activity in plasma and serum. The present sequence is a rabbit PMP based antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compsns. for treating infections sensitive to beta-lactam antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 5; Length 13;
Pred. No. 0.42;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.4%; Score 49; DB 2; Length 18; 76.9%; Pred. No. 0.56; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR13929 standard; protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-00484020.
91US-00655321.
                                                                                                                                                                                                                                                                                                                                                                  75.4%;
83.3%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ALYKKLFKKLLK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ALYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blake JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-281214/38.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                        Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-1991;
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26-NOV-1991
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Matches
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AAR13929

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AAR13929

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Gaps
                                                                                                                                                                                                                        for potentiating antimicrobial agents active
                                                                  Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein; antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rabbit platelet microbicidal protein, PMP-2, based peptide #10.
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 2
Pred. No. 0.6;
0; Mismatches
                                                    Antimicrobial peptide RP-10 SEQ ID NO:12.
                                                                                                                                                                            (HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                                                                                                                                Disclosure; Page 112; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG69898 standard; peptide; 13 AA.
       AAY57474 standard; peptide; 13 AA
                                                                                                                                                             98US-00025319
                                                                                                                                              99WO-US003350
                                                                                                                                                                                                                                                                                                                                                                                                              73.8%;
90.9%;
                                                                                                                                                                                                                        Antimicrobial peptides for against bacteria and fungi.
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-OCT-2002 (first entry)
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Best Local Similarity 90.3
Best Local 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LYKRLFKKLKK 12
                                                                                                Oryctolagus cuniculus.
                                                                                                                                                                                           Yeaman MR, Shen AJ;
                                                                                                                                                                                                          WPI; 1999-527417/44
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13 AA;
                                                                                                                WO9942119-A1.
                                                                                                                                              17-FEB-1999;
                                                                                                                                                             18-FEB-1998;
                                     25-FEB-2000
                                                                                                                               26-AUG-1999
                                                                                         Synthetic.
                     AAY57474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG69898;
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ABG69898
AAY57474
        8X4X6X8
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us-09-648-816b-13.rag

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(HARB-) HARBOR-UCLA RES & EDUCATION INST.
                                                                                                                                      Disclosure; Page 131; 221pp; English.
                                                                                                                             multiple antibiotic resistance.
                                                                          25-AUG-2000; 2000US-00648816.
                                                                 24-AUG-2001; 2001WO-US041877
                                                                                                                                                                                                                                                                                                                   90.98;
                                                                                                                                                                                                                                                                                                                  Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                 2 LYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                       LYKRLFKKLLK 12
                            Oryctolagus cuniculus.
Synthetic.
                                                                                               Yeaman MR, Shen AJ;
                                                                                                        WPI; 2002-590659/63.
                                                                                                                                                                                                                                                                                                   Sequence 13 AA;
                   mutant; mutein.
                                            WO200255554-A2
                                                      18-JUL-2002.
                                                                                                                                                                                                                                                                                                             Query Match
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The present invention relates to antiviral peptides containing a domain of 10-25 amino acids, where half the domain is positively charged and the other half is uncharged. The present sequence is an antiviral peptide of the invention. Oligomers consisting of at least two peptides coupled together are also included in the invention. The peptides are useful for treating viral infections such as human immunodeficiency virus (HIV) and herpes simplex virus (HSV) and for the treatment of cold sores, aphthous ulcers and viral bronchial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, histatin, DH5, antimicrobial peptide; endocarditis;
anti-infection; antiinflammatory; anti-repulsion; antifungal; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiviral peptides comprising a domain of 10-25 amino acids, half of which is positively charged and half uncharged, useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Veerman ECI, Van 'thof W, Nibbering PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.8%; Score 46; DB 3; Length 28; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                       Antiviral, antiulcer, human immunodeficiency virus, HIV, herpes simplex virus; HSV; cold sore; aphthous ulcer; viral bronchial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which is positively charged and half uncharged, useful
human immunodeficiency virus and herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human histatin 5 carboxy terminal based peptide 18.
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                                                                                                                                                                                                                                                                                                                                                                             /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TEWE-) STICHTING TECH WETENSCHAPPEN
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                     16-NOV-2000 (first entry)
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                                                                                                          Antiviral peptide #18.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200032629-A2
                                                                                                                                                                                                                                                                                                                             Key
Modified-site
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AAB13952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU08314
  쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an antimicrobial peptide composition for use against organisms such as bacteria and fungi comprising a peptide of 5-150 amino acide core sequence (derived from PMP-1 and PMP-2, platelet microbiodial protein), and retromers, truncations, extensions, combinations, fusions and their derivatives. The possible structures are fully described in the specification. Also included are (1) an antimicrobial agents active against organisms such as a crear and fungi comprising a peptide of 13-74 containing an amino acid core sequence selected from truncations of the peptides described above, and retromers, extensions, combinations and fusions; and (2) antimicrobial peptides for potentiating antimicrobial agents useful as individual antimicrobial agents that enhance the antimicrobial agents that enhance the antimicrobial agents that enhance the antimicrobial are in a conventional antimicrobials, agents that enhance the antimicrobial for potentiating that enhance the antimicrobial for potentiate or restore efficancy of conventional antimicrobials, agents that enhance the antimicrobial for potentials of prior art have generally been considered to have undesirable toxicity, immunogenicity and short to hology techniques. Antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides of prior art have generally been considered to have undesirable toxicity, immunogenicity and short are based upon natural antimicrobial peptides that have potent and broad spectrum activity against pathogens exhibiting multiple antibiotic resistance. They exhibit lower inherent mammallan cell toxicity and shortness of effectiveness due to biodegradation, retaining activity and shortness of effectiveness due to biodegradation, retaining activity in plasma and covercome problems of toxicity, immunogenicity, and shortness of effectiveness due to biodegradation, retaining activity in plasma and effective antimicrobial peptides 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antimicrobial peptide composition for the prevention and treatment of infections caused by organisms, such as bacteria and fungi, exhibiting
                            Antimicrobial, platelet microbiocidal protein, PMP-1, PMP-2, bacterial infection, fungal infection, fungicide, disinfectant, preservative, foods, cosmetic, multiple antibiotic resistance, rabbit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.6;
0; Mismatches
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Gaps

; 0

Location/Qualifiers

Key

AAB13952 standard; peptide; 28 AA.

RESULT 9
AAB13952
ID AAB:

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This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alpha-helical structure and is believed to act as an ionophore, making holes in bacterial call membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compsns. for treating infections sensitive to beta-lactam antibiotics -comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                               Compsns. for treating infections sensitive to beta-lactam antibiotics -comprise beta-lactam antibiotic and cationic oligopeptide, useful against Enterobacteriaceae, Pseudomonas aeruginosa etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      numan platelet factor 4 C-13 fragment; amphipathic alpha helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 2; Length 18; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                    Blake JJ, Cosand WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR13928 standard; protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blake JJ, Cosand WL;
                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 44; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 44; 64pp; English
                                                                                                                                                                         (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                        90US-00484020.
91US-00655321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.2%;
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                                                               90US-00484020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-281214/38.
                                                                                                                                                                                                                                                           WPI; 1991-281214/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 AA;
                                                               23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-1991;
                                                                                                                              19-FEB-1991;
                      05-SEP-1991.
                                                                                                          23-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
26-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Darveau RP,
                                                                                                                                                                                                                    Darveau RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9112815-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR13928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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AAR13928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to medical device for application onto or into a body of a patient, coated with one or more naturally occurring peptides or proteins or synthetic peptides or their analogues having antimicrobial activity. The medical device is useful for application onto or into body of a patient and includes endotracheal tubes, intravenous catheters, or urinary catheters, syringe needles, contact lenses, prosthetic implants, cut as heart valves, bone implants, contact lenses, prosthetic implants, cut substitutes, dental implants and spinal implants. The medical device is also suitable for veterinary use. The peptide coated implants have antimiferammation and anti-repulsion activity, resulting in avoiding or inhibiting tissue loss after implantation and prevent bone degradation around the implants e.g. endocarditis. Cystatin-derived peptides inhibit both the proteolytic activity and growth of peptides inhibit both the proteolytic activity and growth of peptides inhibit both the proteolytic activity and growth of peptides have increased antibacterial, antifungal and antiviral activity. Sy counteracted and the medical device with an antimicrobial peptide or protein, the chance of the infection, including biofilm infection is effectively counteracted and the body of the patient is not oversensitive degainst and particular and particular and antiviral activity and growth of counteracted and the body of the patient is not oversensitive degainst and particular and antiviral activity and growth of antipare and antiviral activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                          Medical device, in particular implants and contact lenses for application into body of a patient, is coated with natural or synthetic antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       against such peptides. The present sequence is a synthetic oligomeric antimicrobial peptide based on human histatin 5 (DH5) carboxy terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.8%; Score 46; DB 4; Length 29; 100.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                        Veerman ECI, Van't Hof W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ....
                                        /note= "Lys is amidated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 7; 22pp; English
                      /label= OTHER
                                                                                                                                                                         12-JAN-2001; 2001WO-NL000019.
                                                                                                                                                                                                                  12-JAN-2000; 2000NL-01014071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100...
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cationic oligopeptide #3
                                                                                                                                                                                                                                                                                                        /an Nieuw Amerongen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKRLFKKLK 11
                                                                                                                                                                                                                                                           (AMPH-) AM-PHARMA BV
                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514579/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29 AA;
                                                                                   WO200156627-A1
Modified-site
                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
26-NOV-1991
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RESULT 11 AAR1392

BXSXXXXXXXX

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Gaps

Gape

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Indels

5

Mismatches Score 43; Pred. No.

Length 18;

DB 2;

66.2%; 75.0%;

Query Match
Best Local Similarity 75...
Best Good 9; Conservative

1 ALYKRLFKKLKK 12 1 ||||:| ||| | 1 ALYKKLLKKLLK

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This is a specific example of a cationic oligopeptide suitable for use in compositions with beta-lactam antibiotics. The peptide has an alphahelical structure and is believed to act as an ionophore, making holes in bacterial cell membranes. The peptide and antibiotic act synergistically. See AAR13924-R13930 and AAR13936-7. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antimicrobial compsns. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with
                                                                                                                                                                                                                                                                                                                              Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; cancer; endocrinology; antibodiotic; antibody; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panasik N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pugh C,
                                                                                                              Length 18;
                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                           Antibacterial peptide C18G for immunoadapter synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schatz RW,
                                                                                                             Score 43; DB 2;
Pred. No. 5.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shekhani MS, Firca JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 39; Page 150; 227pp; English.
                                                                                                                                                                                                                                        AAW10351 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US010227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00482191.
                                                                                                             Query Match
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                          1 ALYKRLFKKLKK 12
                                                                                                                                                                        WPI; 1997-077224/07.
                                                                                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin
                                                                                                                                                                                                                                                                                     22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                    WO9640251-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stafford D;
                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                AAW10351;
                                                                                                                                                                                                               RESULT 13
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Limulus antilipopolysaccharide factor; LALF; diagnosis: endotoxin; bacterial infection; antibacterial; fimbriae-binding compound; sepsis.

Antibacterial peptide C18G SEQ ID NO:2.

(first entry)

11-APR-2000

AAY68001;

AAY68001 standard; peptide; 18 AA.

RESULT 14

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Gaps

g

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The present invention describes a threspeture formulation compression of the present invention describes a threspeture formulation compression is a method of treatment for bacterial disease comprising: (a) providing a subject with symptoms of bacterial disease with one or more fimbriae-binding compounds comprising a mannose of an anomeric configuration, an alpha-aromatic or heteroaromatic ring attached to the mannose by a glycosidic or pseudoglycosidic linkage and a functional group which provides a site for chemical modification remote from the mannose and a pharmaceutically carrier; and (b) administering the fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compound to the subject. Administration of one or more fimbriae-binding compounds can be used for treating subjects with symptoms of and for subjects at risk from bacterial diseases. Treatment of and prevention of blood-borne and toxin mediated diseases in particular sepsis in humans the effects of endotoxin is also possible. The compounds may also be used to identify bacteria according to their cell binding specificity's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agglutination of yeast cells induced by type 1 pili bearing bacteria. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through conjugation to reporter substances such as dyes, luminescent or fluorescent molecules and enzymes. The compounds also inhibit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a therapeutic formulation comprising N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 3
Pred. No. 5.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 39; Col 84; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
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Therapeutic formulation comprising N-(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside or its cysteinyl derivative useful for diagnosing and treating bacterial diseases.

Shekhani MS, Anderson B, Firca JR;

WPI; 2000-115173/10.

(OPHI-) OPHIDIAN PHARM INC

96US-00760903. 96US-00760903.

06-DEC-1996; 06-DEC-1996;

US5998381-A. 07-DEC-1999

Synthetic.

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Gaps

.. 0

2; Indels

9; Conservative 1 ALYKRLFKKLKK 12

ò

Sequence 18 AA

by adding a Cys-amide to the carboxy terminus. This was used to produce an immunoadapter conjugate. Making a conjugate comprises covalently linking a surface-binding ligand (SBL) to a hapten via a spacer to form a ligand-spacer-lapten (LSH) compound, and reacting the compound with immunoglobulin (Ig) under conditions that allow for non- covalent binding of the Ig to the hapten of the compound. The conjugate can be used for the diagnosis, prevention and treatment of microbial infections, e.g. neurology, cancer and endocrinology, where Ig targeting can provide desired therapeutic effects. The methods for producing a conjugate can use small molecule targeting ligands to efficiently direct otherwise unreactive Ig to microbial targets. This targeting allows Ig to react with microbial structures that may not normally be accessible to Ig, or are incapable of stimulating antibody production

present sequence is an antibacterial peptide C18G, which was modified

Limulus antilipopolysaccharide factor; LALF; diagnosis; endotoxin; bacterial infection; antibacterial; fimbriae-binding compound; sepsis.

Antibacterial peptide C19G SEQ ID NO:3.

(first entry)

11-APR-2000

AAY68002;

AAY68002 standard; peptide; 19 AA.

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1 ALYKKILKKILK 12

g

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produce an immunoadapter conjugate. Making a conjugate comprises covalently linking a surface-binding ligand (SBL) to a hapten via a spacer to form a ligand-spacer-hapten (LSB) compound, and reacting the compound with immunoglobulin (1g) under conditions that allow for non-covalent binding of the Ig to the hapten of the compound. The conjugate can be used for the diagnosis, prevention and treatment of microbial infections, e.g. sepsis, influenza, virenian or fungemia. They can also be used in neurology, cancer and endocrinology, where Ig targeting can provide desired therapeutic effects. The methods for producing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conjugate can use small molecule targeting ligands to efficiently direct otherwise unreactive Ig to microbial targets. This targeting allows Ig to react with microbial structures that may not normally be accessible to Ig, or are incapable of stimulating antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial compsns. for diagnosis and therapy - comprising microbial surface binding ligand-spacer-hapten, non-covalently associated with
                                                                                                                                                               Antimicrobial; immunoglobulin; surface binding ligand; hapten; sepsis; influenza; viremia; fungemia; neurology; cancer; endocrinology; antibodiotic; antibody; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Panasik N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is a peptide designated C19G. This was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pugh C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.2%; Score 43; DB 2; Length 19; 75.0%; Pred. No. 5.4; 2; Indels iive '1; Mismatches 2; Indels
                                                                                                                                  Antibacterial peptide C19G for immunoadapter synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Firca JR, Schatz RW,
                                                                                                                                                                                                                                                                                                         /note= "In amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 39; Page 150; 227pp; English.
                                                                                                                                                                                                                                                                       Location/Qualifiers
                               AAW10352 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US010227.
                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00482191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shekhani MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OPHI-) OPHIDIAN PHARM INC.
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 75.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-077224/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin
                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams JA,
Stafford D;
                                                                                                                                                                                                                                                                                                                                          WO9640251-A1
                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
                                                                                                   22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1996.
                                                                                                                                                                                                                                         Synthetic
                                                                 AAW10352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
RESULT 15
              AAW10352
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(phenylalanyl)-4-aminophenyl-alpha-D-mannopyranoside (1). Also described is a method of treatment for bacterial disease comprising: (a) providing a subject with symptoms of bacterial disease with one or more finbriae-binding compounds comprising a mannose of an anomeric configuration, an alpha-arcmatic or heteroarcmatic ring attached to the mannose by a glycosidic or pseudoglycosidic linkage and a functional group which provides a site for chemical modification remote from the mannose and provides a site for chemical modification remote from the mannose and promaraceutically carrier; and (b) administration of one or more fimbriae-binding compounds can be used for treating subjects with symptoms of and for subjects at risk from bacterial diseases. Treatment of and prevention of blood-borne and toxin mediated diseases in particular sepsis in humans and other animals can be carried diseases in particular sepsis in humans to identify bacteria according to their cell binding specificity's to identify bacteria according to their cell binding specificity's through conjugation to reporter substances such as dyes, luminescent or fluorescent molecules and enzymes. The compounds also inhibit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Therapeutic formulation comprising N-{phenylalanyl}-4-aminophenyl-alpha-D -mannopyranoside or its cysteinyl derivative useful for diagnosing and treating bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agglutination of yeast cells induced by type 1 pili bearing bacteria. The present sequence is used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a therapeutic formulation comprising N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 3; Length 19;
Pred. No. 5.4;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Shekhani MS, Anderson B, Firca JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB13951 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 39; Col 84; 89pp; English
                                                                                                                                                                                                                                                                                                     96US-00760903.
                                                                                                                                                                                                                                                                                                                                         96US-00760903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                            (OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALYKKLIKKLIK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-115173/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 AA;
                                                                                                                                                                                                                                                                                                     06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                         06-DEC-1996;
                                                                                                                                                                                                                                US5998381-A
                                                                                                                                                                                                                                                                    17-DEC-1999
                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB13951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
AAB13951
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8
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Gaps

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|||||:| ||| | ALYKKLLKKLLK 12 1 ALYKRLFKKLKK 12

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RESULT 16 AAY68002

us-09-648-816b-13.rag

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(AMPH-) AM-PHARMA BV.
                                                                                                            WPI; 2001-514579/56
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29 AA;
WO200156627-A1
                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB83730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB83730
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                  The present invention relates to antiviral peptides containing a domain of 10-25 amino acids, where half the domain is positively charged and the other half is uncharged. The present sequence is an antiviral peptide of the invention. Oligomers consisting of at least two peptides coupled together are also included in the invention. The peptides are useful for treating viral infections such as human immunodeficiency virus (HIV) and herpes simplex virus (HSV) and for the treatment of cold sores, aphthous ulcers and viral bronchial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, histatin, DHS, antimicrobial peptide; endocarditis,
anti-infection, antiinflammatory, anti-repulsion, antifungal; antiviral.
                                                                                                                                                                                                                                                       oŧ
                                                                                                                                                                                                                                           Antiviral peptides comprising a domain of 10-25 amino acids, half of which is positively charged and half uncharged, useful for treatment human immunodeficiency virus and herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                          Veerman ECI, Van 'thof W, Nibbering PH;
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 3; Length 28;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
               Antiviral; antiulcer; human immunodeficiency virus; HIV; herpes simplex virus; HSV; cold sore; aphthous ulcer; viral bronchial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human histatin 5 carboxy terminal based peptide 17.
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                          /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= OTHER
/note= "Lys is amidated"
                                                                                                                                                                                       (TEWE-) STICHTING TECH WETENSCHAPPEN
                                                                    Location/Qualifiers
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU08313 standard; peptide; 29 AA
                                                                                                                                                                                                                                                                                  Example 1; Page 7; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         64.6%;
88.9%;
                                                                                                                                                  99WO-NL000732
                                                                                                                                                                    98NL-01010692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.>
88.>
8, Conservative
                                                                                                                                                                                                          Van Nieuw Amerongen A,
Antiviral peptide #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YKRLFKKLK 11
                                                                                                                                                                                                                            WPI; 2000-412289/35.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28 AA;
                                                                                                            WO200032629-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Synthetic.
                                                                                                                                                  01-DEC-1999;
                                                                                                                                                                    01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-2001
                                                                                                                               08-JUN-2000
                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU08313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 18
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the interaction transcribed with one or more naturally occurring peptides or proteins or synthetic peptides or their analogues having antimicrobial activity. The medical device is useful for application onto or into body of a patient and includes endotracheal tubes, intravenous catheters, curinary catheters, syrings endotracheal tubes, intravenous catheters, curinary catheters, syrings enedles, contact lenses, prosthetic implants, such as heart valves, bone implants, voice prostheses, pace makers, joint substitutes, dental implants and appint implants and spinal implants. The medical device is also suitable for veterinary use. The peptide coated implants have anticinfection, antinflammation and anti-repulsion activity, resulting in avoiding or inhibiting tissue loss after implantation and prevent bone degradation around the implants e.g. endocarditis. Cystatin-derived peptides inhibit both the proteolytic activity and growth of peptides have increased antibacterial, antifungal and antiviral activity. By coating the medical device with an antimicrobial peptide or protein, the patient is not oversensitive against cuch peptides or proteins. Resistant bacterial strain is not formed against such peptides. The present sequence is a synthetic oligomeric antimicrobial peptide based on human histatin 5 (DHS) carboxy terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                 Medical device, in particular implants and contact lenses for application into body of a patient, is coated with natural or synthetic antimicrobial peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to medical device for application onto or into a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apolipoprotein A-1; Apo; atherosclerosis; Alzheimer's disease; acquired immunodeficiency syndrome; AIDS; osteoporosis; rheumatoid arthritis; biofilm formation; antiatherosclerotic; antiinflammatory; antileprotic; tuberculostatic; dermatological; osteopathic; antirheumatic; antiarthritic; antibacterial; virucide; fungicide; antiparasitic; vulnerary; immunosuppressive; vasotropic; anti-HIV; nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 12;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                            Van't Hof W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apolipoprotein A-1 mimetic peptide SEQ ID NO 29.
                                                                                                                                                                                                                                                                 Veerman ECI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB83730 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 7; 22pp; English.
12-JAN-2001; 2001WO-NL000019
                                                                                       12-JAN-2000; 2000NL-01014071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                            Jan Nieuw Amerongen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YKRLFKKLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 YKRLFKELK 22
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rheumatoid arthritis; biofilm formation; antiatherosclerotic;

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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                               Novel apolipoprotein A-1 mimetic peptide useful for ameliorating symptom of atherosclerosis in a mammal, comprises at least one class A amphipathic helix and a D-amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein A-1; Apo; atherosclerosis; Alzheimer's disease; acquired immunodeficiency syndrome; AIDS; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 5; Length 14;
Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apolipoprotein A-1 mimetic peptide SEQ ID NO 36.
                               note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                      Anantharamaiah GM, Navab M;
                                                              /note= "C-termnal amide"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB83737 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 85; 149pp; English
                                                                                                                                                           23-AUG-2001; 2001WO-US026497.
                                                                                                                                                                                        24-AUG-2000; 2000US-00645454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | ::|:|||:|
1 AFYDKVFEKLKEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                       WPI; 2002-463036/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14 AA;
                                                                                            WO200215923-A1
 Key
Modified-site
                                            Modified-site
                                                                                                                                                                                                                                                      Fogelman AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-2002
                                                                                                                           28-FEB-2002
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The invention relates to an apolipoprotein (apo) A-1 mimetic peptide (I, ABB83703-ABB83786) that ameliorates a symptom of atherosclerosis, CC Camprising a sequence of 10-30 amino acids, at least one class A camphipathic helix, at least one D amino acid residue and which protects a phospholipid against oxidation by an oxidising agent. (I) is not the D-18A peptide, DWLKARYDKVAEKIKARP. (I) is useful for ameliorating a symptom of atherosclerosis in a mammal diagnosed as having one or more symptoms of atherosclerosis, or at risk for atherosclerosis and for mitigating or preventing a coronary complication (a symptom of atherosclerosis)

CC preventing a coronary complication (a symptom of atherosclerosis)

CC preventing a coronary complication (a symptom of atherosclerosis)

CC preventing a coronary complication (a symptom of atherosclerosis)

CC preventing a coronary complication (a symptom of atherosclerosis)

CC preventing a coronary disease, such as leprosy, tuberculosis, systemic recurrent inflammatory disease, such as leprosy, tuberculosis, systemic coronary disease, Alzheimer's disease and acquired immunodeficiency syndrome disease, Alzheimer's disease and acquired immunodeficiency syndrome coronary coloring cobstructive pulmonary disease, coronary calcification, calcific cortic stenosis, osteoporosis, rheumatod arthritis, or inflammatory response associated with bacterial, viral, fungal infection, an organ cranpalant, a wound, an implanted prosthesis, parasitic infection, an organ cranple, has elevated serum half-life and readily administered by oral coute even when the amino and/or carboxy termini are blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel apolipoprotein A-1 mimetic peptide useful for ameliorating symptom of atherosclerosis in a mammal, comprises at least one class A amphipathic helix and a D-amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
antiinflammatory; antileprotic; tuberculostatic; dermatological; osteopathic; antirheumatic; antiarthritic; antibacterial; virucide; fungicide; antiparasitic; vulnerary; immunosuppressive; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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53.8%; Pred. No. 8.5;
cive , 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fogelman AM, Anantharamaiah GM, Navab M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C-termnal amide"
                                                                                                                                       anti-HIV; nootropic; neuroprotective
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE39735 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 86; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-2001; 2001WO-US026497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2000; 2000US-00645454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.8%;
Matches 7; Conservative ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFYDKVFEKLKEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-463036/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200215923-A1
                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2002
                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE39735
ID AAE3
XX
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complication; atherosclerosis; inflammation; leprosy;

(first entry)

'note= "Optionally N-terminal acetyl" /note= "Optionally C-terminal amide"

Location/Qualifiers

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systemic lupus erythematosus, idiopathic pulmonary fibrosis; scleroderma, polymyalgia rheumatica, chronic obstructive pulmonary disease, ADS; acquired immune deficiency syndrome; tuberculosis; polyarteritis nodosa, Alzheimer's disease; coronary calcification; calcific aortic stenosis;
                                                                                                                                             rheumatoid arthritis; osteoporosis; cardiant; neuroprotective; nootropic; vasotropic; gastrointestinal; dermatological.
                                         SFnew peptide #24 used to ameliorate symptoms of atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fogelman AM, Anantharamaiah GM,
                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2001; 2001US-00896841
                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2000; 2000US-00645454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-720035/68.
                                                                                                                                                                                                                                     Misc-difference 1
                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                           US2003045460-A1
                                                                                                                                                                                          Unidentified
             18-DEC-2003
                                                                                                                                                                                                                                                                                                                                         06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                               (FOGE/)
(ANAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAVA/)
disease, AIDS, osteoporosis, coronary calcification, calcific aortic stenosis and rheumatoid arthritis. The present sequence is a peptide used to ameliorate one or more symptoms of atherosclerosis
                                                                                                systemic lupus erythematosus; idiopathic pulmonary fibrosis; scleroderma; polymyalgia rheumatica; chronic obstructive pulmonary disease; AIDS; acquired immune deficiency syndrome; tuberculosis; polyarteritis nodosa; Alzheimer's disease; coronary calcification; calcific aortic stenosis; rheumatoid arthritis; osteoporosis; cardiant; neuroprotective; nootropic; vasotropic; gastrointestinal; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide, which protects phospholipid against oxidation by oxidizing agent, used for preparing composition for treating or preventing coronary complication associated with acute phase response to inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel peptides having 10-30 amino acids and comprising at least one class A amphipathic helix or D amino acid residue, protecte a phospholipid against oxidation by an oxidising agent and is not the D-18A peptide. Peptides of the invention are useful to treat or prevent a coronary complication, particularly atherosclerosis
                                                                                    complication; atherosclerosis; inflammation; leprosy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             symptoms, associated with an acute phase response to an inflammation, particularly leprosy, tuberculosis, systemic lupus erythematcosus, polymyalgia rheumatica, polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's
                                                       SFnew peptide #17 used to ameliorate symptoms of atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 7; Length 14;
Pred. No. 8.5;
                                                                                                                                                                                                                                                                'note= "Optionally N-terminal acetyl"
                                                                                                                                                                                                                                                                                              /note= "Optionally C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Navab M;
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 29; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anantharamaiah GM,
                                                                                                                                                                                                                                                                                                                                                                                     29-JUN-2001; 2001US-00896841.
                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-2000; 2000US-00645454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              FOGELMAN A M.
ANANTHARAMAIAH G M.
                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-720035/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                      Therapy; coronary
                                                                                                                                                                                                                                                  Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAVAB M.
                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                            US2003045460-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pogelman AM,
                                                                                                                                                                                                       Unidentified
                             18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                        06-MAR-2003.
 AAE39735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (FOGE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NAVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANAN/)
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FOGELMAN A M. ANANTHARAMAIAH G M.

NAVAB M.

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The present invention relates to novel peptides having 10-30 amino acids and comprising at least one class A amphipathic helix or D amino acid residue, protectes a phospholipid against oxidation by an oxidising agent and is not the D-18A peptide. Peptides of the invention are useful to treat or prevent a coronary complication, particularly atherosclerosis symptoms, associated with an acute phase response to an inflammation, particularly leprosy, tuberculosis, systemic lupus erythematosus, polymyalgia rheumatica, polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's disease, AlDS, osteoporosis, coronary calcification, calcific aortic stenosis and rheumatoid arthritis. The present sequence is a peptide used to ameliorate one or more symptoms of atherosclerosis
New peptide, which protects phospholipid against oxidation by oxidizing agent, used for preparing composition for treating or preventing coronary complication associated with acute phase response to inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 7;
Pred. No. 8.5;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI41463 standard; peptide; 14 AA.
                                                                                                                         Claim 10; Page 29; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.1%;
ilarity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFYDKVFEKLKEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI41463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI41463
ID ADI4
XX ADI4
AC ADI4
XX
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Gaps

. 0

2; Indels

Mismatches

1 ALYKRLFKKLKKF 13 | | ::|:|||:| 1 AFYDKVFEKLKEF 13

셤 8

Conservative

AAE39742 standard; peptide; 14 AA.

AAE39742

AAE39742 ID AAE3 XX AC AAE3

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/note= "N-terminal acetyl"
                    Location/Qualifiers
                                                            /note= "C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | ::|:||:|
1 AFYDKVFEKLKEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKRLFKKLKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                        WPI; 2004-061012/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003171277-A1.
                                                                                 US2003229015-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14 AA;
                              Modified-site
                                                  Modified-site
                                                                                                                                             24-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-2004
                                                                                                    11-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM79444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM79444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of stimulating the formation and cycling of pre-beta high density lipoprotein-like particles and/or promoting lipid transport and detoxification in a mammal comprising administering to the mammal a peptide or a concatamer of a peptide. The method is useful in stimulating the formation and cycling of pre-beta high density lipoprotein-like particles and/or promoting lipid transport and detoxification in a mammal for treating osteoporosis or atherosclerosis. The present sequence represents the amino acid sequence of a class A peptide analogue.
                                                                                                                                                                                                                                                                                                                                  Stimulating the formation and cycling of pre-beta high density ilpoproteain-like particles or promoting lipid transport and detoxification in a mammal by administering to the mammal a peptide or a concatamer of a peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pre-beta high density lipoprotein-like particle, lipid transport, lipid detoxification, osteoporosis, atherosclerosis.
                                      pre-beta high density lipoprotein-like particle, lipid transport, lipid detoxification; osteoporosis, atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.1%; Score 41; DB 8; Length 14; 53.8%; Pred. No. 8.5; 2; Indels tive 4; Mismatches 2; Indels
                                                                                                              /note= "N-terminal acetyl"
                                                                                                                                                                                                                                                                                           Navab M;
                                                                                                                                    /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; SEQ ID NO 29; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class A peptide peptide analogue #28.
                    Class A peptide peptide analogue #21
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI41470 standard; peptide; 14 AA
                                                                                                                                                                                                                                                                                          Fogelman AM, Anantharamaiah GM,
                                                                                                                                                                                                                             2001US-00896841
2001WO-US026497
                                                                                                                                                                                                                                                   28-JUN-2002; 2002US-00187215
                                                                                                                                                                                                16-OCT-2002; 2002US-00273386
                                                                                                                                                                                                                    2000US-00645454
22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFYDKVFEKLKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                               WPI; 2004-061012/06.
                                                                                                                                                        US2003229015-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14 AA;
                                                                                                   Modified-site
                                                                                                                         Modified-site
                                                                                                                                                                                                                               29-JUN-2001;
                                                                                                                                                                                                                    24-AUG-2000;
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                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI41470;
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ADI41470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis; D-18A peptide; acute phase response; inflammation; tuberculosis; AlDS; Alzheimer's disease; scleroderma; osteoporosis; rheumatoid arthritis; bacterial infection; viral infection; parasitic infection; fungal infection; parasitic infection; fungal infection; organ transplant; wound; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stimulating the formation and cycling of pre-beta high density lippoprotein-like particles or promoting lipid transport and detoxification in a mammal by administering to the mammal a peptide concatamer of a peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endotoxic shock syndrome; implanted prosthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 8;
Pred. No. 8.5;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                     Fogelman AM, Anantharamaiah GM, Navab M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-atherosclerosis class A peptide #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; SEQ ID NO 36; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM79444 standard; peptide; 14 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of a class A peptide analogue.
                                                                                                         29-JUN-2001; 2001US-00896841.
23-AUG-2001; 2001WO-US026497.
28-JUN-2002; 2002US-00187215.
                                                                          2000US-00645454.
16-OCT-2002; 2002US-00273386
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53.8%;
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The invention relates to a new peptide that ameliorates a symptom of atherosclerosis comprising an amino acid sequence that: (i) comprises 10-30 amino acids, at least one class A amphipathic helix and D amino acid residue; (ii) protects a phospholipid against oxidation by an oxidising agent; and (iii) is not the D-18A peptide. The peptide further comprises a protecting group coupled to the amino or carboxyl terminus. It has greater than about 50% amino acid sequence identity with human or mouse apo A-1. The peptide is useful for preparing a composition for ameliorating a symptom of atherosclerosis or mitigating or preventing a coronary complication associated with an acute phase response to an inflammation in a mammal. Mitigating or preventing a coronary complication associated with an acute phase response to an inflammation in a mammal, where the coronary complication is a symptom of the same polypeptide in combination with an all L-form of the same polypeptide. The acute phase response is a symptom of a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propose a propo
                                                                                                                                                                                                                                                                                     New peptide, useful for preparing a composition for ameliorating a symptom of atherosclerosis or mitigating or preventing a coronary complication associated with an acute phase response to an inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, a disease comprising tuberculosis, AIDS, Alzheimer's disease, scleroderma, osteoporosis or rheumatoid arthritis, or a condition comprising bacterial, viral, parasitic or fungal infection, organ transplant, wound, sepsis, endotoxic shock syndrome or implanted prosthesis. The present sequence represents a class A peptide of the
                                                                                                                                                                                                 Navab M;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; SEQ ID NO 36; 92pp; English.
                                                                                                                                                                                                 Anantharamaiah GM,
                                         28-JUN-2002; 2002US-00187215.
                                                                                   2000US-00645454
2001US-00896841
                                                                                                                                                     (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                             WPI; 2004-119156/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14 AA;
                                                                                      24-AUG-2000;
29-JUN-2001;
                                                                                                                                                                                                 Fogelman AM,
11-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                a mammal
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Score 41; DB 8; Length 14;
Pred. No. 8.5;
                      2; Indels
                        4; Mismatches
   63.1%;
                                                         1 AFYDKVFEKLKEF 13
                                            1 ALYKRLFKKLKKF 13
           Best Local Similarity 53.6
Matches 7; Conservative
  Query Match
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atherosclerosis; D-18A peptide; acute phase response; inflammation; tuberculosis; AIDS; Alzheimer's disease; scleroderma; osteoporosis; rheumatoid arthritis; bacterial infection; viral infection; parastic infection; fungal infection; parastic infection; fungal infection; organ transplant; wound; sepsis;
                                                                                                                                                                                                                          endotoxic shock syndrome; implanted prosthesis.
                                                                                                                           Anti-atherosclerosis class A peptide #28.
                               ADM79437 standard; peptide; 14 AA.
                                                                                            (first entry)
                                                                                              03-JUN-2004
                                                                                                                                                                                                                                                         Synthetic
                                                              ADM79437;
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US2003171277-A1

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The invention relates to a new peptide that ameliorates a symptom of atherosclerosis comprising an amino acid sequence that: (1) comprises 10-30 amino acids, at least one class A amphigathic helitz and D amino acid residue; (ii) protects a phospholipid against oxidation by an oxidising agent; and (iii) is not the D-18A peptide. The peptide further comprises a protecting group coupled to the amino or carboxyl terminum. It has greater than about 50% amino acid sequence identity with human or mouse apo A-1. The peptide is useful for preparing a composition for amelioration a symptom of atherosclerosis or mitigating or preventing a coronary complication associated with an acute phase response to an inflammation in a mammal. Where the coronary complication is a symptom of the same polypeptide. The acute phase response is atherosclerosis comprises administering the polypeptide in combination with an all L-form of the same polypeptide. The acute phase response is a inflammatory response associated with a recurrent inflammatory disease, a disease comprising tuberculosis, Alzheimer's disease, a disease comprising themeroid arthritis, or a condition comprising bacterial, viral, parasitic or fungal infection, organ transplant, wound, seppis, endocaci schock syndrome or implanted of the processing the present sequence represents a class A peptide of the
                                                                                                                                                                                                                                                                                                                                                                                                New peptide, useful for preparing a composition for ameliorating a symptom of atherosclerosis or mitigating or preventing a coronary complication associated with an acute phase response to an inflammation
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apoA-I like peptide; atherosclerosis; statin; antiatherosclerotic;
cerebroprotective; osteopathic; dermatological; noctropic;
neuroprotective; anti-HIV; stroke; polymyalgia rheumatica;
polyarteritis nodosa; scleroderma; lupus erythematosus;
idiopartic pulmonary fibrosis; chronic obstructive pulmonary disease;
Alzheimer's disease; AIDS; coronary calcification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 8; Length 14;
Pred. No. 8.5;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                            Fogelman AM, Anantharamaiah GM, Navab M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; SEQ ID NO 29; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.1%;
53.8%;
                                                             28-JUN-2002; 2002US-00187215
                                                                                                                          24-AUG-2000; 2000US-00645454.
29-JUN-2001; 2001US-00896841.
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                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
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1 AFYDKVFEKLKEF
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                                                                                                                                                                                                                                                                                                                                         WPI; 2004-119156/12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in a mammal.
11-SEP-2003
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Gaps

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Indels

5

Mismatches

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7; Conservative
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Modified-site
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Matches
                                                                                                                                                                                                                                                                                                                                            RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                   ADS87801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eliminating decalcification of a bone and by inducing recalcification of a bone. (1) is useful for inhibiting a symptom of a disease such as polymyalgia rheumatica, polyarteritis nodosa, scleroderma, lupus erythematosus, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's disease, AlDS, coronary calcification, or calcific aortic stenosis. The present sequence represents an apoA-I like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reduce or eliminate one or more symptoms of osteoporosis by reducing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcific aortic stenosis. The present sequence represents an apoA-I like peptide, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel synthetic apo-A-I like peptides (e.g., D-4F), having class A amphipathic helix, stimulates formation and cycling of pre-beta high density lipoprotein-like particles and thus useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mammal, where (I) is administered in a concentration sufficient
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                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                        /note= "acetylated"
                                                                                                                                                                                                                                                                                                                                  /note= "amidated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2002; 2002US-00273386.
25-APR-2003; 2003US-00423830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-2003; 2003WO-US032442
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                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                     Modified-site
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                                                 Synthetic
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DB 8; Length 14;

Score 41; DB 8 Pred. No. 8.5;

63.1**%**; 53.8**%**;

Best Local Similarity

Query Match

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dermatological, nootropic, neuroprotective and anti-HIV activities, and can be used to stimulate the formation and cycling of pre-beta high density lipoprotein-like particles, to promote lipid transport and detoxification, to prevent formation of oxidised phospholipids, to reduce decalcification of bone, and to induce recalcification of bone. (I) is useful for mitigating one or more symptoms of atherosclerosis in a mammal (human or non-human) by administering (I) to the mammal, where (I) is in an excipient and administered as a unit dosage formulation. The mammal is a mammal diagnosed as having one or more symptoms of atherosclerosis or at risk for stroke or atherosclerosis. (I) is useful for enhancing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptides (I) that ameliorate one or more symptoms of atherosclerosis. Also described is a formulation (II) comprising: a statin; and a peptide or a concatamer of a peptide that: ranges in length from 10-30 amino acids; comprises at least one class A amphipathic helix; protects a phospholipid against oxidation by an oxidiating agent; and is not the D-18A peptide. (I) has antiatherosclerotic, cerebroprotective, osteopathic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes synthetic apolipoprotein (apo) A-I like
                                                                                                                                                                                                                                                                                                                                                                                                                              obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel synthetic apo-A-I like peptides (e.g., D-4F), having class A amphipathic helix, stimulates formation and cycling of pre-beta high density lipoprotein-like particles and thus useful for treating
                                                                                                                                                                                                                                                                                                                apolipoprotein A-I; apoA-I; apolipoprotein A-I like peptide; apoA-I like peptide; atherosclerosis; statin; antiatherosclerotic; cerebroprotective; osteopathic; dermatological; nootropic; neuroprotective; anti-HIV; stroke; polymyalgia rheumatica; polyarteritis nodosa; scleroderma; lupus erythematosus; idiopathic pulmonary fibrosis; chronic obstructive pulmonary disease; Alzheimer's disease; AlbS; coronary calcification;
                                                                                                                                                                                                                                                                                Atherosclerosis ameliorating apoA-I like peptide SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Navab M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "acetylated"
                                                                                                                                                  ADS87801 standard; peptide; 14 AA.
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25-APR-2003; 2003US-00423830.
                                                                                                                                                                                                                                      (first entry)
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1 ALYKRLFKKLKKF
                                          1 AFYDKVFEKLKEF
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            chosen from cerivastatin, atorvastatin, simvastatin, pravastatin, fluvastatin, locastatin, rosuvastatin, and pitavastatin, [I] is administered simultaneously with the statin, or administered before or after the statin. (I) and/or the statin are administered as a unit dosage formulation. (I) is useful for mitigating one or more symptoms associated with atherosclerosis in a mammal by administering (I) and statin to the mammal, where the amount of statin is lower than the amount of statin administered without the peptide. The peptide is lower than the peptide administered without the statin. (I) is useful for reducing or inhibiting one or more symptoms of osteoporosis in a mammal by administering (I) to the mammal, where (I) is administered in a concentration sufficient to reduce or eliminate one or more symptoms of osteoporosis by reducing or eliminating decalcification of a bone and by inducing recalcification of
                                                                                                                                                                                                                             a bone. (I) is useful for inhibiting a symptom of a disease such as polymyalgia rheumatica, polyarteritis nodosa, scleroderma, lupus erythematosus, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's disease, AlbS, coronary calcification, or calcific aortic stenosis. The present sequence represents an apoA-1 like peptide, which is used in the exemplification of the present invention.
activity of a statin in a mammal by coadministering (I) with the statin
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial; antifungal; antitumour; pharmaceuticals; antibiotics; antiparasitic; spermicides; burns; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 8; Length 14;
Pred. No. 8.5;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amphiphilic peptide to inhibit growth of a target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "acylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR22864 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-00554422.
91US-00725331.
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                                                                                                                                                                                                                                                                                                                                                                                    63.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blondelle S;
                                                                                                                                                                                                                                                                                                                                                                      | | ::|:|||:|
1 AFYDKVFEKLKEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                                                                   Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Modified-Bite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghten RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
22-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR22864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR2286
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Method for inhibiting target cell and virus growth - comprises administering amphiphilic peptide compsns, useful for treating viral and phytopathogenic infections, tumours and burns.

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                           The amphiphilic peptide (SEQ ID NO 43) was prepd. by standard solid phase methods. The peptide is an analogue of the peptide having SEQ ID NO 3 (ARR22824), with His substituted for Leu at position 4. Substitution and deletion analogues of this peptide have increased biological activity and are effective as pharma ceuticals e.g. antibiotics for bacterial, fungal or viral infections, or in spermicides or antitumour or antiparasitic agents. Additionally the peptides can be used in wound healing compsns. or for treating burns or other skin or eye infections. See also AAR22822-89. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of sperm and hence have application in a spermicide preparation. They also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. AAR20969 and AAR20970 were published in Haighten and Ostresh, Bio Chromatography, Vol 2, issue 2, page 80-83, 1987. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphiphilic peptide; anti-microbial; anti-viral; anti-tumour; spermicide; wound healing; sterilant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for inhibiting target cell and virus growth - comprises administering amphiphilic peptide compsns, useful for treating viral and phytopathogenic infections, tumours and burns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The peptides of the invention are effective pharmaceuticals having anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of amphiphilic peptide SEQ ID No. 43 which may be a C-terminal amide and maybe acetylated at N-terminus.
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                         Score 41; DB 2;
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR21380 standard; peptide; 18 AA
Claim 9; Page 51; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 51; 72pp; English.
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                                                                                                                                                                                                                                                            63.1%;
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                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                 2 LYKRLFKKLKK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-064700/08.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                            Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 30
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& × 0 0 0 0 0 0 0 0 0 0 0 × 8
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The invention relates to an apolipoprotein (apo) A-1 mimetic peptide (I, ABB83703-ABB83708) that ameliorates a symptom of atherosclerosis, comprising a sequence of 10-30 amino acids, at least one class A amphipathic helix, at least one D amino acid residue and which protects a phospholipid against oxidation by an oxidising agent. (I) is not the D-18A peptide, DWLKARYDKVARKLKEAR. (I) is useful for ameliorating a symptom of atherosclerosis in a mammal diagnosed as having one or more symptoms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel apolipoprotein A-1 mimetic peptide useful for ameliorating symptom
     polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis,
(AIDS), polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis chronic obstructive pulmonary disease, coronary calcification, calcific acrtic stenosis, osteoporosis, rheumatorid arthritis, or inflammatory response associated with bacterial, viral, fungal infection, an organ transplant, a wound, an implanted prosthesis, parasitic infection, sepsis, endotoxic shock syndrome, and biofilm formation. (I) is highly stable, has elevated serum half-life and readily administered by oral route even when the amino and/or carboxy termini are blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apolipoprotein A-1; Apo; atherosclerosis; Alzheimer's disease; acquired immunodeficiency syndrome; AIDS; osteoporosis; rheumatoid arthritis; biofilm formation; antiatherosclerotic; antiinflammatory; antileprotic; tuberculostatic; dermatological; osteopathic; antirheumatic; antiarthritic; antibacterial; virucide; fungicide; antiparasitic; vulnerary; immunosuppressive; vasotropic; anti-HIV; nootropic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of atherosclerosis in a mammal, comprises at least one class A amphipathic helix and a D-amino acid.
                                                                                                                                                                                                                                                                       DB 5; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein A-1 mimetic peptide SEQ ID NO 11.
                                                                                                                                                                                                                                                                                        Pred. No. 11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-termnal amide"
                                                                                                                                                                                                                                                                       Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB83712 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 85; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2000; 2000US-00645454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2001; 2001WO-US026497
                                                                                                                                                                                                                                                                       63.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                 1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                                                                                                                                                                                               S AFYDKVFEKLKEF 17
                                                                                                                                                                                                                                                                                      Local Similarity 53.8
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-463036/49.
                                                                                                                                                                                                                       Sequence 18 AA;
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                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                      Matches
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     888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an apolipoprotein (apo) A-1 mimetic peptide (I, ABB83703-ABB83786) that ameliorates a symptom of atheroselerosis, comprising a sequence of 10-30 amino acids, at least one class A amphipathic helix, at least one D amino acid residue and which protects a phospholipid against oxidation by an oxidising agent. (I) is not the D-18 A peptide, DWLKAFYDKVARKLKBAF. (I) is useful for ameliorating a symptom of atheroselerosis in a mammal diagnosed as having one or more symptom of atheroselerosis, or at risk for atheroselerosis and for mitigating or preventing a coronary complication (a symptom of atheroselerosis) associated with an acute phase response to an inflammation in a mammal. The acute phase response is an inflammatory response associated with a ceurrent inflammatory disease, such as leprosy, tuberculosis, systemic lupus erythematosus, polymyalgia rheumatica, polymatteritis nodosa, clubus erythematosus, polymyalgia rheumatica, polymyarteritis nodosa, clease, Alzheimer's disease and acquired immunodeficiency syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel apolipoprotein A-1 mimetic peptide useful for ameliorating symptom of atherosclerosis in a mammal, comprises at least one class A amphipathic helix and a D-amino acid.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein A-1, Apo, atherosclerosis, Alzheimer's disease, acquired immunodeficiency syndrome; AIDS; osteoporosis; rheumatoid arthritis; biofilm formation; antiatherosclerotic; antiinflammatory; antileprotic; tuberculostatic; dermatological; osteopathic; antirheumatic; antiarthritic; antibacterial; virucide; fungicide; antiparasitic; vulnerary; immunosuppressive; vasotropic;
                                                                                                                             .
                                                                           Length 18;
                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apolipoprotein A-1 mimetic peptide SEQ ID NO 18.
                                                                           DB 2;
                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "N-terminal acetyl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Navab
                                                                           Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-HIV; nootropic; neuroprotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          ABB83719 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-2001; 2001WO-US026497
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                                                                           63.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                          8; Conservative
                                                                                                                                                                          2 LYKRLFKKLKK 12
                                                                                                                                                                                                   3 LHKKLLKKLKK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-463036/49.
                                                                           Query Match
Best Local Similarity
                                Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                            ABB83719;
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                RESULT 31
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preventing a coronary complication (a symptom of atherosclerosis)

preventing a coronary complication (a symptom of atherosclerosis)

associated with an acute phase response to an inflammation in a mammal.

The acute phase response is an inflammation in a mammal.

The acute phase response is an inflammatory response associated with a recurrent inflammatory disease, such as leprosy, tuberculosis, systemic lupus erythematosus, polymyalgia rheumatica, polyarteritis nodosa,

cleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's disease and acquired immunodeficiency syndrome (AIDS), polyarteritis nodosa, scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, coronary calcification, calcific chronic obstructive pulmonary disease, coronary calcification, cartic stenosis, osteoporosis, rheumatoid arthritis, or inflammatory response associated with bacterial, viral, fungal infection, an organ transplant, a wound, an implanted prosthesis, parasitic infection, caspois, endotoxic shock syndrome, and biofilm formation. (I) is highly stable, has elevated serum half-life and readily administered by oral croute even when the amino and/or carboxy termini are blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       systemic lupus erythematosus; idiopathic pulmonary fibrosis; scleroderma; polymyalgia rheumatica; chronic obstructive pulmonary disease; AIDS; acquired immune deficiency syndrome; tuberculosis; polyarteritis nodosa; Alzheimer's disease; coronary calcification; calcific aortic stenosis; rheumatoid arthritis; osteoporosis; cardiant; neuroprotective; nootropic; vasotropic; gastrointestinal; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide, which protects phospholipid against oxidation by oxidizing agent, used for preparing composition for treating or preventing coronary complication associated with acute phase response to inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Therapy; coronary complication; atherosclerosis; inflammation; leprosy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFnew peptide #6 used to ameliorate symptoms of atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                            63.1%; Score 41; DB 5; Length 18; 53.8%; Pred. No. 11; 2; Indels ive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Optionally N-terminal acetyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Optionally C-terminal amide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE39724 standard; peptide; 18 AA.
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(ANAN/) ANANTHARAMAIAH G M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S AFYDKVFEKLKEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 1
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 33
AAE39724
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                              and comprising at least one class A amphipathic helix or D amino actains residue, protects a phospholipid against oxidation by an oxidising agent and is not the D-18A peptide. Peptides of the invention are useful to treat or prevent a coronary complication, particularly atherosclerosis symptoms, associated with an acute phase response to an inflammation, polymyalgia rheumatica, polymyalgia special, opporteritis nodosa, scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's disease, ALDS, osteoporosis, coronary calcification, calcific aortic stenosis and rheumatoid arthritis. The present sequence is a peptide used to ameliorate one or more symptoms of atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       systemic lupus erythematosus, idiopathic pulmonary fibrosis, scleroderma, polymyalgia rhematica, chronic obstructive pulmonary disease, AIDS, acquired immune deficiency syndrome, tuberculosis, polyarteritis nodosa, Alzheimer's disease, coronary calcification, calcific stenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agent, used for preparing composition for treating or preventing coronary complication associated with acute phase response to inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis; osteoporosis; cardiant; neuroprotective; nootropic; vasotropic; gastrointestinal; dermatological.
                                           The present invention relates to novel peptides having 10-30 amino acids and comprising at least one class A amphibathic helix or D amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptide, which protects phospholipid against oxidation by oxidizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Therapy; coronary complication; atherosclerosis; inflammation; leprosy;
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                         Score 41; DB
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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                Claim 10; Page 29; 59pp; English.
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                                                                                                                                                                                                                                                                                                                         63.1%;
53.8%;
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ANAN/) ANANTHARAMAIAH G M.
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5 AFYDKVFEKLKEF 17
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                                                                                                                                                                                                                                                                                                                                                           7; Conservative
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                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                       Sequence 18 AA;
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ADI41452;
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                                                                             symptoms, associated with an acute phase response to an inflammation, particularly leprosy, tuberculosis, systemic lupus erythematosus, polymyalgia rheumatica, polymretriis nodosa, scleroderma, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's disease, ALDS, osteoporosis, coronary calcification, calcific acric stenosis and rheumatoid arthriis. The present sequence is a peptide used to ameliorate one or more symptoms of atherosclerosis
                    The present invention relates to novel peptides having 10-30 amino acids and comprising at least one class A amphipathic helix or D amino acid residue, protects a phospholipid against oxidation by an oxidising agent and is not the D-18A peptide. Peptides of the invention are useful to treat or prevent a coronary complication, particularly atherosclerosis
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                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of stimulating the formation and cycling of pre-beta high density lipoprotein-like particles and/or
                                                                                                                                                                                                                                                                                                                                                                                                                   pre-beta high density lipoprotein-like particle, lipid transport, lipid detoxification, osteoporosis, atherosclerosis.
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                                                                                                                                                                                              Score 41; DB 7; Length 18; Pred. No. 11;
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                                                                                                                                                                                                                       4; Mismatches
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Claim 10; Page 29; 59pp; English.
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2001US-00896841.
2001WO-US026497.
2002US-00187215.
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53.8%;
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AFYDKVFEKLKEF 17
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                                                                                                                                                                          Sequence 18 AA;
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29-JUN-2001;
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ADI41445
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promoting lipid transport and detoxification in a mammal comprising administering to the mammal a peptide or a concatamer of a peptide. The method is useful in stimulating the formation and cycling of pre-beta high density lipoprotein-like particles and/or promoting lipid transport and detoxification in a mammal for treating osteoporosis or atherosclerosis. The present sequence represents the amino acid sequence of a class A peptide analogue.
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lipid detoxification; osteoporosis; atherosclerosis.
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                                                                                                                                                                                                                                                                                      Score 41; DB
Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class A peptide peptide analogue #10.
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2001US-00896841.
2001WO-US026497.
2002US-00187215.
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    1 ALYKRLFKKLKKF 13
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                                                                                                                                                                                                                                     Sequence 18 AA;
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Modified-site
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The invention relates to a new peptide that ameliorates a symptom of atherosclerosis comprising an amino acid sequence that: (i) comprises 10-30 amino acids, at least one class A amphipathic helix and D amino acid residue; (ii) protects a phospholipid against oxidation by an oxidising agent; and (iii) is not the D-18A peptide. The peptide further comprises or greater than about 50% amino acid sequence identity with human or mouse apo A-1. The peptide to the amino or carboxyl terminus. It has apo A-1. The peptide is useful for preparing a composition for ameliorating a symptom of atherosclerosis or mitigating or preventing a corporation associated with an acute phase response to an inflammation in a mammal. Mitigating or preventing a coronary complication associated with an acute phase response to an inflammation in a mammal. Where the coronary complication is a symptom of a mammal, where the coronary complication is a symptom of a mammal. Where the coronary complication is a symptom of a mammal. The same polypeptide in combination with an all L-form of the same polypeptide. The acute phase response is an inflammatory response associated with a recurrent inflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis; D-18A peptide; acute phase response; inflammation; tuberculosis; AIDS; Alzheimer's disease; scleroderma; osteoporosis; rheumatoid arthritis; bacterial infection; viral infection; parasitic infection; tungal infection; parasitic infection; tungal infection; organ transplant; wound; sepsis;
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                                                                                                                                         Gaps
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                                                                 Score 41; DB 8; Length 18;
Pred. No. 11;
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29-JUN-2001; 2001US-00896841.
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                                                                    63.1%;
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                                                                                                   Local Similarity 53.8
Les 7; Conservative
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Sequence 18 AA;
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                                                                    Query Match
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ADM79426
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The invention relates to a new peptide that ameliorates a symptom of atherosclerosis comprising an amino acid sequence that: (1) comprises 10-30 amino acids, at least one class A amphipathic helix and D amino acid residue; (ii) protectes a phospholipid against oxidation by an oxidising agent; and (iii) is not the D-18A peptide. The peptide further comprises a protecting group coupled to the amino or carboxyl terminus. It has greater than about 50% amino acid sequence identity with human or mouse apo A-1. The peptide is useful for preparing a composition for ameliorating a symptom of atherosclerosis or mitigating or preventing a coronary complication associated with an acute phase response to an inflammation in a mammal. Mitigating or preventing a coronary complication associated with an acute phase response to an inflammation in a mammal. The complication is a symptom of atherosclerosis comprises administering the polypeptide in combination in a mammal. And all Liform of the same polypeptide. The acute phase response is an inflammatory response associated with a recurrent inflammatory disease, a disease comprising tuberculosis, AlDS, Alzheimer's disease, comprising tuberculosis, AlDS, Alzheimer's disease, comprising bacterial, viral, parasite or fungal infection, organ transplant, wound, sepsis, endotoxic shock syndrome or implanted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atherosclerosis; D-18A peptide; acute phase response; inflammation; tuberculosis; AIDS; Alzheimer's disease; scleroderma; osteoporosis; rheumatoid arthritis; bacterial infection; viral infection; parasitic infection; fungal infection; organ transplant; wound; sepsis; endotoxic shock syndrome; implanted prosthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide, useful for preparing a composition for ameliorating a symptom of atherosclerosis or mitigating or preventing a coronary complication associated with an acute phase response to an inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; SEQ ID NO 11; 92pp; English.
                                                                                                                                                                                                                                                                                                          ADM79419 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2002; 2002US-00187215.
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29-JUN-2001; 2001US-00896841.
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                                        Sequence 18 AA;
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invention.
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RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes synthetic apolipoprotein (apo) A-I like peptides (I) that ameliorate one or more symptoms of atherosclerosis. Also described is a formulation (II) comprising: a statin, and a peptide or a concatamer of a peptide that: ranges in length from 10-30 amino acids; comprises at least one class A amphipathic helix; protects a phospholipid against oxidation by an oxidising agent; and is not the D-18A peptide. (I) has antiatherosclerotic, cerebroprotective, osteopathic, dermatological, nootropic, neuroprotective and anti-HIV activities, and can be used to stimulate the formation and cycling of pre-beta high density lipoprotein-like particles, to promote lipid transport and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoA-I like peptide, atherosclerosis, statin, antiatherosclerotic, cerebroprotective, osteopathic, dermatological, nootropic, neuroprotective, anti-HIV, stroke, polymyalgia rheumatica; polyarteritis nodosa; scleroderma, lupus erythematosus; didopathic pulmonary fibrosis, chronic obstructive pulmonary disease; Alzheimer's disease; AlDS; coronary calcification;
                                                                                                                                                           Gaps
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  prosthesis. The present sequence represents a Class A peptide of the
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                                                                                                              Length 18;
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Pred. No. 11;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2002; 2002US-00273386.
25-APR-2003; 2003US-00423830.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calcific aortic stenosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-365082/34.
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                                                                      Sequence 18 AA;
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                         invention.
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detoxification, to prevent formation of oxidised phospholipids, to reduce decalcification of bone, and to induce recalcification of bone. (1) is useful for mitigating one or more symptoms of atherosclerosis in a mammal (human or non-human) by administering (1) to the mammal, where (1) is in an excipient and administered as a unit dosage formulation. The mammal is a mammal diagnosed as having one or more symptoms of atherosclerosis or at risk for stroke or atherosclerosis. (1) is useful for enhancing the chosen from cerivastatin, atorvastatin, simvastatin, pravastatin, chosen from cerivastatin, atorvastatin, and pitavastatin, pravastatin, fluvastatin, lovastatin, rosuvastatin, and pitavastatin, rosuvastatin, atorvastatin, or administered before or after the statin. (1) and/or the statin are administered before or after the statin. (1) is useful for mitigating one or more symptoms associated with a mammal by administering (1) and statin is lower than the peptide coministered without the statin is lower than the amount of statin administered without the statin is lower than the peptide administered without the statin is lower than the peptide administered without the statin is a mammal by administering or inhibiting one or more symptoms of osteoporosis in a mammal by administering or inhibiting or the mammal, where (1) is administered in a concentration sufficient to the mammal, where (1) is administered in a concentration sufficient to the mammal, where (1) is administered in a concentration sufficient to the mammal or more symptoms of estating or process or eliminate one or more symptoms of estating or stating or stating or stating or stating or stating or success or elements of stating or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible or successible o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eliminating decalcification of a bone and by inducing recalcification of a bone. (I) is useful for inhibiting a symptom of a disease such as polymyalgia rheumatica, polyarteritis nodosa, scleroderma, lupus erythematosus, idiopathic pulmonary fibrosis, chronic obstructive pulmonary disease, Alzheimer's disease, AlDS, coronary calcification, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coronary calcification, or erepresents an aboA-I like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcific aortic stenosis. The present sequence represents an apoA-I like peptide, which is used in the exemplification of the present invention.
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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The present invention describes synthetic apolipoprotein (apo) A-1 like present invention describes synthetic apolipoprotein (apo) A-1 like periods (1) that ameliorate one or more symptoms of atherosclerosis.

Also described is a formulation (II) comprising; a statin; and a peptide or a concatamer of a peptide that: ranges in length from 10-10 anno cardes or cardes to exhapt a concatamer of a peptide that: ranges in length from 10-10 anno cardes or cardes to exhapt a concatamer or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or cardes or 
                                                                                                                                                                       Novel synthetic apo-A-I like peptides (e.g., D-4F), having class A amphipathic helix, stimulates formation and cycling of pre-beta high density lipoprotein-like particles and thus useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 8
Pred. No. 11;
4; Mismatches
                                                                                    Navab M;
                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 11; 81pp; English.
                                                                                    Anantharamaiah GM,
                                                                                                                                                                                                                                            atherosclerosis or osteoporosis.
25-APR-2003; 2003US-00423830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.0
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFYDKVFEKLKEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKRLFKKLKKF 13
                                       (REGC ) UNIV CALIFORNIA
                                                                                                                              WPI; 2004-365082/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
                                                                                       Fogelman AM,
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                Gaps
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8; Length 18;
               2; Indels
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AAB13953 standard; peptide; 28 AA.

histatin 5; bacterial; fungal; yeast infection;

99WO-NL000045.

26-JAN-1999; 27-JAN-1998;

98NL-01008139

AAY28969 standard; peptide; 14 AA.

RESULT 42

AAY28969

(first entry)

04-OCT-1999

AAY28969;

Antimicrobial peptide 5.

salivary peptide

#X#XBX#X8X##XBX#X8X#

WO9937678-A2

Synthetic.

29-JUL-1999

Antimicrobial;

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16-NOV-2000 (first entry)
                                                                              Antiviral peptide #19.
                                       AAB13953;
RESULT 41
AAB13953
ID AAB13
XX
AC AAB13
XX
DT 16-NO
XX
DE Antiv
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The present invention relates to antiviral peptides containing a domain of 10-25 amino acids, where half the domain is positively charged and the other half is uncharged. The present sequence is an antiviral peptide of the invention. Oligomers consisting of at least two peptides coupled together are also included in the invention. The peptides are useful for treating viral infections such as human immunodeficiency virus (HIV) and herpes simplex virus (HSV) and for the treatment of cold sores, aphthous ulcers and viral bronchial infections
                                                                                                                                                                                                                                                                                                                                                                                          Antiviral peptides comprising a domain of 10-25 amino acids, half of which is positively charged and half uncharged, useful for treatment of human immunodeficiency virus and herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps.
                                                                                                                                                                                                                                                                                                                               Van 'thof W, Nibbering PH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
              virus, HIV;
           Antiviral, antiulcer, human immunodeficiency virus, HI herpes simplex virus; HSV; cold sore; aphthous ulcer; viral bronchial infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 63.1%; Score 41; DB 3 Local Similarity 100.0%; Pred. No. 16; es 8; Conservative 0; Mismatches
                                                                                                                                        /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                               Veerman ECI,
                                                                                                                                                                                                                                                                                                (TEWE-) STICHTING TECH WETENSCHAPPEN
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 26; Page 5; 20pp; English.
                                                                                                                                                                                                                                                                  98NL-01010692
                                                                                                                                                                                                                                    99WO-NL000732
                                                                                                                                                                                                                                                                                                                               Van Nieuw Amerongen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YKRLFKKL 10
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                                                                                                                                                                      WO200032629-A2
                                                                                                                        Modified-site
                                                                                                                                                                                                                                    01-DEC-1999;
                                                                                                                                                                                                                                                                  01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28
                                                                                                                                                                                                     08-JUN-2000
                                                                           Synthetic
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Matches
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Helmerhorst

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The invention relates to antimicrobial peptides containing a domain of 10 the other half are uncharged, while most in the other half are uncharged. The positively charged, while most in synthesised by modifying the C-terminal sequence of histarin 5 peptide. The peptides are used to treat bacterial, fungal or yeast infections. Typical applications are control of Candida and of bacteria in the mouth, on the skin, in cattle and in foods. These antimicrobial peptides are subject to proteolysis and, being rather small, can be produced relatively inexpensively. They have practically no hemolytic action. The present sequence represents a specific example of the antimicrobial
                                                                                                     New antimicrobial peptides with two domains containing mostly positively charged or uncharged amino acids, e.g. for treating bacterial or fungal infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiviral peptides comprising a domain of 10-25 amino acids, half of which is positively charged and half uncharged, useful for treatment of human immunodeficiency virus and herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Veerman ECI, Van 'thof W, Nibbering PH;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 2; Length 14;
Pred. No. 12;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antiviral; antiulcer; human immunodeficiency virus; HIV; herpes simplex virus; HSV; cold sore; aphthous ulcer; viral bronchial infection.
                                           Veerman ECI, Van't Hof W,
            (TEWE-) STICHTING TECH WETENSCHAPPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEWE-) STICHTING TECH WETENSCHAPPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB13939 standard; peptide; 14 AA
                                                                                                                                                                   Claim 10; Page 19; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                61.5%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-NL000732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type 1 antiviral peptide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Nieuw Amerongen A,
                                           Van Nieuw Amerongen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-412289/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Claim 15; Page 7; 20pp; English.

Gaps

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The present invention relates to antiviral peptides containing a domain of 10-25 amino acids, where half the domain is positively charged and the other half is uncharged. The present sequence is a type 1 antiviral peptide. Oligomers consisting of at least two peptides coupled together are also included in the invention. The peptides are useful for treating viral infections such as human immunodeficiency virus (HIV) and herpes simplex virus (HSV) and for the treatment of cold sores, aphthous ulcers and viral bronchial infections
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel conjugates of an antifungal peptide and a mucoadhesive polymer which have antifungal and cytostatic activity. The conjugates can be used to treat tumors and yeast, fungal and bacterial infections of the oral cavity, skin and vagina, especially yeast infections caused by Candida albicans and bacterial infections caused by Staphylococcus aureus, especially the methicillin-resistant strain MRSA. The polymer provides prolonged residence times at the site of infection, which compensates for the lower activity of the conjugates compared with the free peptides. AAY50848-Y50865 represent peptides used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antifungal peptide; mucoadhesive polymer; cytostatic; treatment; tumor; yeast infection; fungal infection; bacterial infection; oral cavity; skin; vagina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide conjugates useful for treating yeast, fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Der Reijden WA;
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                                                                                                                                                                                                              Gaps
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                                                                                                                                                                               Length 14;
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                                                                                                                                                                                                              Indels
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                                                                                                                                                                                , DB 3;
. 12;
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Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Veerman ECI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TEWE-) STICHTING TECH WETENSCHAPPEN.
                                                                                                                                                                                                                                                                                                                                                         AAY50852 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 9; 23pp; Dutch.
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                                                                                                                                                                                61.5%;
88.9%;
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ilarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Nieuw Amerongen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infections and tumors.
                                                                                                                                                                                                                                             4 KRLFKKLKK 12
                                                                                                                                                                                                                                                                           1 KRLFKELKK 9
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Matches 8; Conserv
                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antifungal peptide
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                                                                                                                                                   Sequence 14 AA;
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                                                                                                                                                                                                                Matches
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AAY77083 standard; peptide; 14 AA.
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KRLFKKLKK 12
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1 KRLFKELKK 9
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                                                                                                                                                                                                                                                        AAY77083;
                                                                                                                                        RESULT 45
                                                                                                                                                                MAY77083

MAY77083

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The invention relates to a novel bone material for the prevention and treatment of osteomyelitis. This material makes use of a resorbable calcium phosphate cement, and a new class of antibiotic agents, the antimicrobial peptides (AMPB). The AMPB consist of an amino acid chain containing a domain of 10-25 amino acids, where the majority of the amino acids of the one half of the domain are positively charged amino acids (hydrophilic) and the majority of the amino acids of the other half of the domain are uncharged amino acids (hydrophilic) and the majority of the amino acids of the other half of the domain are uncharged amino acids (hydrophilic). The AMPB can be the surrounding area over a period of time. After curing, the bone material forms bone cement, and can serve as bone replacement. The bone material can be used for the prevention and treatment of infections of bone (osteomyelitis) and the surrounding soft tissues. The peptides have a wide spectrum of amibacterial and antifungal activity, even against mechicillin-resistant Stabylococcus aureus (MRSA), Pseudomonas acruginosa, and amphotericin-Bresistant Candida albicans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             granules which release antibiotics. However, PMMA granules are non-
resorbable, requiring an additional operation to remove them. Sequences
AAY77081-Y77088 represent type I AMPS, which form laterally amphipathic
alpha helices (i.e. a maximum hydrophobic moment of 100 degrees), and
which are claimed for use in the bone material of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         have low toxicity. Prior art methods of preventing bone/soft tissue infections after surgery make use of polymethyl methacrylate (PMMA)
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Antimicrobial peptide; AMP type I; alpha helix; amphipathic; antibiotic; antibacterial; antifungal; bone infection; treatment; prevention; bone material; bone cement; bone replacement; osteomyelitis; soft tissue infection; orthopaedic surgery.
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Antimicrobial peptide 5, used to treat and prevent bone infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Nieuw Amerongen A, Wuisman PIJM;
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|||||:||| 1 KRLFKELKK 9

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Search completed: May 16, 2005, 08:38:33 Job time : 55.1293 secs

Sequence 14 AA;

Query Match
Best Local Similarity 88.9
Matches 8; Conservative

4 KRLFKKLKK 12

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Gaps

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61.5%; Score 40; DB 3; Length 14; 88.9%; Pred. No. 12; ive 1; Mismatches 0; Indels

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TYPE: PRT
ORGANISM: Artificial Sequence
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JS-09-525-269A-13
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Best Local S
Matches 13
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                                                          May 16, 2005, 08:21:21; Search time 13.8966 Seconds (without alignments) 69.833 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/ROTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-525-269A-11

US-08-233-203-10

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US-08-760-903-2

US-08-760-903-2

US-08-760-903-3

US-08-760-903-3

US-08-760-903-3

US-08-645-454-29

US-09-645-454-11

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US-09-645-454-11

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                                                                                                                                                           513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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seq length: 74
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63.1
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OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon OTHER INFORMATION: microbiocidal domains from platelet microbial OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
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| Sequence 11, Application US/09525269A
| Patent No. 6743769 |
| GENERAL INPORMATION: APPLICANT: Yeaman, Michael R. |
| APPLICANT: Yeaman, Michael R. |
| APPLICANT: Shen, Alexander J. |
| TITLE OF INVENTION: Metapeptides and Derived ITILE OF INVENTION: Metapeptides |
| TITLE OF INVENTION: MORBRE: US/09/52,269A |
| CURRENT APPLICANION NUMBER: US/09/025,319 |
| PRIOR FILING DATE: 1998-02-18 |
| NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 65; DB 4; Lilarity 100.0%; Pred. No. 0.00098; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yeaman, Michael R.
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Matimicrobial Peptides and Dex;
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 13
US-07-725-331-54
US-07-725-331-55
US-07-725-331-55
PCT-US91-05047-47
PCT-US91-05047-47
PCT-US91-05047-54
PCT-US91-05047-55
US-07-725-331-5
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US-07-725-331-22
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FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                        1 ALYKRLFKKLKKF 13
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Best Local Similarity 90.9
Matches 10; Conservative
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1 ALYKKLLKKLLKF
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US-09-525-269A-12
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APPLICANT: Darveau, Richard P.
APPLICANT: Darveau, Anne J.
APPLICANT: Cosand, Welly L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                  CTHER INFORMATION: Antimicrobiocidal peptide designed in part upon CTHER INFORMATION: microbiocidal domains from platelet microbial; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits US-09-525-269A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.4%; Score 49; DB 1;
Best Local Similarity 76.9%; Pred. No. 0.33;
Matches 10; Conservative 1; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11 LENGTH: 13
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 266/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08233203 Patent No. 5409898
                                                                                                                                                                                                                                       75.4%;
                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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LENGTH: 18 amino acids
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Best Local Similarity
Matches 10; Conserva
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HYPOTHETICAL:
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ZIP: 98121
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STATE:
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us-08-233-203-7
; Sequence 7, Application US/08233203
; Patent No. 540999
; GENERAL INFORMATION:
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washin--
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OTHER INFORMATION: Antimicrobiocidal peptide designed in part upon
OTHER INFORMATION: microbiocidal domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-12
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Sequence 12, Application US/09525269A

Patent No. 6743769

GENERAL INFORMATION:
APPLICANT: Seaman, Michael R.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
TITLE OF INVENTION: Metapeptides
FILE REFERENCE: 66742-025 (HRS614)
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 12
LENTH: 13
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COMPUTER READABLE FORM:
MEDIUM TUPER Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
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0; Gaps

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Sequence 2, Application US/08760903
| Patent No. 598381
| GENERAL INFORMATION:
| APPLICANT: SHEKHANI, MOHAWMED S. APPLICANT: FIRCA, JOSEPH R. APPLICANT: ANDERSON, BYRON, TITLE OF INVENTION: COMPOUNDS THAT BIND BACTERIAL PILLI NUMBER OF SEQUENCES: 9
| CORRESPONDENCE ADDRESS: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: 
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                                                                                                                                 DB 1; Length 18;
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                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
FILING DATE: 06-DEC-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SOUMOFF, CYNTHIA
REGISTRATION NUMBER: 0PHD-02557
TELECOMMUNICATION NUMBER: 0PHD-02557
TELECOMMUNICATION NUMBER: 0PHD-02557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-838
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    Score 43; DB 1
Pred. No. 2.6;
1; Mismatches
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Pred. No. 2
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Sequence 2, Application US/08482191
Sequence 2, Application US/08482191
Setent No. 6579696
APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: SCHATZ, ROBERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UNITED STATES OF AMERIC ZIP: 94104
COMPUTER READABLE FORM:
COMPUTER: FLODDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.2%;
75.0%;
                                                                                                                                    66.2%;
75.0%;
                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 9, Conservative
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Best Local Similarity 75.0
Matches 9; Conservative
      peptide
YES
                                                                                                                                                                                                                                                            1 ALYKRLFKKLKK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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STRANDEDNESS: si
      ; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-233-203-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-760-903-2
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Patent No. 540989
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98121
MEDIUM TYPER READABLE FORM:
MEDIUM TYPER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB :
Pred. No. 2.6;
1; Mismatches
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERNICE/DOCKET NUMBER: 0N0063A
TELEPHONE: 206/728-4800
TELEPHONE: 206/448-475
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 514.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTOCNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.2%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                             18 amino acida
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ALYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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US-08-233-203-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
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                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
TILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFESTENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUCHWARD.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,903
PTI.ING DATE: 06-DEC-1996
                                                       UNITED STATES OF AMERICA
                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 75.v.
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                     COMPUTER READABLE FORM:
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STRANDEDNESS: si
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                                                         COUNTRY:
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APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WILLIAMS, JAMES A.
APPLICANT: SHEKIANI, MCHANMED S.
APPLICANT: PIRCA, JOSEPH R
APPLICANT: PIRCA, JOSEPH R
APPLICANT: PUGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK WR., NICHOLAS
APPLICANT: PUGH, CHARLES
APPLICANT: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES:
ADDRESSE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STRATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 18;
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SOFTWAREN APPLICATION DATA:

APPLICATION NUMBER: US/08/482,191
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/164,067
FILING DATE: US 08-DEC-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/995,388
FILING DATE: 21-DEC-1992
ATTORNEY/AGENT INPORMATION:

NAME: CRRENIL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEI/NOBL,
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                       STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-482-191-2
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                                                                                                                                                                                                                                                                         Indels
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APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: FIRCA, JOSEPH R
APPLICANT: FORM. CHARLES
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUPTRY: UNITED STATES OF AMERICA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.2%; Score 43;
                                                                                                                                                                                                                Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
FILING DATE:
APPLICATION NUMBER: US 08/482,191
FILING DATE: 07-40N-1995
APPLICATION NUMBER: US 08/169,701
FILING DATE: 17-DEC-1993
PRICR APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRICR APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
FILING DATE: 12-DEC-1992
FILING DATE: 21-DEC-1997
ATTORNEY AGENT INFORMATION:
WANTER CARRET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPHD-01280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application PC/TUS9610227
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                66.2%;
19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 amino acids
                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                   1 ALYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKKLIKKLIK 12
                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-482-191-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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APPLICANT: SHEKHANI, MOHAMMED S.
APPLICANT: SHEKHANI, MOSEPH R.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: PUGH, CHARLES
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: PANASIK JR., NICHOLAS
APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: PREVENTION AND TREATMENT OF SEPSIS
CORDER PROVENTION: PREVENTION AND TREATMENT OF SEPSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNEY: CALLFORALA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,191
FILING DATE: U7-JUN-1995
CLASSIFICATION NUMBER: US 08/169,701
PILING DATE: 17-DEC-1993
PRIOR APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 08/164,067
FILING DATE: 08-DEC-1993
PRIOR APPLICATION NUMBER: US 08/164,067
FILING DATE: US DEC-1993
PRIOR APPLICATION NUMBER: US 07/995,388
FILING DATE: 1-DEC-1993
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT INFORMATION:
AMERICAL DATE: 1-DEC-1992
ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT ATCHNEY/AGENT 
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220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.2%; Score 43; DB 75.0%; Pred. No. 2.7; tive 1; Mismatches
                         NAME: SOUMOFF, CYNTHIA
RECISTRATION NUMBER: 38,314
REFERENCE/DOCKET NUMBER: OPHD-02557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-01280
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAN FRANCISCO
CALIFORNIA
Y: UNITED STATES OF AMERICA
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Patent No. 6579696
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TELEFAX: (415) 397-8338
INPORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
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                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: WILLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
STREET: 22
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Sequence 43, Application US/07725331

Patent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie

TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof

NUMBER OF SEQUENCES:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow

STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.1%; Score 41; DB 1; Length 18; 72.7%; Pred. No. 5.1;
DB 4; Length 14;
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                                            Indels
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                      Pred. No. 4.1;
4; Mismatches
    Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER: 09/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECHONE: 3126165418
TELEPHONE: 312616540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/09645454
Patent No. 664220
GRNERAL INFORMATION:
APPLICANT: Fogelman, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
  63.1%;
53.8%;
Query Match 63.1
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                      1 ALYKRLFKKLKKF 13
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1 AFYDKVFEKLKEF 13
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Matches 8; Conservative
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3 LHKKLLKKLKK 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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APPLICANT: Anancharamaiah, Gattadahalli
APPLICANT: Anancharamaiah, Gattadahalli
APPLICANT: Anancharamaiah, Gattadahalli
APPLICANT: Navab, Mohamad
TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
FILE REFERENCE: 4077-91120004
CURRENT APPLICATION NUMBER: US/09/645,454
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 36
                                                                                                                                                                                                                                                      APPLICANT: Fogelman, Alan
APPLICANT: Fogelman, Alan
APPLICANT: Fogelman, Alan
APPLICANT: Ananharamaiah, Gattadahalli
APPLICANT: Ananharamaiah, Gattadahalli
APPLICANT: Navab, Mohamad
TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
TITLE OF INVENTION: 0711200US
CURRENT APPLICATION: 08-124
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.0
SEQ ID NO 29
LENGTH: 14
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                          Gaps
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                      2; Indels
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NAME/KEY: misc feature
LOCATION: (1). (1)
OTHER INFORMATION: A is blocked with an acetyl
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: A is blocked with an acetyl NAME/KEY: misc_feature LOCATION: (14)...(14)

LOCATION: (14)...(14)

OTHER INFORMATION: F is blocked with an amide US-09-65-45-45-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) LOCATION: (14); OTHER INFORMATION: F is blocked with an amide US-09-645-454-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 4
Pred. No. 4.1;
4; Mismatches
    Pred. No. 2.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: synthetic peptide NAME/KEY: misc feature LOCATION: (1). (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/09645454 Patent No. 6664230 GENERAL INFORMATION:
APPLICANT: Fogelman, Alan
                                                                                                                                                                                                              Sequence 29, Application US/09645454 Patent No. 6664230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.1%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
  Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | ::|:|||:|
1 AFYDKVFEKLKEF 13
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                1 ALYKRLFKKLKK 12
                                                                                        RESULT 14
US-09-645-454-36
                                                                                                                                                                        RESULT 13
US-09-645-454-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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TYPE: PRT ORGANISM: Artificial Sequence
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STRANDEDNESS:
                                                                                                                                                                                                 COUNTRY: USA
ZIP: 60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US91-05047-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fogelman, Alan
APPLICANT: Rogelman, Alan
APPLICANT: Navab, Mohamad,
APPLICANT: Navab, Mohamad
TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
FILE REFERENCE: 407T-911200US
FURENT FILING APPLICATION NUMBER: US/09/645,454
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 18
            APPLICANT: Navab, Mohamad,
TITLE OF INVENTION: Orally Administered Peptides to Ameliorate Atherosclerosis
FILE REFERENCE: 4077-91120003
CURRENT APPLICATION NUMBER: US/09/645,454
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 18
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Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 4; Length 18;
Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: synthetic peptide
NAME/KEY: misc. feature
(1). (1). (1)
OTHER INFORMATION: E is blocked with an acetyl
                                                                                                                                                                                                                                                          ) OTHER INFORMATION: synthetic peptide
) NAWE/KEY: misc_feature
| LOCATION: (1)...(1)
| OTHER INFORMATION: D is blocked with an acetyl
| NAME/KEY: misc_feature
| LOCATION: (18)...(18)
| OTHER INFORMATION: F is blocked with an amide
| US-09-645-454-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , LOCATION: (18)...(18); OTHER INPORMATION: F is blocked with an amide US-09-645-454-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
Anantharamaiah, Gattadahalli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application PC/TUS9105047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 17
US-09-645-454-18
US-09-645-454-18
; Sequence 18, Application US/09645454
; Patent No. 6664230
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houghten, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.1%;
53.8%;
                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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5 AFYDKVFEKLKEF 17
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Best Local Similarity 53.8
Matches 7; Conservative
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5 AFYDKVFEKLKEF 17
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                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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Gaps
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Amphiphilic Peptide Compositions and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Van Nieuw Amerongen, Arie
APPLICANT: Van Nieuw Amerongen, Arie
APPLICANT: Veerman, Engelmundus Cornelis Ignatius
APPLICANT: Veerman, Engelmundus Cornelis Ignatius
APPLICANT: Ven't Hof, Wilem
APPLICANT: Helmerhorst, Eva Josephine
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: 702 001448
CURRENT APPLICATION NUMBER: US/09/601,124
CURRENT APPLICATION NUMBER: PCT/NL99/00045
PRIOR APPLICATION NUMBER: PCT/NL99/00045
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Microsoft Word 97 SR-2
SEQ ID NO 3
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: May be a C-terminal amide, m
OTHER INFORMATION: be acetylated at N-terminus.
                                                              CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow STREBT: 180 North Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
2
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Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                 MEDIUM TIPE: FIORPY GIBN
COMPUTER: TEAPLY GIBN
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEATENT Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                   Analogues Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION:
TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09601124
Patent No. 6638531
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 18 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|:| |||||
3 LHKKLLKKLKK 13
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ORGANISM: Artificial Sequence AFATURE: OFFICE OF ON ONE SIGE, hydrophic on the OTHER INFORMATION: Peptide of Type I (hydrophobic on one side, hydrophilic on the OTHER INFORMATION: other side) having antimicrobial activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 14
COTHER INFORMATION: Modified peptide having antimicrobial activity
COTHER INFORMATION: Two identical amino acid chains of this composition
COTHER INFORMATION: are linked to one substituted lysine molecule at this point.
US-09-601-124-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van Nieuw Amerongen, Arie
APPLICANT: Van Nieuw Amerongen, Arie
APPLICANT: Van Veerman, Engelmundus Cornelis Ignatius
APPLICANT: Van V Hof, Wilem
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: 702 001448
CURRENT APPLICATION NUMBER: US/09/601,124
CURRENT FILING DATE: 1909-01-13
FRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 21
SOUTHARRE: Microsoft Word 97 SR-2
SEQ ID NO 7
IENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09601124
Patent No. 6638531
GENERAL INFORMATION:
APPLICANT: Van Nieuw Amerongen, Arie
APPLICANT: Van THOUW Amerongen, Arie
APPLICANT: Van Thou, Willen
APPLICANT: Veerman, Engelmundus Cornelis Ignatius
APPLICANT: Veerman, Engelmundus Cornelis Ignatius
APPLICANT: Veerman, Engelmundus Cornelis Ignatius
APPLICANT: Veerman, Engelmundus Cornelis Ignatius
APPLICANT: Helmerhorst, Reva Josephine
TITLE OF INVENTION: Antimicrobial Peptides
FILER REPERENCE: 702 001448
CURRENT APPLICATION NUMBER: US/09/601,124
CURRENT FILING DATE: 1209-01-26
NUMBER OF SEQ ID NOS: 21
SOFTHARE: Microsoft Word 97 SR-2
SEC ID NO I GENERAL INFERDICATION INCOMENTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.0%; Score 39; DB Best Local Similarity 100.0%; Pred. No. 8.2 Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0%; Pred. No. 8.2
Matches 8; Conservative 0; Mismatches
                                                                Sequence 7, Application US/09601124
Patent No. 6638531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE: NAME/KEY: BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KRLFKKLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KRLFKKLK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 22
US-09-601-124-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-601-124-7
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; FEATURE:
; OTHER INFORMATION: Peptide of Type I (hydrophobic on one side, hydrophilic on the
; OTHER INFORMATION: other side) having antimicrobial activity
US-09-601-124-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley, L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                      4; Length 14;
                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                               Score 40; DB 4
Pred. No. 5.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1
Pred. No. 7.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATOMNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERNICE/DOCKET NUMBER: 0N0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08233203 Patent No. 5409898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61.5%;
80.0%;
                                                                                                                                                               Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
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                                                                                                                                                                                                                                                                                                                                     Washington
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 98121
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Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FBE-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOR, BRIAN W.
REGISTRATION NUMBER: 32,928
PERFERENCE/DOCKET NUMBER: ON0063A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: OI TELECOMMUNICATION TELEPHONE: 206/728-4800 TELEPRX: 206/448-4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                       3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.7°
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYKRLFKKLKK 12
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                 COMPUTER READABLE FORM:
                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                           Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60601
                                                                                                          98121
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-233-203-12
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                                  Sequence 11, Application US/08233203
| Patent No. 5409898
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Darveau, Richard P. |
| APPLICANT: Blake, James J. |
| APPLICANT: Blake, James J. |
| APPLICANT: Blake, James J. |
| TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM |
| TITLE OF INVENTION: ANTIBIOTICS |
| NUMBER OF SEQUENCES: 12 |
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08233203
Patent No. 540898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Cosand, Wesley L.
TITLE OF INVENTION: COMPOSITONS AND METHODS FOR TREATING
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Bristol-Myers Squibb Company, Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                 ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: POOR, BRIAN W.
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 32,928
REGISTRATION NUMBER: 000063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LYKRLFKKLKK 12
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                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-233-203-12
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Gaps
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Patent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:
ADDRESSER: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 13;
1; Mismatches
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OTHER INFORMATION: May be a C-terminal amide, and/or may OTHER INFORMATION: be acetylated at N-terminus. PUBLICATION INFORMATION: AUTHORS: Houghten, R. AUTHORS: Ostresh, J. JOURNAL: Bio Chromatography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Minamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB F
Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: GAMBON, EGWARD P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 412156-80
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 18F05418
TELEPHONE: 312616540
TELEPHONE: 312616540
TELEPHONE: 312616540
TELEPHONE: 117 AMINO AG:
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ZIP: 60601
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/07725331 Patent No. 5294605
                                                                 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                   TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LYKRLFKKLKK 12
  3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
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  TELEFAX:
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GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Richard
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: E Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 14; Pred. No. 12;
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
BEATURE:
OTHER INFORMATION: May be a C-terminal amide, a
OTHER INFORMATION: be acetylated at N-terminus.
PUBLICATION INFORMATION:
AUTHORS: HOUGhten, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 1991077
FILING DATE: 1991077
PRIOR APPLICATION: 514
PRIOR APPLICATION DATE: 090/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 421250-80
TELECOMMUNICATION:
TELEPHONE: 3126165418
                 FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US 07/554,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             TELEPHONE: 3126165418
TELEPAX: 3126165460
INFORMATION FOR SEG ID NO: 1: SEQUENCE CHARACTERISTICS: LENCTH: 14 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bio Chromatography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 180 North Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL:
VOLUME: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US91-05047-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-725-331-1
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RESULT 29
US-07-725-331-54
Sequence 54, Application US/07725331
Sequence 54, Application US/07725331
Sequence 54, Application US/07725331
Sequence 54, Application US/07725331
Setter No. 5294605
SEXERAL INFORMATION:
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Ampliphilic Peptide Compositions and TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-725-331-55

Sequence 55, Application US/07725331

Sequence 55, Application US/07725331

Patent NO. 52944605

APPLICANT: Houghten, Richard

APPLICANT: Blondelle, Sylvie

TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,

ADDRESSEE: & Milnamow

STREET: 180 NO. 52944605th Stetson

CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%; Score 38; DB 1; Length 17; ilarity 72.7%; Pred. No. 14; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: C-terminal amide, acetylated CTHER INFORMATION: at N-terminus. US-07-725-331-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165460
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LYKRLFKKLKK 12
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 47, Application US/07725331

Fatent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 17;
Pred. No. 14;
1; Mismatches 2; Indels
                                                                                                                                             Score 38; DB 1; Length 17;
Pred. No. 14;
1; Mismatches 2; Indels
                                                           C-terminal amide, acetylated at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: C-terminal amide, acetylated; OTHER INFORMATION: at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIPICATION: 514
PRIOR APPLICATION DATE:
APPLICATION UNMERR: US 07/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFRATE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                  58.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                             Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LYKRLPKKLKK 12
| |:| |||||
                    peptide
                                                                                                                                                                                                                                       2 LYKRLFKKLKK 12
                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LLKKLLKKLKK 12
                                                         OTHER INFORMATION:
; OTHER INFORMATION:
US-07-725-331-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid STRANDEDNESS:
                MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                  RESULT 28
US-07-725-331-47
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Gaps

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Gaps
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APPLICANT: Houghten, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: C-terminal amide, acetylated at
                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: C-terminal amide, acetylated OTHER INFORMATION: at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow STREET: 180 North Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Score 38;
Pred. No.
                                                                421250-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application PC/TUS9105047 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60601
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 4212:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 3126165418
TELEPRAK: 312616540
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFRENCE/DOCKET NUMBER: 4212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEPHONE: 3126165460
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                                                                                                                                                                                                                                                                                                                                                                                                            58.5%;
ATTORNEY/AGENT INFORMATION:
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TYPE: AMINO ACID
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 58.5
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLKKLLKKLKK 13
                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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PCT-US91-05047-46
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; Patent No. 5294605
; GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
; TITLE OF INVENTION: Ampliphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
STREET: 180 No. 5294605th Stetson
; CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%; Score 38; DB 1; Length 17; 72.7%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: C-terminal amide, acetylated OTHER INFORMATION: at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                               CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312616540
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION: 514
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/554,422
APPLICATION TOWNER: US 07/554,422
                                                                                                                                             SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.5
Best Local Similarity 72.7
Matches 8; Conservative
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LYKRLFKKLKK 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                  FILING DATE:
                                        60601
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US-07-725-331-56
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PCT-US91-05047-55
; Sequence 55, Application PC/TUS9105047
; GENREAL INFORMATION:
; APPLICANT: Houghten, Richard
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Analogues Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
; STREET: 180 North Stetson
; CITT: Chicago
                     Blondelle, Sylvie
FRNTION: Amphiphilic Peptide Compositions and
FENTION: Analogues Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: C-terminal amide, acetylated OTHER INFORMATION: at N-terminus.
                 APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Composit
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
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Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFRENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEFAX: 3126165418
TELEFAX: 3126165418
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
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Best Local Similarity 72.7%;
Matches 8; Conservative 1
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MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                  USA
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COUNTRY:
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                                                                                                                                                                                                                                                                                  Sequence 47, Application PC/TUS9105047
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
FITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
MUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6 Milnamow
STREET: 180 North Stetson
CITY: Chicago
                                                               Score 38; DB 5; Length 17;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.5%; Score 38; DB 5; Length 17; 72.7%; Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: C-terminal amide, acetylated OTHER INFORMATION: at N-terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 14;
1; Mismatches
                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIPICATION B14
PRIOR APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421250-80
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; OTHER INFORMATION: N-terminus.
PCT-US91-05047-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gameon, Edward P. REGISTRATION NUMBER: 29,381 REPERENCE/DOCKET NUMBER: 42: TELECOMMUNICATION INFORMATION: TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                             Query Match 58.5%;
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 72.7.
8. Conservative
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LLKKLLKKLKK 12
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LYKRLFKKLKK 12
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2 LLKKLLKKLKK 12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 34
PCT-US91-05047-54
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Length 17; Indels

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; Sequence 3, Application US/07725331
; Patent No. 5294605
; GENERAL INFORMATION:
    APPLICANT: Houghten, Richard
    APPLICANT: Houghten, Richard
    APPLICANT: Houghten, Richard
    APPLICANT: Houghten, Sylvie
    TITLE OF INVENTION: Amphiphilic Peptide Compositions and
    TITLE OF INVENTION: Analogues Thereof
    NUMBER OF SEQUENCES: 68
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: & Milnamow
    STREET: 180 No. 5294605th Stetson
    CITT: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May be a C-terminal amide, and/or may be acetylated at N-terminus.
                                                                                                                                                                                                                                                        Score 38; DB 5; Length 17;
Pred. No. 14;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.5%; Score 38; DB 1; Length 18; 72.7%; Pred. No. 14; 1; Mismatches 2; Indels
                                                                                                                                                                     CTHER INFORMATION: C-terminal amide, acetylated NTHER INFORMATION: at N-terminus.

PCT-US91-05047-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
  56:
                                                                                                                                                                                                                                                        Query Match 58.5%;
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                          TYPE: AMINO ACID STRANDEDNESS:
TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                               17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 3126165418
TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             2 LYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                          3 LLKKLLKKLKK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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COTHER INFORMATION:
US-07-725-331-3
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STRANDEDNESS:
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PCT-US91-05047-56

Sequence 56, Application PC/TUS9105047

GENERAL INFORMATION:

APPLICANT: Houghten, Richard

APPLICANT: Blondelle, Sylvie

TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: & Milnamow

ADDRESSEE: & Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 5; Length 17;
Pred. No. 14;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal amide, acetylated at N-terminus.
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ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US91/05047
               SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REGISTRATION NUMBER: 29,381
REFERNICE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FILING DATE: 19910717

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422

FILING DATE: 19-ULL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: 421250-80

TELEPHONE: 3126165418
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.5%;
72.7%;
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                                                                                                                                                                                                                                                                                                                       TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LYKRLFKKLKK 12
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COTHER INFORMATION:
PCT-US91-05047-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
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May be a C-terminal amide, and/or may be acetylated at N-terminus, Xaa is Met or methionine sulfoxide.
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APPLICANT: Houghten, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10xity 72.7%; Pred. No. 14; Conservative 1; Mismatches 2. r-1-
                                                      ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow STREET: 180 No. 5294605th Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow
IITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIPICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/554,422
PILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEPAX: 3126165460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 180 No. 5294605th Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYKRLFKKLKK 12
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                              COUNTRY:
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                                                                                                                                  CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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be acetylated at N-terminus, Xaa is
Met or methionine sulfoxide.
                                                                                                                                                                    Sequence 5, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Amalogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Milnamow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
US-07-725-311-6
US-07-725-311-6
Sequence 6, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Houghten, Sylvie
ITILE OF INVENTION: Amphiphilic Peptide Compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.5%; Score 38; DB 1; Length 18; Best Local Similarity 72.7%; Pred. No. 14; Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 514
PRIGR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: GAMBON, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELECHONE: 3126165418
TELEFAN: 312616540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 66601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEM: Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                3 LLKKLLKKLKK 13
                         2 LYKRLFKKLKK 12
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OTHER INFORMATION:
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                RESULT 38
US-07-725-331-5
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Gaps

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Gaps
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be acetylated at N-terminus, Xaa is
Met or methionine sulfoxide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 18;
Pred. No. 14;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dressler, Goldsmith, Sutker, Shore, ADDRESSEE: & Milnamow STREET: 180 No. 5294605th Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEPAX: 3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILIN Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/07725331
Patent No. 5294605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                      58.5%;
                                                                                  LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                3 LLKKLLKKLKK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                        2 LYKRLFKKLKK 12
                                                                                                                                                                                                     ; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-07-725-331-18
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CTHER INFORMATION:
CTHER INFORMATION:
US-07-725-331-19
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                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
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Patent No. 5294605

GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              May be a C-terminal amide, and/or may be acetylated at N-terminus, .Xaa is Met or methionine sulfoxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 18; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
FELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
                                                                                                                                                                                                                                                          421250-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
SUFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
                                                                                                   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REERENCE/DOCKET NUMBER: 4212:
TELECOMMUNICATION INPORMATION:
TELEPAK: 3126165418
TELEPAK: 3126165418
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LXKKLLKKLKK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LYKRLFKKLKK 12
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CTHER INFORMATION:
CTHER INFORMATION:
US-07-725-331-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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US-07-725-331-18
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421250-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 4212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEPAX: 3126165460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
  APPLICANT: Houghten, Richard
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.7-
Rest Local Similarity 72.7-
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MOLECULE TYPE: peptide
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CTHER INFORMATION:
CTHER INFORMATION:
US-07-725-331-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                60601
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STATE:
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                                                                                                                                                                                                Sequence 20, Application US/07725331
Fatent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May be a C-terminal amide, and/or may
be acetylated at N-terminus, Xaa is
Met or methionine sulfoxide.
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Pred. No. 14;
1; Mismatches 2; Indels
  58.5%; Score 38; DB 1; Length 18; 72.7%; Pred. No. 14;
                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 44
18-07-725-311-21
18-04 Sequence 21, Application US/07725331
Patent No. 5294605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 3126165460
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 72.7.

Since 8, Conservative
                  Best Local Similarity 72. Matches 8, Conservative
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LLKKLLKKLKK 13
                                                                              2 LYKRLFKKLKK 12
                                                                                                    3 LLKKLLKKLKK 13
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COTHER INFORMATION:
COTHER INFORMATION:
US-07-725-331-20
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US-07-725-331-20
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Query Match
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| Patent No. 5294605
| GENERAL INPORMATION:
| APPLICANT: Houghten, Richard
| APPLICANT: Blondelle, Sylvie
| TITLE OF INVENTION: Amphiphilic Peptide Compositions and TITLE OF INVENTION: Analogues Thereof
| NUMBER OF SEQUENCES: 68 | CORRESPONDENCE ADDRESSE: ADDRESSEE: & Milnamow STREET: 180 No. 5294605th Stetson CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            May be a C-terminal amide, and/or may
be acetylated at N-terminus, Xaa is
Met or methionine sulfoxide.
APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sutker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 18; 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.5%; Score 38; 72.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/554,422
FILING DATE: 19-ULL-1990
FILING DATE: 19-ULL-1990
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IMP C compatible
COMPUTER: IMP C compatible
COMPUTER: IMP C compatible
COMPUTER: IMP C compatible
COMPUTER: IMP C compatible
COMPUTER: IMP C compatible
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFCATION NUMBER: US/07/725,331
FILING DATE:
FILING DATE:
CLASSIFCATION NUMBER: US/07/554,422
FILING DATE:
CLASSIFCATION NUMBER: 42,381
FILING DATE: 19-1010-1990
ATTOCHEVATION NUMBER: 23,381
FEGISTRATION NUMBER: 23,381
FEGISTRATION NUMBER: 23,381
FEGISTRATION NUMBER: 23,381
FEGISTRATION NUMBER: 22,381
FEGISTRATION NUMBER: 32,381
FEGISTRATION NUMBER: 32,381
FEGISTRATION NUMBER: 32,381
FEGISTRATION NUMBER: 32,381
FEGISTRATION: May be a C-terminal amide, and/or may OTHER INFORMATION: Met or methionine sulfoxide.

COTHER INFORMATION: Methionine sulfoxide.

COTHER INFORMATION: Methionine sulfoxide.

COTHER INFORMATION: Methionine sulfoxide.

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                                                                                                                                                                                                                                                                                                                                527782
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                 OM.protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                         1 ALYKRLFKKLKKF 13
                                                                                                                                                                   US-09-648-816B-13
65
                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 74
                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

frodata/1/pubpaa/US10A PUBCOMB.pep. /ptodata/1/pubpaa/US10B PUBCOMB.pep. /ptodata/1/pubpaa/US10E PUBCOMB.pep. /ptodata/1/pubpaa/US10D\_PUBCOMB.pep.

/cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:

# SUMMARIES

|   | ;                          | App1             | Appl              | Appl              | Appl              | Appl             | Appl             | Appl             | Appl             | Appl              | Appl              | Appl             | Appl             | Appl             |
|---|----------------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|
|   | _ [                        | 8,               | 7.                | 29,               | 36,               | 29,              | 36,              | 29,              | 36,              | 11,               | 18,               | 1,               | 18,              | 11,              |
|   | Description                | Sequence 1       | Sequence 17, Appl | Sequence          | Sequence          | Sequence         | Sequence         | Sequence         | Sequence         | Sequence          | Sequence          | Sequence         | Sequence         | Sequence         |
|   | ΩI                         | US-09-872-864-18 | US-09-872-864-17  | US-09-896-841A-29 | US-09-896-841A-36 | US-10-187-215-29 | US-10-187-215-36 | US-10-273-386-29 | US-10-273-386-36 | US-09-896-841A-11 | US-09-896-841A-18 | US-10-187-215-11 | US-10-187-215-18 | US-10-273-386-11 |
|   | DB                         | 6                | 0                 | 10                | 10                | 14               | 14               | 15               | 15               | 10                | 10                | 14               | 14               | 15               |
|   | Query<br>Match Length DB I | 29               | 29                | 14                | 14                | 14               | 14               | 14               | 14               | 18                | 18                | 18               | 18               | 18               |
| æ | Query<br>Match             | 70.8             | 64.6              | 63.1              | 63.1              | 63.1             | 63.1             | 63.1             | 63.1             | 63.1              | 63.1              | 63.1             | 63.1             | 63.1             |
|   | Score                      | 46               | 42                | 41                | 41                | 41               | 41               | 41               | 41               | 41                | 41                | 41               | 41               | 41               |
|   | Result<br>No.              | -                | 8                 | ღ                 | 4                 | S                | 9                | 7                | 80               | 6                 | 10                | 11               | 12               | 13               |

|         | 13   | Sequence 9, Appli | e<br>O | Sequence 2, Appli | 4    | Sequence 45, Appl | 4       | Sequence 97, Appl | 129,     | Sequence 41, Appl | 46,  | 47,  | 4             | 46,     | 47,    | 41,      | 46,     | 47,      | 10,  | Sequence 31, Appl | 38,      | 31,     | 38,     | Sequence 31, Appl | 38,     | 98,              | 24                | Ċ         | ý                | 5             | Sequence 20, Appl |
|---------|------|-------------------|--------|-------------------|------|-------------------|---------|-------------------|----------|-------------------|------|------|---------------|---------|--------|----------|---------|----------|------|-------------------|----------|---------|---------|-------------------|---------|------------------|-------------------|-----------|------------------|---------------|-------------------|
| 73-386- | -872 | US-09-872-864-9   | -10-2  | US-10-627-314-2   | -66- | -10-              | 10-273- | -10-273-          | -10-688- | US-09-896-841A-41 | -09- |      | -10-187-215-4 | 10-187- | -10-18 | -10-273- | 10-273- | -10-273- | -10  | -968-60-          | -968-60- | 10-187- | 10-187- | 273-              | 10-273- | US-10-273-386-98 | US-09-865-989-241 | -09-865-9 | US-09-896-841A-6 | -09-896-841A- | US-09-896-841A-20 |
| 15      | σ    | σ                 | 12     | 16                | 2    | 14                | 12      | 15                | 11       | 2                 | 2    | 2    | 14            | 14      | 14     | 12       | 12      | 12       | 15   | 2                 | 10       | 14      | 14      | 12                | 15      | 15               | 2                 | 10        | 20               | 10            | 10                |
| 18      | 53   | 14                | 14     | 14                | 18   | 18                | 18      | 18                | 69       | 18                | 18   | 18   | 18            | 18      | 18     | 18       | 18      | 18       | 18   | 14                | 14       | 14      | 14      | 14                | 14      | 14               | 18                | 18        | 18               | 18            | 18                |
| 63.1    | 63.1 | 0.09              | 0.09   | 0.09              | 0.09 | 60.09             | 0.09    | 0.09              | 60.09    | 58.5              | 58.5 | 58.5 | 58.5          | 58.5    | 58.5   | 58.5     | 58.5    | 58.5     | 58.5 | 56.9              | 56.9     | 56.9    | 56.9    | 56.9              | 56.9    | 56.9             | v                 | 56.9      | 56.9             | 56.9          | 56.9              |
| 41      | 41   | 39                | 39     | 39                | 39   | 39                | 39      | 39                | 39       | 38                | 38   | 38   | 38            | 38      | 38     | 38       | 38      | 38       | 38   | 37                | 37       | 37      | 37      | 37                | 37      | 37               | 37                | 37        | 37               | 37            | 37                |
| 14      | 15   | 16                | 11     | 18                | 19   | 20                | 21      | 22                | 23       | 24                | 25   | 56   | 27            | 28      | 53     | 30       | 31      | 32       | 33   | 34                | 32       | 36      | 37      | 38                | 39      | 40               | 41                | 42        | 43               | 44            | 45                |

## ALIGNMENTS

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                                                                                 GENERAL INCOCACALITY AND MENUM APPLICANT: APPLICANT: AMERONGEN, ARIE VAN NIEUW APPLICANT: AMERONGEN, ENERLINDUS CORNELIS IGNATIUS APPLICANT: VAN Y THOF, WILLLEM APPLICANT: VIBNERING, PETER HENDRICUS ITILE OF INVENTION: ANTIVIRAL PEPTIDES FILE REFERENCE: EPP-004.01

FULER REPRENCE: EPP-004.01

CURRENT APPLICATION NUMBER: DCT/ML99/00732

PRIOR APPLICATION NUMBER: PCT/ML99/00732

PRIOR PILLING DATE: 1999-12-01

PRIOR PILLING DATE: 1998-12-01

NUMBER OF SEQ ID NOS: 20

SOUTHARR: PALENTING VET. 2.1

SEQ ID NO IS BLOOK OF THE PARENTING NUMBER: MINIOTOS OF THE PARENTING DATE: 1998-12-01

SEQ ID NO IS BLOOK OF THE PARENTING NUMBER: MINIOTOS OF THE PARENTING DATE: 1998-12-01

SEQ ID NO IS BLOOK OF THE PARENTING NUMBER: MINIOTOS OF THE PARENTING DATE: 1998-12-01

SEQ ID NO IS BLOOK OF THE PARENTING NUMBER: PARENTING DATE: 1998-12-01

SEQ ID NO IS BLOOK OF THE PARENTING NUMBER: PARENTING DATE: 1998-12-01
                     Sequence 18, Application US/09872864
Patent No. US20020111305A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT. ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: AMIDATION US-09-872-864-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
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LOCATION: (29)
JS-09-872-864-18
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FOGELAWN, ALAN
APPLICANT: NAVABA, MCHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
CURRENT APPLICATION NUMBER: US/09/896,841A
PRIOR APPLICATION NUMBER: US 09/645,454
PRIOR PAPLICATION NUMBER: US 09/645,454
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
SOFTWARER PATENTIN VERBION 3.0
SEQ ID NO 36
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: synthetic or recombinant class A peptide
               Sequence 36, Application US/09896841A Publication No. US20030045460A1
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.1%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ALYKRLFKKLKKF 13
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1 AFYDKVFEKLKEF 13
JS-09-896-841A-36
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Publication No. US20030045460A1
Fublication No. US20030045460A1
Fublication No. US20030045460A1
Fublication No. US20030045460A1
GARBEAL INFORMATION:
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: ANANTHARAMAIAH
APPLICANT: ANANTHARAMAIAH
APPLICANT: NANTHON: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
TITLE OF INVENTYON: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
CURRENT APPLICATION NUMBER: US/09/896,841A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/645,454
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
SOFTWARRE: PATCHTIN VERSION 3.0
SOFTWARRE: PATCHTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 10; Length 14;
Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 29;
                                                                                        APPLICANT: VEERMAN, ENGELMUNDUS CORNELIS IGNATIUS
APPLICANT: VEERMAN, ENGELMUNDUS CORNELIS IGNATIUS
APPLICANT: VAN 'T HÔF' WILLEM
APPLICANT: NIBBERING, PETER HENDRICUS
TITLE OF INVENTION: ANTIVIRAL PEPTIDES
FILE REFERENCE: EPP-004.01
CURRENT APPLICATION NUMBER: US/09/872,864
CURRENT PLING DATE: 2001-06-01
PRIOR PILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 17
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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Pred. No.
                  Sequence 17, Application US/09872864 Patent No. US20020111305A1 GENERAL INFORMATION:
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88.9%;
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53.8%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
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Best Local Similarity 53.8
Matches 7; Conservative
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Gaps

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Length 14;

Score 41; DB 10; Pred. No. 6.9; 4; Mismatches 2;

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Sequence 29, Application US/10187215

Publication No. US20030171277A1

GENERAL INFORMATION:
APPLICANT: NAVABA, WORAMAN
APPLICANT: ANAVAHARAMAIAH, GATTADAHALLI
APPLICANT: ANAVAB, WORAMAN
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
TILE REFERENCE: 407T-911220US
CURRENT APPLICATION NUMBER: US/09/696,841
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2000-08-24
NUMBER OF SEC ID NOS: 87
SOFTWARE: PatentIn version 3.0
SEQ ID NO 29
LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Pred. No. 6.9;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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1 AFYDKVFEKLKEF 13
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US-10-187-215-36
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1 AFYDKVFEKLKEF 13

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US-09-896-841A-11
; Sequence 11, Application US/09896841A
; Sequence 11, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INPORMATION:
; APPLICANT: FOCSELMAN, ALAN
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; PILE REFERENCE: 407T-911220PC
; CURRENT APPLICATION NUMBER: US/09/896,841A
; CURRENT FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/645,454
; RIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 86
; SOCITANAE: PatentIn version 3.0
; SEQ ID NO 11
LENGTH: 18
                                                 GENERAL INFORMATION:
APPLICANT: FOGELMAN, ALAN M.
APPLICANT: FOGELMAN, ALAN M.
APPLICANT: FOGELMAN, ALAN M.
APPLICANT: ANATHRARMATH, GATTADAHALLI M.
APPLICANT: ANATHRARMATH, GATTADAHALLI M.
APPLICANT: NAVAB, MCHANAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REPRENCE: 407t-911230US
CURRENT APPLICATION NUMBER: DCT/US01/26497
FRIOR PILING DATE: 2002-06-29
FRIOR PILING DATE: 2002-06-29
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-29
FRIOR PILING DATE: 2001-06-29
FRIOR FILING DATE: 2000-08-24
FRIOR FILING DATE: 2000-08-24
FRIOR FILING DATE: 2000-08-24
FRIOR FILING DATE: 2000-08-24
FRIOR APPLICATION NUMBER: 09/645,454
FRIOR FILING DATE: 2000-08-24
FRIOR FILING DATE: 2000-08-24
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FRIOR APPLICATION NUMBER: 09/645,454
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FRIOR APPLICATION NUMBER: 09/645,454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
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Pred. No. 8.8;
4; Mismatches 2;
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Pred. No. 6.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Synthetic D peptides US-10-273-386-36
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US-09-896-841A-18
; Sequence 18, Application US/09896841A
Sequence 36, Application US/10273386 Publication No. US20030229015A1
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 53.8%;
Matches 7; Conservative
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1 AFYDKVFEKLKEF 13
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                                                                        APPLICANT: ANANTHARAMALH, GATTADAHALLI
APPLICANT: ANANTHARAMALH, GATTADAHALLI
APPLICANT: NAVAB, MOHANAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REFERENCE: 4077-91122003
CURRENT APPLICATION NUMBER: US/10/187,215
CURRENT FILING DATE: 2002-06-28
PRIOR PILING DATE: 2010-06-29
PRIOR PILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PACENTIN VERSION 3.0
SEQ ID NO 36
LENGTH: 14
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Publication No. US20030229015A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROGELMAN, ALAN M.
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
APPLICANT: NANAND, WORMAND
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REFERENCE: 407c-911230US
CURRENT ELLING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: DCT/US01/26497
PRIOR APPLICATION NUMBER: 10/187,215
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-28
PRIOR PELLING DATE: 2001-06-28
PRIOR FILING DATE: 2001-06-28
PRIOR FILING DATE: 2001-06-29
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PRIOR FILING DATE: 2001-06-29
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PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-24
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Pred. No. 6.9;
4; Mismatches 2; Indels
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Publication No. US20030171277A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 53.8%;
Matches 7; Conservative
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AFYDKVFEKLKEF 13
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1 AFYDKVFEKLKEF 13
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Best Local Similarity 53.8
Matches 7; Conservative
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SOFTWARE: Patentin version
SEQ ID NO 29
LENGTH: 14
                                                                  APPLICANT: FOGELMAN, ALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial
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US-10-273-386-29
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Gaps

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Gaps ö

RESULT 8 US-10-273-386-36

Gaps

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FITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
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APPLICANT: ANANTHARANALH, GATTADAHALLI M.
APPLICANT: ANANTHARANALH, GATTADAHALLI M.
APPLICANT: NAVAB, MOHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REFERENCE: 407t-91120US
CURRENT APPLICATION NUMBER: US/10/273,386
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: PCT/US01/26497
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Pred. No. 8.8;
4; Mismatches 2; Indels
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               FILE REFERENCE: 4077-911220US
CURRENT APPLICATION NUMBER: US/10/187,215
CURRENT FILING DATE: 2002-06-28
FRIOR APPLICATION NUMBER: US 09/896,841
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
LENGTH: 18
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APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic D peptides US-10-273-386-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 10/187,215
PRIOR PLING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 09/896,841
PRIOR FILING DATE: 2001-06-29
PRIOR PRILING DATE: 2001-06-29
PRIOR PILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentin version 3.2
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-273-386-11
; Sequence 11, Application US/10273386
; Publication No. US20030229015A1
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                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.1%;
Best Local Similarity 53.8%;
Matches 7; Conservative
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Matches 7; Conservative
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5 AFYDKVFEKLKEF 17
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                              APPLICANT: FOGELMAN, ALAN
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: NAVAB, MOHAWAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REFERENCE: 407T-911220PC
CURRENT APPLICATION NUMBER: US/09/896,841A
CURRENT APPLICATION NUMBER: US 09/645,454
PRIOR APPLICATION NUMBER: US 09/645,454
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 18
LENGTH: 18
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APPLICANT: FOGSLAAN, ALAN
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: NAVAB, MOHAMAD
APPLICANT: NAVAB, MOHAMAD
APPLICANT: NAVAB, MOHAMAD
TILLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REPERENCE: 407T-911220US
CURRENT APPLICATION NUMBER: US/10/187,215
PRIOR APPLICATION NUMBER: US 09/896,841
PRIOR APPLICATION NUMBER: US 09/645,454
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 87
SOUTWARE: PATENTIN VESSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: synthetic or recombinant class A peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 10; Length 18;
Pred. No. 8.8;
4; Mismatches 2; Indels
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Pred. No. 8.8;
4; Mismatches 2; Indels
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APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: NAVAB, MOHAWAD
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Publication No. US20030171277A1
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53.8$;
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ORGANISM: Artificial Sequence
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Best Local Similarity 53.8%;
Matches 7; Conservative
US20030045460A1
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5 AFYDKVFEKLKEF 17
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Best Local Similarity 53.8
Matches 7; Conservative
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GAPELICANT: FOGELMAN, ALAN M.

APPLICANT: FOGELMAN, ALAN M.

APPLICANT: ANANTHARAMALAH, GATTADAHALLI M.

APPLICANT: NAVAB, MOHAMAD

TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY

FILE REPERENCE: 407t-911230US

CURRENT FILING DATE: 2002-10-16

CURRENT PELLING DATE: 2002-10-16

PRIOR PILING DATE: 2002-06-29

PRIOR FILING DATE: 2002-06-29

PRIOR PLILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR PLILING DATE: 2001-06-39

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                                                                                                          GENERAL INFORMATION:
APPLICANT: WARRONGEN, ARIE VAN NIEUW
APPLICANT: VERNAN, ENGELAUNDUS CORNELIS IGNATIUS
APPLICANT: VAN T HOF, WILLER
APPLICANT: VAN T HOF, WILLER
TOTALE OF INVENTION: ANTIVIRAL PEPTIDES
FILE REFERENCE: EPP-004.01
CURRENT APPLICATION NUMBER: US/09/872,864
CURRENT PILLING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/NL99/00732
PRIOR RILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: NIJ010692
PRIOR APPLICATION NUMBER: 20
PRIOR PILING DATE: 1998-12-01
SOFTWARE: PATENTIN VOR: 20
LENGTH: 14
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Pred. No. 14;
5; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 99, Application US/10273386 Publication No. US20030229015A1 GENERAL INFORMATION:
                                   Sequence 9, Application US/09872864 Patent No. US20020111305A1 GENERAL INFORMATION:
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46.2%;
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Best Local Similarity 46.2
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1 AFYEKVFEKFKEF 13
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Matches 8; Conservative
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APPLICANT: NAVAB, MOHAMAD

TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REPERENCE: 407t-911230US
CURRENT APPLICATION NUMBER: US/10/273,386
CURRENT PILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: PCT/USO1/26497
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
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; Batent No. US20020111305A1
; GENERAL INNORMATION:
   APPLICANT: AMERONGEN, ARIE VAN NIEUW
; APPLICANT: VEERWAN', ENGELMUNDUS CORNELIS IGNATIUS
; APPLICANT: VEERWAN', ENGELMUNDUS CORNELIS IGNATIUS
; APPLICANT: VAN 'T HOP', WILLEM
; APPLICANT: VAN 'T HOP', WILLEM
; APPLICANT: NIBBERING, PETER HENDRICUS
; TITLE OF INVENTION: ANTIVIRAL PEPTIDES
; FILE REFERENCE: EPP-004.01
; CURRENT APPLICATION NUMBER: US/09/872,864
; CURRENT FILING DATE: 2001-06-01
; PRIOR FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1998-12-01
; SEQ ID NO S: 20
; SOFTWARE: PALENTIN Ver. 2.1
; SEQ ID NO 129
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Pred. No. 8.8;
4; Mismatches 2,
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Best Local Similarity 53.8%;
Matches 7; Conservative
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OTHER INFORMATION: AMIDATION
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S AFYDKVFEKLKEF 17
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Matches 8; Conserva
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APPLICANT: FOCSELMAN, ALAN M.
APPLICANT: FOCSELMAN, ALAN M.
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI M.
APPLICANT: NAVAB, MOHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REFERENCE: 407c-9112304
CURRENT APPLICATION NUMBER: US/10/273,386
CURRENT APPLICATION NUMBER: 2002-10-16
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2000-06-29
PRIOR PRILING DATE: 2000-06-29
PRIOR PRILING DATE: 2000-06-29
PRIOR PLING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentin version 3.2
SEQ ID NO 45
                      APPLICANT: NAVAE, MORAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REPERBNES: 4077-91122002
CURRENT APPLICATION NUMBER: US/10/187,215
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 09/896,841
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
SEQ ID NO 45
LENGTH: 18
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Pred. No. 18;
5; Mismatches 2
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US-10-273-386-45
ANANTHARAMAIAH, GATTADAHALLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45, Application US/10273386 Publication No. US20030229015A1 GENERAL INFORMATION:
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46.2%;
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.0%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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5 AFYEKVFEKFKEF 17
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Best Local Similarity
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1. Sequence 45, Application US/09896841A

2. Sequence 45, Application US/09896841A

3. Bublication No. US20030045460A1

5. GENERAL INFORMATION:

APPLICANT: POGELMAN, ALAN

APPLICANT: NAVAB, MOHAMAD

7 TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS

7 TITLE OF INVENTION: 08-102-00-06-29

CURRENT FILING DATE: 2000-06-29

PRIOR PELING DATE: 2000-06-24

7 NUMBER OF SEQ ID NOS: 86

7 SOFTWARE: Patentin version 3.0

7 SEQ ID NO 45

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                                                                                                                                                              TITLE OF INVENTION: Bone cement
FILE REFERENCE: Bone cement
FILE REFERENCE: Bone cement
CURRENT APPLICATION NUMBER: US/10/627,314
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: EP 01200363.8
PRIOR FILING DATE: 2001-02-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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                                                                                                 Sequence 2, Application US/10627314
Publication No. US20040131678A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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AFYEKVFEKFKEF 17
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Best Local Similarity
Matches 8; Conservat
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Matches 6; Conserv
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RESULT 20

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APPLICANT: ANANTHARMALIAN, GATTADAHALLI
APPLICANT: NAVAB, MOHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
CURRENT APPLICATION NUMBER: US/09/896,841A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/645,454
PRIOR PILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 46
LENGTH: 18
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Sequence 47. Application WS/09896841A
Sequence 47. Application No. US20030045460A1
Sequence 47. Application No. US20030045460A1
SEQUENCE NO. US20030045460A1
SEQUENCE INFORMATION:
APPLICANT: POGELMAN, ALAN
APPLICANT: NAVAB, MOHAWAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REPREBENCE: 4077-911220PC
CURRENT APPLICATION NUMBER: US/09/896,841A
CURRENT FILING DATE: 2001-06-29
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS FILE REFERENCE: 407T-911220PC
CURRENT APPLICATION NUMBER: US/09/896,841A
CURRENT PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/645,454
PRIOR PILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 41
LENGTH: 18
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Pred. No. 26;
4; Mismatches 3;
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PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
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Publication No. US20030045460A1
GENERAL INFORMATION:
APPLICANT: FOGELMAN, ALAN
                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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46.2%;
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Best Local Similarity 46.2
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-09-896-841A-46
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                                                  APELICANT: MANABATION CRAILLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REPERENCE: 407-911230U3
CURRENT APPLICATION NUMBER: US/10/273,386
CURRENT FILING DATE: 2002-10-16
PRIOR PAPLICATION NUMBER: D0/187,215
PRIOR PELING DATE: 2002-06-29
PRIOR PELING DATE: 2002-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2000-08-24
PRIOR PELING DATE: 2000-08-24
SOFTWARE: PRECENTION NUMBER: 09/645,454
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PRECENTIN VERSION 3.2
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APPLICANT: HALE, KATHERINE S.
APPLICANT: HALE, KATHERINE S.
APPLICANT: JOHNSTON. STEPHEN A.
ITTLE OF INVENTION: MCCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF THE GENUS TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF THE GENUS TITLE OF INVENTION: BORRELIA FILE OF INVENTION: BORRELIA GURRENT APPLICATION NUMBER: US/10/688,058
CURRENT APPLICATION NUMBER: US/10/688,058
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 129
LENGTH: 69
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Pred. No. 18;
5; Mismatches 2; Indels
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            FOGELMAN, ALAN M.
ANANTHARAMAIAH, GATTADAHALLI M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-97
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APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: NAVAB, MOHAMAD
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US-10-688-058-129
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46.2%;
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Best Local Similarity 46.2
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5 AFYEKVFEKFKEF 17
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52 YKKPYKELKQF 62
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ORGANISM: Artificial
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Best Local Similarity
Matches 6; Conserv
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US-10-688-058-129
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US-09-896-841A-41
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Sequence 46, Application US/10187215

Publication No. US20030171277A1

Sequence 46, Application US/10187215

Publication No. US20030171277A1

APPLICANT: POGELMAN, ALAN

APPLICANT: NAVABANANAIAH, GATTADAHALLI

APPLICANT: NAVAB, MOHAMAD

TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS

FILE REFERENCE: 407T-911220US

CURRENT PFLICATION NUMBER: US/0/187,215

CURRENT PILING DATE: 2002-06-28

PRIOR PELICATION NUMBER: US/09/896,841

PRIOR PELICATION NUMBER: US/09/645,454

PRIOR PLICATION NUMBER: US/09/645,454

PRIOR PLING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin version 3.0

SEQ ID NO 46

LENGTH: 18
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APPLICANT: ROGELAWA, ALAN
APPLICANT: ANANTHARAWAIAH, GATTADAHALLI
APPLICANT: ANANAB, WIGHAND
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REFERENCE: 407T-911220US
CURRENT APPLICATION NUMBER: US/10/187,215
CURRENT APPLICATION NUMBER: US 9/896,841
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATENTIN VOS: 87
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                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Synthetic or recombinant class A peptide
US-09-896-841A-47
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Sequence 41, Application US/10187215; Publication No. US20030171277A1
; GENERAL INFORMATION:
SOFTWARE: Patentin version 3.0 SEQ ID NO 47 LENGTH: 18
                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Seguence
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5 AFYEKFFEKFKEF 17
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Best Local Similarity
Matches 6; Conserva
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LENGTH: 18
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; FUDLICALION NO. USZUUJUL/12/141
; GENERAL INFORMATION:
APPLICANT: FOGELMAN, ALAN
APPLICANT: ROALINAMAIAH, GATTADAHALLI
APPLICANT: NAVAB, WOHAMAI
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
TITLE DE INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
CURRENT APPLICATION NUMBER: US/01/0187,215
CURRENT PILING DATE: 2002-06-29
FRIOR PELING DATE: 2001-06-29
FRIOR PELING DATE: 2001-06-29
FRIOR APPLICATION WHERE: US/09/645,454
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 47
LENGTH: 18
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Publication No. US20030229015A1

GENERAL INFORMATION:

APPLICANT: ANDNTHARMAIAH, GATTADAHALLI M.

APPLICANT: ANANTHARMAIAH, GATTADAHALLI M.

APPLICANT: ANANTHARMAIAH, GATTADAHALLI M.

APPLICANT: NAVAB, MOHAMAD

FILE REFERENCE: 407C-911230US

CURRENT PAPLICATION NUMBER: US/10/273,386

CURRENT PILING DATE: 2002-10-16

PRIOR APPLICATION NUMBER: 001-06-29

PRIOR APPLICATION NUMBER: 00/4897

PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 103

SOFTWARRE: PATCHIN VERSION 3.2

SEQ ID NO 41
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; TYPE: PRT; ORGANISM: Artificial Sequence; PRTURE: PRATURE: PRATURE: CTHER INFORMATION: Synthetic or recombinant class A peptide US-10-187-215-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: synthetic or recombinant class A peptide US-10-187-215-47
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Pred. No. 26;
4; Mismatches
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Pred. No. 26;
4; Mismatches
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Publication No. US20030171277A1
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Best Local Similarity 46.2%;
Matches 6; Conservative
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Best Local Similarity 46.2%;
Matches 6; Conservative
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18 amino acids
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5 AFYEKFFEKFKEF 17
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial
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Best Local Similarity
Matches 6; Conserv
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| APPLICANT: FOGELMAN, ALAN M. |
| APPLICANT: FOGELMAN, ALAN M. |
| APPLICANT: ANANTHARMAIAH, GATTADAHALLI M. |
| APPLICANT: NAVAB, MOHAMAD, |
| APPLICANT: NAVAB, MOHAMAD, |
| APPLICANT: NAVAB, MOHAMAD, |
| TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY |
| FILE REFERENCE: 407c-911230US |
| CURRENT APPLICATION NUMBER: US/10/273,386 |
| PRIOR PILING DATE: 2001-06-29 |
| PRIOR PILING DATE: 2001-06-29 |
| PRIOR PILING DATE: 2001-06-29 |
| PRIOR PILING DATE: 2001-06-29 |
| PRIOR FILING DATE: 2000-08-24 |
| PRIOR FILING DATE: 2000-08-24 |
| NUMBER OF SEQ ID NOS: 103 |
| SOFTWARE: PatentIn version 3.2 |
| LENGTH: 18 |
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APPLICANT: POSELMAN, ALAN M.
APPLICANT: NAVAB, MOHAWAD
APPLICANT: NAVAB, MOHAWAD
TITLE OF INVENTION: NAVABLAD ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REPERENCE: 407-911230US
CURRENT APPLICATION NUMBER: US/10/273,386
CURRENT PILING DATE: 2002-10-16
PRIOR PPLICATION NUMBER: PCY/US01/26497
PRIOR PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 10/187,215
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Pred. No. 26;
4; Mismatches 3; Indels
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                                                                                                                             ) OTHER INFORMATION: Synthetic D peptides US-10-273-386-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Synthetic D peptides US-10-273-386-46
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APPLICATION NUMBER: 09/896,841
FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 46, Application US/10273386; Publication No. US20030229015A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 47, Application US/10273386; Publication No. US20030229015A1; GENERAL INFORMATION:
                                                                                                                                                                                                                               Query Match 58.5%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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5 AFYEKFFEKFKEF 17
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Best Local Similarity 46.2
Matches 6; Conservative
                                  TYPE: PRT ORGANISM: Artificial
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US-10-273-386-46
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                                                                                                     FEATURE:
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LENGTH:
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Gaps
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APPLICANT: Enright, Frederick M.
APPLICANT: Elzer, Philip H.
APPLICANT: Elzer, Philip H.
APPLICANT: Elzer, Philip H.
APPLICANT: Hammer, Robert P.
TITLE OF INVENTION: Short Amphipathic Peptides with
TITLE OF INVENTION: Activity
TITLE OF INVENTION: Against Bacteria and Intracellular Pathogens
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. Runnels
STREET: P. O. Box 2471
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                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                    3; Indels
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PUBLICATION INFORMATION:
AUTHORS: Blondelle, Sylvie E.
AUTHORS: Houghten, Richard A.
TITLE: Design of Model Amphipathic Peptides Having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/414,342
                                                                                                                                                                                                                                                                                       DB 15;
26;
                                                                                                                                                                                                                                                                                     Score 38; DB 1
Pred. No. 26;
4; Mismatches
                                                                                                                                                                                                                   ; OTHER INFORMATION: Synthetic D peptides US-10-273-386-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/796,123
FILING DATE: 06-FEB-1997
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: 09/645,454
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentin version 3.2
SEQ ID NO 47
LENGTH: 18
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REGISTRATION NUMBER: 33451
REFERENCE/DOCKET NUMBER: 9619
TELECOMMUNICATION INFORMATION:
TELEPACN: (504) 346-3221
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/10414342
Publication No. US20040059088A1
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46.2%; Pred. No. 29; ive 4; Mismatches
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Best Local Similarity 46.2%;
Matches 6; Conservative
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                                                                1 ALYKRLFKKLKKF 13
  Best Local Similarity 46.2
Matches 6; Conservative
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Sequence 38, Application US/09896841A

Sequence 38, Application No. US20030045460A1

Publication No. US20030045460A1

GENERAL INFORMATION:
APPLICANT: FOGELMAN, ALAN

APPLICANT: NAVMB, MOHAMAD

TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCIEROSIS

FILE REFERENCE: 4077-931220PC

CURRENT APPLICATION NUMBER: US/09/896,841A

CURRENT FILING DATE: 2000-06-29

PRIOR PELING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 86

SOFTWARE: PALENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FOGELMAN, ALAN
APPLICANT: ANANTHARAMAIAH, GATTADAHALLI
APPLICANT: NANTHARAMAIAH, GATTADAHALLI
APPLICANT: NANSH, MOHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REFERENCE: 407T-911220PC
CURRENT APPLICATION NUMBER: US/09/896,841A
CURRENT FILING DATE: 2001-06-29
PRIOR RILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PATENTIN VETRION 3.0
SEQ ID NO 31
LENGTH: 14
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Pred. No. 29;
4; Mismatches 3; Indels
                                                                                                                         58.5%; Score 38; DB 15; Length 18; 72.7%; Pred. No. 26; ive 1; Mismatches 2; Indels
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US-09-896-841A-31
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US-09-896-841A-38
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    VOLUME: 31
PAGES: 12688-12694
DATE: 1992
RELEVANT RESIDUES IN SEQ ID NO: 10: FROM 1 TO 18
                                                                                                                                                                                                                                                                                                           RESULT 34
US-09-896-841A-31
Sequence 31, Application US/09896841A
Publication No. US20030045460A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 46.2%;
Matches 6; Conservative
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2 AFYDKVFEKFKEF 14
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                                                                                                                                                                                                             2 LYKRLFKKLKK 12
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                                                                                     US-10-414-342-10
  VOLUME:
PAGES:
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LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Sequence 31, Application US/10187215
; bublication No. US20030171277A1
; bublication No. US20030171277A1
; bublication No. US20030171277A1
; denbeat inproperties
; publication No. US20030171277A1
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: NAVAB, MORAMAD
; TILE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REPERBNGE: 407T-911220US
; CURRENT APPLICATION NUMBER: US/10/187,215
; CURRENT APPLICATION NUMBER: US 09/096,841
; PRIOR APPLICATION NUMBER: US 09/096,841
; PRIOR APLICATION NUMBER: US 09/045,454
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3.1
: LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 38, Application US/10187215

Sequence 38, Application US/10187215

Publication No. US20030171277A1

GENERAL INFORMATION:

APPLICANT: POGELAMN, ALAN

APPLICANT: NAVAB, MOHAMAD

TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS

FILE REPERENCE: 4077-911220US

CURRENT APPLICATION NUMBER: US/10/187,215

CURRENT APPLICATION NUMBER: US 09/686,841

PRIOR PILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Petentin version 3.0

SEQ ID NO 38

LENGTH: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: synthetic or recombinant class A peptide
US-10-187-215-31
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Pred. No. 29;
4; Mismatches 3; Indels
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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OPERATING SYSTEM: D
            Query Match 56.9%;
Best Local Similarity 46.2%;
Matches 6; Conservative
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1 AFYDKVFEKFKEF 13
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1 AFYDKVFEKFKEF 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: ROCKLAMN, ALAN M.
APPLICANT: ROCKLAMN, ALAN M.
APPLICANT: NAVAH, MOHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REFERENCE: 4070-911230US
CURRENT PAPLICATION NUMBER: US/10/273,386
CURRENT FILING DATE: 2002-10-16
FRIOR PELING DATE: 2001-06-29
FRIOR PELING DATE: 2002-06-28
FRIOR PELING DATE: 2001-06-29
FRIOR PELING DATE: 2001-06-29
FRIOR RELING DATE: 2001-06-29
FRIOR RELING DATE: 2000-08-24
NUMBER OF SEQ 1D NOS: 103
NUMBER OF SEQ 1D NOS: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.9%; Score 37; DB 15; Length 14; 46.2%; Pred. No. 29; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic D peptides US-10-273-386-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Synthetic D peptides
US-10-273-386-38
                                                                                                     Sequence 31, Application US/10273386 Publication No. US20030229015A1 GENERAL INFORMATION:
ALYKRLFKKLKKF 13
                 | | ::|:| |:|
1 AFYDKVFEKFKEF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ALYKRLFKKLKKF 13
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ORGANISM: Artificial
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ORGANISM: Artificial
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Best Local Similarity
Matches 6; Conserv
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US-10-273-386-38
                                                                                       US-10-273-386-31
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APPLICANT: ANANTHARMAINH, GATTADAHALLI M.
APPLICANT: ANANTHARMAINH, GATTADAHALLI M.
APPLICANT: ANANTHARMAINH, GATTADAHALLI M.
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES SYNERGIZE STATIN ACTIVITY
FILE REFERENCE: 407t-911230US
CURRENT APPLICATION NUMBER: US/10/273,386
CURRENT APPLICATION NUMBER: US/210-16
PRIOR APPLICATION NUMBER: 10/107,215
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2000-08-44
PRIOR FILING DATE: 2000-08-3
SOFTWARE: PALCATION NUMBER: 09/645,454
PRIOR FILING DATE: 2000-08-3
SOFTWARE: PALCATION NUMBER: 09/645,454
PRIOR FILING DATE: 2000-08-3
SOFTWARE: PALCATION NUMBER: 09/645,454
PRIOR FILING DATE: 2000-08-3
SOFTWARE: PALCATION NUMBER: 09/645,454
PRIOR FILING DATE: 2000-08-3
SOFTWARE: PALCATION NUMBER: 09/645,454
PRIOR FILING DATE: 2000-08-3
SOFTWARE: PALCATION NUMBER: 09/645,454
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Cornut, Isabelle
Metz, Gunther
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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   Length 14;
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Score 37; DB 15;
Pred. No. 29;
4; Mismatches 3
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Pred. No. 29;
4; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic D peptides US-10-273-386-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 241, Application US/09865989
Publication No. US20030008827A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                            S-10-273-386-98
Sequence 98, Application US/10273386
Publication No. US20030229015A1
GENERAL INFORMATION:
APPLICANT: FOGELMAN, ALAN M.
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Sequence 6, Application US/09896841A Publication No. US20030045460A1 GENERAL INFORMATION:
                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 245:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn version 3.0
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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5 AFYDKVFEKFKEF 17
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5 AFYDKVFEKFKEF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.9
Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                                                                                                      US-09-865-989-245
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SOFTWARE: Pat
SEQ ID NO 13
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Cornut, Isabelle
Metz, Gunther, APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: APOLIPOPROTEIN TO TREAT DYSLIPIDEMIC DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                   NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 10;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: FISH COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
                                     APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: No. US20030008827Ale; SEQUENCE DESCRIPTION: SEQ ID NO: 241: US-09-865-989-241
                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 245, Application US/0965989; Publication No. US20030008827A1
GENERAL INFORMATION: APPLICANT: Dasseux, Jean-Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                     TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                              TELERAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 241:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.9%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 46.2*
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | ::|:| |:|
AFYDKVFEKFKEF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                       CURRENT
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13. Application US/09896841A

Sequence 13, Application US/09896841A

Sequence 13, Application No. US20030045460A1

PUDICATION No. US20030045460A1

GENERAL INFORMATION:
APPLICANT: FOGELMAN, ALAN

APPLICANT: NANTHARAMATAH, GATTADAHALLI

APPLICANT: NAVAB, MOHAMAD

TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS

FILE REFERENCE: 407T-911220PC

CURRENT APPLICATION NUMBER: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FOGELMAN, ALAN
APPLICANT: FOGELMAN, ALAN
APPLICANT: ANAWTHARARAIAH, GATTADAHALLI
APPLICANT: NAVABA, MOHAMAD
TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
FILE REPERRORC: 4077-9112200C
CURRENT APPLICATION NUMBER: US/09/896,841A
CURRENT FILING DATE: 2001-06-29
PRIOR PEPLICATION NUMBER: US 09/645,454
PRIOR PEPLICATION NUMBER: US 09/645,454
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PALENTIN VETSION 3.0
SEQ ID NO 6
LENGTH: 18
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                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                             Indels
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                                                                                                                        Score 37; DB 10;
Pred. No. 37;
4; Mismatches 3
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TOPOLOGY: linear
MOLECULE TYPE: No. US20030008827Ale
SEQUENCE DESCRIPTION: SEQ ID NO: 245:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37;
Pred. No. 3
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RESULT 45
US-09-6841A-20
; Sequence 20, Application US/09896841A
; Publication No. US20030045460A1
; GENERAL INFORMATION:
; APPLICANT: FOGELMAN, ALAN
; APPLICANT: ANATHARAMIAH, GATTADAHALLI
; APPLICANT: NAVAB, MOHAMAD
; TITLE OF INVENTION: ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; TITLE OF INVENTION ORALLY ADMINISTERED PEPTIDES TO AMELIORATE ATHEROSCLEROSIS
; FILE REPERENCE: 407T-911220PC
; CURRENT FILING DATE: 2001-06-29
; PRIOR PAPLICATION NUMBER: US 09/645,454
; PRIOR PAPLICATION NUMBER: US 09/645,454
; NUMBER OF SEQ ID NOS: 86
; SOFTHARE: PALENTIN VEXSION 3.0
; SEQ ID NO 20
; LENTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic or recombinant class A peptide
US-09-896-841A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: synthetic or recombinant class A peptide US-09-896-841A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 56.9%; Score 37; DB 10; Length 18; Best Local Similarity 46.2%; Pred. No. 37; Matches 6; Conservative 4; Mismatches 3; Indels
                                                                                                                       Query Match

56.9%; Score 37; DB 10; Length 18;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 16, 2005, 09:23:44
Job time : 49.8621 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                          1 ALYKRLFKKLKKF 13
                                                                                                                                                                                                                                                     S AFYDKVFEKFKEF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALYKRLFKKLKKF 13
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

May 16, 2005, 08:21:21 ; Search time 11.2069 Seconds (without alignments) 111.611 Million cell updates/sec Run on:

US-09-648-816B-13 65 Title: Perfect score:

1 ALYKRLFKKLKKF 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

22893 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Description           | dkų    |        | hypothetical | hypothetical |        | hypothetical |        | hypotheti | hypothetical |        | conserved hyp | gene e25 pro | transposase B |        |        | hypothetical p | dermaseptin - |        |        | cecropin A precurs |       | degenerate tr | hypothetical |        | calsequestrin, fas |        |        |      | himothetical prote |
|-----------|-----------------------|--------|--------|--------------|--------------|--------|--------------|--------|-----------|--------------|--------|---------------|--------------|---------------|--------|--------|----------------|---------------|--------|--------|--------------------|-------|---------------|--------------|--------|--------------------|--------|--------|------|--------------------|
| SUN       | Ω                     | 838596 | S46847 | G69787       | H70218       | E90557 | B90857       | A85763 | F82833    | G82355       | T08133 | E69437        | T03342       | AC3599        | T03065 | H97839 | T48105         | A40298        | B70252 | T07212 | CKMTA              | CKWKA | H97935        | T07326       | 872280 | B27499             | A69538 | AB0756 | ~    | F64318             |
|           | DB                    | 7      | -      | 7            | 7            | ~      | ~            | ~      | N         | ~            | ~      | N             | N            | N             | ~      | 7      | ~              | ~             | ~      | ~      | -                  | Н     | ~             | ~            | ~      | 7                  | ~      | 0      | 7    | ~                  |
|           | Query<br>Match Length | 57     | 71     | 71           | 36           | 20     | 9            | 9      | 32        | 55           | 65     | 68            | 53           | 23            | 61     | 62     | 69             | 34            | 34     | 57     | 63                 | 64    | 42            | 51           | 51     | 26                 | 26     | 57     | 57   | 28                 |
| ٠         | Query<br>Match        | 63.1   | 55.4   | 53.8         | 52.3         | 52.3   | 50.8         | 50.8   | 49.2      | ٠            | 49.2   | 49.2          | 47.7         | 47.7          | 47.7   | 47.7   | 47.7           | 46.2          | 46.2   | 46.2   | 46.2               | 46.2  | 44.6          | 44.6         | •      | 44.6               | 44.6   | 44.6   | 44.6 | 44.6               |
|           | Score                 | 41     | 36     | 35           | 34           | 34     | 33           | 33     | 32        | 32           | 32     | 32            | 31           | 31            | 31     | 31     | 31             | 30            |        | 30     |                    | 30    | 29            | 59           | 29     | 29                 | 29     | 29     | 53   | 29                 |
|           | Result<br>No.         | 7      | 0      | e            | 4            | ស      | 9            |        | œ         | σı           | 10     | 11            | 12           | 13            | 14     | 15     | 16             | 17            |        | 19     |                    | 21    | 22            | 23           | ~      | . 25               | 56     | 27     | 28   | 59                 |

# ALIGNMENTS

| RESULT 1<br>838596<br>hypothetical protein 57 (rps2 3' region) - euglenid (Astasia longa) plastid | C;Species: plastid Astasia longa<br>C;Cate: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004<br>C;Accesion: S38596 | R;Gockel, G.; Baier, S.; Hachtel, W.<br>submitted to the EMBL Data Library, November 1993<br>A;Reference number: S38590 | A;Accesale nr. 534596<br>Molecule type: DNA<br>A;Residues: 1-57 <goc><br/>A;Cross-references: UNIPROT:P34774; EMBL:X75651; NID:g414852; PID:g414861</goc> | Score 41; DB 2; Length 57;<br>Pred; No. 6.1;                                    | /; Conservative 3; mismatches 2; indeib 0; caps 0; 1 LYKRLFKKLKKF 13 :  :  :   :   :   :   :   :   :   : |
|---------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------|
| RESULT 1<br>S38596<br>hypothetical protein 57                                                     | C.Species: plastid Astas<br>C.Date: 31-Dec-1993 #seq<br>C.Accesion: S38596                                                            | R;Gockel, G.; Baier, S.; Hi<br>submitted to the EMBL Data<br>A;Reference number: S38590                                 | A;Accession: S38596<br>A;Molecule type: DNA<br>A;Residues: 1-57 <goc><br/>A;Cross-references: UNIP</goc>                                                  | C;Keywords: chloroplast; plastid<br>Query Match<br>Best Local Similarity 58.3%; | Marches                                                                                                  |

hypothetical protein JGR - variola major virus (strains India-1967 and Harvey)

NiAlternate names: 28R protein; A52R protein (middle)
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Species: variola major virus
C;Spacession: S4684; JQ1859
R;Kolykhalov, A.A.; Blinov, V.M.; Frolov, I.V.; Totmenin, A.V.; Shchelkunov, S.N.; Sanda)
Submitted to the EMBL Data Library, April 1992
A;Reference number: S46842
A;Reference number: S46842
A;Reference number: S46847

A;Molecule type: DNA A;Residues: 1-71 «KOL» A;Cross-references: UNIPROT:Q89619; EMBL:X67118; NID:g516399; PIDN:CAA47548.1; PID:g5164( A;Experimental source: strain India-1967, isolate Ind3 R;Blinov, V.M. Bubmitted to GenBank, November 1992 A;Reference number: A36859 A;Accession: E36854

A;MOJECULE LYDE: DNA
A;Residues: 1.71 cBLI>
A;Residues: 1.71 cBLI>
A;Residues: 1.71 cBLI>
A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49105.1; PID:g457055
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Aguado, B.; Selmes, I.P.; Smith, G.L.
C, Gen. Virol. 73, 2887-2902, 1992
A;Title: Nuclocide sequence of 21.8 kbp of variola major virus strain Harvey and compar: A;Reference number: JQ1832; MUID:93057361; PMID:1331292

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CiSpecies: Mycoplasma pulmonis
CiSpecies: Advanced by 101 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
CiAccession: B90557
Richambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
Nucleic Acids Res. 29, 2145-2153, 2001
A;Itle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q98QJ6; GB:AL445566; PID:g14089779; PIDN:CAC13538.1; GSPDB:GR
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. Day Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genom A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q8X7A7; GB:BA000007; PIDN:BAB35249.1; PID:g13361291; GSPDB:GA
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ypothetical protein EC81826 [imported] - Escherichia coli (strain O157:H7, substrain RIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ηγροthetical protein MYPU_3650 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Bscherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C.Accession: B90857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 2; Le.
Pred. No. 1.2e+02;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 2;
Pred. No. 72;
4; Mismatches 1
                                                                                                                                    DB 2;
                                                                                                                                                                                                   4; Mismatches
                                                                                                                                    Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.3%;
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                                                                                                                                    52.3%;
50.0%;
A; Experimental source: strain B31 C; Genetics:
                                                                                                     Query Match
Best Local Similarity 50.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50...
From S; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||: || |:||
ALFIRLLKRLK 19
                                                                                                                                                                                                                                                                         3 YKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                        27 FKKFFEKIKK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 YKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 YKKLYENIKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
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A;Residues: 1-60 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Genetic code: SGC3
                                                                     A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: MYPU 3650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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A85763
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G69787

hypothetical protein ydiN - Bacillus subtilis

C;Species: Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G69787

C;Accession: G69787

R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc

A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

A; Authors: Callger, D.; Fritz, C.; Fujita, M.; Kurita, K.; Lapidus, A.; Layinois, A.; Authors: Lamber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Saco, T.; Scanlon, A.; Aluthors: Schleich, S.; Schroeter, R.; Scoffone, R.; Tognoni, J.; Sekowska, A.; Seror

A; Authors: Yobhikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Vollyama, A.; Liu, E.; Tognoni, A.; Tosato, V.; Yoshida, M.; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A; Acterial anumber: A69580; MUID:98044033; Phun: Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis and Parallalis a
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Whypothetical protein BBB20 - Lyme disease spirochete plasmid B/cp26

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Accession: H70218

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Pecerson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580, 586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:050991; GB:AE000792; NID:g3253098; PIDN:AAC66341.1; PID:g268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:034608; GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12424. A;Experimental source: strain 168
                                                                                                                                                                                                                                                                         ö
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70218
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: LNA
A;Residues: 1-36 cKLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-71 <KUN>
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                                                                                                                                                                                                   Score 36; DB 1; Length 71; Pred. No. 48; 2; Indels 3; Mismatches 2; Indels
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Pred. No. 69;
2; Mismatches 2; Indels
                                  A;Molecule type: DNA
A;Residues: 1-67 <AGUs
A;Experimental source: strain Harvey
C;Superfamily: variola major virus hypothetical protein J6R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.8%;
                                                                                                                                                                                                   Query Match 55.4%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                    3 YKRLFKKLKKF 13
| | | | | :::| |
21 YGRLFNEIRKF 31
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FKVLYKLLKKF
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Best Local Similarity
Matches 7; Conserva
   A; Accession: JQ1859
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Gaps ; 0

Length 50; Indels ö

Gaps

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Length 60 Indels

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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 49.2%;
Similarity 85.7%;
6; Conservative
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-65 < ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: VC0169
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrarc, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajina, J.P.; Kriager, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Matuthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.W.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Aththors: da Silva, A.C.R.; da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; S.
                                                                                                  Riperna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85763
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-60 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PBESULT 8
F9233
hypothetical protein XF0218 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;NOTE: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q8X7A7; GB:AE005174; NID:g12515550; PIDN:AAG56565.1; GSPDB:GA;Experimental source: strain 0157:H7, substrain BDL933 C;Genetics:
A;Genetics:
probable transposase (partial) 22563 [imported] - Escherichia coli (strain O157:H7, subs
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q9PGT0, GB:AE003875; GB:AE003849; NID:g9105019; PIDN:AAF8303
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Pred. No. 1.2e+02;
2; Mismatches 2; Indels
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Pred. No. 1e+02
4; Mismatches
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Best Local Similarity 63.0
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Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ALYKRLFKKLK 11
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C, Genetics:
A, Gene: XF0218
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A;Molecule type: DNA
A;Residues: 1-32 <SIM>
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RESULT 9 G82355 hypothetical protein VC0169 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

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Rifeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. J., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A,Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A,Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Robsidues: 1-55 <HEI>
A;Cross-references: UND:G9654569; PIDN:AAF93344:
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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Plant J. 9, 625-637, 1996
A,Title: Charaterisation of anther-expressed genes encoding a major class of extracellula A,Reference number: 216361, MUID:96237453, PMID:8653113
A,Accession: T08133
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A,Experimental source: cv. Topas; inflorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: B65437
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, G;Accession: B65437
G;Accession: RD; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Releischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. algodek, Z. Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Sanith, H.O.; Woese, C.R.; Vencer, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T08133
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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ilarity 45.5%; Pred. No. 1.9e+02;
Conservative 5; Mismatches 1;
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C;Keywords: extracellular protein; pollen
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A;Cross-references: UNIPROT:Q92GK3; GB:AE006914; PIDN:AAL03658.1; PID:g15620245; GSPDB:Gr.C;Genetics:
A;Gene: RC1120
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StRieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24459
                                                                                                                                               C;Accession: T03065
R;Bahr, U.; Tidona, C.A.; Darai, G.
R;Bahr, U.; Tidona, C.A.; Darai, G.
R;Bahr, U.; Tidona, C.A.; 1997
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101
A;Reference number: Z14834; MUID:98141693; PMID:9482589
A;Accession: T03065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-61 <BAH>
A;Cross-references: UNIFROT:055728; EMBL:AF003534; NID:g2738385; PIDN:AAB94439.1; PID:g2
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R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, pecies: Rickettsia conorii
C, Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                      C;Species: Chilo iridescent virus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.7e+02;
2; Mismatches 3; Indels
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oxidase homolog 043L - Chilo iridescent virus
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A;Molecule type: DNA
A;Residues: 1-69 <a href="https://doi.org/10.100/">https://doi.org/10.100/<a href="https://doi.org/">https://doi.org/<a href="https://doi.org/">https://do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 2; 1
Pred. No. 2.7e+02;
7; Mismatches 1.
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Pred. No. 3e+02;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 33.3
Matches 4; Conservative
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6 LKKRINKFIKKF 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T48105
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A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricrutz-Le Cog, A.M.; Cesselin, B.; Commissaire, J.; Anba, J.; Kyriakidis, S.; Chopin, M submitted to the EMBL Data Library, June 1997

**A Description: Sequence and organization of the lactococcal isometric bill70 phage genom A; Reference number: 214903

**A Accession: T03342

**A Status: preliminary; translated from GB/EMBL/DDBJ

**A Status: DNA

**A Status: DNA

**A Status: DNA

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C; Genetics:
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession. AC3599
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
Nazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. US.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
    A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-68 <KLLS
A;Cross-references: UNIPROT:028770; GB:AE000999; GB:AE000782; NID:g2689322; PIDN:AAB8975
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|Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
|Accession: T03342
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41.7%; Pred. No. 2.3e+02;
ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                       Length 68;
                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                             Score 32; DB 2;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                  49.2%;
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Best Local Similarity 60.0-
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Best Local Similarity 41.7
Matches 5; Conservative
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12 LVERFFNRIKOF 23
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4 KELIKELEKF 13
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Best Local Similarity
Matches 6; Conserv
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A, Molecule type: DNA
A, Residues: 1-53 < KUR>
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A, Map position: II
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A; Gene: e25

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C; Genetics:

RESULT 14 T03065

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46.2%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                     17 LYKIKEKFLKKF
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KLFKKIEK 36
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nes 5; Conserv
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-63 <YA2>
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B70252
hypothetical protein BBK08 - Lyme disease spirochete plasmid K/lp36
c; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Species: Borrelia burgdorferi (Lyme disease spirochete)
C; Accession: B70252
C; Accession: B70252
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Feterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, son, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
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C; Species: chloroplast Chlorella vulgaris chloroplast
C; Species: chloroplast Chlorella vulgaris change 21-Jul-2000
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C; Accession: T07212
R; Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A; Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlc
A; Reference number: Z15985; MUID:97303241; PMID:9159184
                                                                                                                         A40298
dermaseptin - Sauvage's leaf frog
dermaseptin - Sauvage's leaf frog)
C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Apr-1998
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Apr-1998
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Apr-1998
R;Mor, A.; Nguyen, V.H.; Delfour, A.; Migliore-Samour, D.; Nicolas, P.
Biochemistry 30, 8824-8830, 1991
A;Title: Isolation, amino acid sequence, and synthesis of dermaseptin, a novel antimicro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:OS0812; GB:AE000788; NID:92690123; PIDN:AAC66154.1; PID:9269
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A40298
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-34 <MOR>
C;Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology
C;Keywords: skin
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; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Ha
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUD: 98065943; PMID: 9403685
A;Accession: B70552
A;Atatus: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-34 <KLE>
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Pred. No. 2.2e+02;
2; Mismatches 2;
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50.0%; Pred. No. 2.2e+02;
iive 3; Mismatches 2;
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Best Local Similarity 60.0
....hes 6; Conservative
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Matches 5; Conservative
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1 ALWKTMLKKL 10
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KKFLEKLKKY 14
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                                                  49
2 LYKRLFKKL 10
                              41 VFKPLFKK
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NiAlternate names: CecAl; CecA2
CiSpecies: Bombyx mori (Bailkworn)
CiDate: 17-Apr-1993 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
CiAccession: JC2295; A60524; JW0074; JW0073
R;Yamano, Y.; Matsumoto, M.; Inoue, K.; Kawabata, T.; Morishima, I.
Biseci. Bistechnol. Biochem. 58, 1476-1478, 1994
A;Title: Cloning of cDNNs for cecropina A. and B, and expression of the genes in the silk
A;Reference number: JC2295; MUID:94369101; PMID:7765280
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A; Mesidues: 27-61 cMOR>
A; Residues: 27-61 cMOR>
A; Residues: 27-61 cMOR>
A; Residues: 27-61 cMOR>
A; Mote: cercopins A! and A2 differ in eletrophoretic mobility but not in sequence or exp.
R; Yamano, Y.; Matsumoto, M.; Sasahara, K.; Sakamoto, E.; Morishima, I.
R; Yamano, Y.; Matsumoto, M.; Sasahara, K.; Sakamoto, E.; Morishima, I.
Biosci. Biotechnol. Biochem. 62, 237-241, 1998
A; Yitle: Structure of genes for cecropin A and an inducible nuclear protein that binds to A; Reference number: JW0073; MUID:98193973; PMID:9512780
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(f. Superfamily: cecropin
C; Superfamily: cecropin
C; Keywords: amidated carboxyl end; antibacterial; hemolymph; hydroxylysine
C; Keywords: amidated carboxyl end; artibacter (SIG)
F; 1-22, Domain: signal sequence #status predicted (SRO)
F; 23-26/Domain: propeptide #status predicted (PRO)
F; 27-61/Product: cecropin A #status experimental
F; 77-Modified site: 5-hydroxylysine (Ly9) #status experimental
F; 61/Modified site: amidated carboxyl end (Leu) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues 1.63 *YMN-
A;Cross-references: UNINEOT:027239; DDBJ:D17394; NID:g1813338; PIDN:BAA04217.1; PID:g122
R;Morishima, I.; Suginaka, S.; Ueno, T.; Hirano, H.
Comp. Biochem: Physiol. B 95, 551-554, 1990
A;Title: Isolation and structure of cecropins, inducible antibacterial peptides, from th
A;Reference number: A60524; MUID:90235568; PMID:2184991
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-57 <WAX>
A;Residues: 1-57 <WAX>
A;Crostorereferences: EMBL:AB001684; NID:g2224352; PIDN:BAA57859.1; PID:g2224375
C;Genetics: A;Genome: chloroplast
C;Keywords: chloroplast
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A;Cross-references: UNIPROT:Q8DQT4; GB:AE007317; PIDN:AAK99316.1; PID:g15458085; GSPDB:Gr
C;Genetics:
A;Gene: IS1239-truncation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: chloroplast Chlorella vulgaris chloroplast
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C; Accession: T07326
R; Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakasl Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A; Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chloroplast A; Reference number: 215985; MUID:97303241; PMID:9159184
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R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyte R;Wilson, R.J.M.; Denny, P.W.; Preiser, P.R.; Rangachari, K.; Roberts, K.; Roy, A.; Whyte A;Title: Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium fall A;Reference number: S72277; MUID:96346169; PMID:8757284
A;Accession: S72280
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A;Note: the nucleotide seguence was submitted to the EMBL Data Library, January 1996
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C;Species: plastid Plasmodium falciparum
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
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A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: H97935 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-42 <KUR> A;Cross-reference
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Pred. No. 4.7e+02;
...----hes 2; Indels
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Pred. No. 4.7e+02;
2; Mismatches 4
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Pred. No. 3.9e+02;
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A,Molecule type: DNA
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Similarity 66.7%;
6; Conservative
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Best Local Similarity 50.0%;
Matches 6; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
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A; Residues: 1-51 <WIL>
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A; Mesidues: 27-63 <STE>
A; Residues: 27-63 <STE>
B; Andreu, D.; Merrifield, R.B.; Steiner, H.; Boman, H.G.
B; Andreu, D.; Merrifield, R.B.; Steiner, H.; Boman, H.G.
Proc. Natl. Acad. Sci. U.S.A. 80, 6475-6479, 1983
A; Title: Solid-phase synthesis of cecropin A and related peptides.
A; Reference number: Asy860; MUID:84044944; PMID:6579533
A; Contents: annotation; chemical synthesis
A; Note: protein carboxyl-terminal composition and amidation determined by mass spectrome C; Comment: Cecropins are a family of basic peptides having lytic and antibacterial activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-64 - KLID>
A; Residues: 1-64 - KLID>
A; Residues: 1-64 - KLID>
A; Cross-references: ENBL: X06672; NID: 99413; PIDN: CAA29871.1; PID: 9671870
B; Hultmark, D.; Engstrom, A.; Bennich, H.; Kapur, R.; Boman, H.G.
B; Hultmark, D.; Engstrom, A.; Bennich, H.; Kapur, R.; Boman, H.G.
A; Hultmark, D.; Engstrom, A.; Bennich, H.; Kapur, R.; Boman, H.G.
A; Title: Insect immunity: isolation and structure of cecropin D and four minor antibacte
A; Reference number: A91121; MUID: 83053366; PMID: 7140755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: cecropin
C; Keywords: amidated carboxyl end; antibacterial; hemolymph
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-26/Domain: propeptide #status predicted <PRO>
F;27-63/Product: cecropin A #status experimental <MAT>
F;63/Modified site: amidated carboxyl end (Lys) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                  ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P01507; GB:M63845; NID:g159196; PIDN:AAA29185.1; PID:g159197 R;Lidholm, D.A.; Gudmundsson, G.H.; Xanthopoulos, K.G.; Boman, H.G. RESS Lett. 226, 8-12, 1987 A;Title: Insect immunity: CDNA clones coding for the precursor forms of cecropins A and A;Reference number: S00208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence and specificity of two antibacterial proteins involved in insect immun
A;Reference number: A93260; MUID:81245158; PMID:7019715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degenerate transposase [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 09-Jul-2004
C;Accession: H97935
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; S.; R;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Iy, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
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                                                                                                                                           NiAlternate frames: cecropin C
C;Species: Hyalophora cecropia (cecropia moth)
C;Date: 24-589-1981 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46420; S00208; A31121; A3260; A01769
R;Gudmundsson, G.H.; Lidholm, D.A.; Asling, B.; Gan, R.; Boman, H.G.
J. Biol. Chem. 266, 11510-11517, 1991
A;Fitle: The cecropin locus: Cloning and expression of a gene cluster encodi
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A;Residues: 27-63 atHL>
A;Residues: 27-63 atHL>
A;Note: cecropin C lacks the carboxyl-terminal blocking group:
R;Steiner, H.; Hultmark, D.; Engstrom, A.; Bennich, H.; Boman, H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 30; DB 1; Length 64;
Pred. No. 4e+02;
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KLFKKIEK 36
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: A40420
A;Molecule type: DNA
A;Residues: 1-64 <GUD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 292, 246-248,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A93260
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Clostridium acetobutylicum
Cispecies: Clostridium acetobutylicum
Cispecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
Cisccesion: G97083
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q97IZ6; GB:AE001437; PIDN:AAK79458.1; PID:g15024437; GSPDB:GP
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence_revision 15-Sep-1996 #text_change 09-Jul-2004
C;Date: 13-Sep-1996 #sequence 0.3.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, L.; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinst, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Rieference number: A64300, MulD:96337999; PMID:8688087
A;Reference number: A64308
A;Accession: F64318
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C;Genetics:
A;Map position: REV146003-145827
                                                                                                                                                                 A;Accession: AB0756
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05749.1; PID:g16503241; GSPDB:GN00176
C;Genetics:
A;Gene: STY2210
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A;Molecule type: DNA
A;Residues: 1-58 <BUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 2; Length 57;
Pred. No. 5.2e+02;
4; Mismatches 2; Indels
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75.0%; Pred. No. 5.2e+02;
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Pred. No. 5.3e+02;
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23 AMYQRLMRREK 33
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         Nature 413, 848-852, 2001
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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A; Status: preliminary
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Os. Dec.1997 #sequence_revision 05-Dec.1997 #text_change 09-Jul-2004
C;Accession: A69538
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                      RESULT 25
calegorestrin, fast skeletal muscle - dog (fragment)
calegorestrin, fast skeletal muscle - dog (fragment)
NiAlternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; laminin-
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: B27499
R;Slupsky, J.R.; Ohnishi, M.; Carpenter, M.R.; Reithmeier, R.A.F.
A;Title: Characterization of cardiac calsequestrin.
A;Reference number: A90520; MUID:88107564; PMID:3427023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:P31236
;Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protei;Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to c;Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi;Superfamily: calsequestrin; skeletal muscle isoform; skeletal muscle
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R;Parkhil, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
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Pred. No. 5.1e+02;
3; Mismatches 3; Indels
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Best Local Similarity 50.0%;
Matches 6; Conservative
13 LYINKYKKLLKY 24
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38 LAERFVKELEKF 49
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23 YKNVFKK 29
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A; Residues: 1-56 < KLE>
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A69538
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A;Gene: SGD:QCR9; UCR9; MIPS:YGR183c
A;Cross-references: SGD:S0003415; MIPS:YGR183c
A;Map position: 7R
A;Genome: nuclear
A;Genome: nuclear
A;Introns: 1/3
C;Superfamily: ubiquinol-cytochrome-c reductase (cytochrome c1) (complex III), nonheme st C;Keywords: membrane-associated complex; mitochondrion; oxidative phosphorylation; oxidor F;2-66/Product: ubiquinol-cytochrome-c reductase chain 9 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dispothetical protein BH3821 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B84127
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirani Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and can also and can be a sequence of the alkaliphilic bacterium Bacillus halodurans and can be a sequence number: Asseterence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-74 <STO>
A;Cross-references: UNIPROT:Q9K6A8; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB0754
A;Experimental source: strain C-125
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C;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Species: 17-Dec-1982 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: A54725; A01711
R;Craig, A.G.; Engetroem, A.; Bennich, H.; Kamensky, I.
Biomed. Environ. Mass Spectrom. 14, 669-673, 1987
A;Title: Plasma desorption mass spectrometry coupled with conventional peptide sequencing A;Reference number: A54725; WUID:88108273; PMID:2962676
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C;Keywords: amidated carboxyl end; antibacterial
F;35/Modified site: amidated carboxyl end (Leu) #status experimental
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A;Residues: 1-35,'S' <QUX>
A;Note: the carboxyl end is blocked and was not sequenced directly
                                                                                                                                                                                                                                                                                                                                               44.6%; Score 29; DB 1; Length 66; 55.6%; Pred. No. 6e+02; cive 2; Mismatches 2; Indels
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Eur. J. Biochem. 127, 219-224, 1982
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Pred. No. 6.7e+02;
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Conservative
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Conservative
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64 LIEKIKKKLKK 74
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Best Local Similarity
Matches 5; Conserv
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Matches 6; Conserv
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A,Gene: BH3821
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A;Residues: 1-66 <HEB>
A;Cross-references: EMBL:272968; NID:g1323323; PIDN:CAA97209.1; PID:g1323324; GSPDB:GN00
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A;Experimental source: strain S288C
C;Genetics:
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A;Molecule type: protein
A;Residues: 2-11 FPH2.
R;Hebing, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64003
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                                                                                                                                                                                                                                                                                                                                                                      C;Spēcies: Glycine max (soybean)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: 105702
R;Hata, S; Izui, K.; Kouchi, H.
Plant J. 13, 267-273, 1998
A;Title: Expression of a soybean nodule-enhanced phosphoenolpyruvate carboxylase gene A;Accession: T05702
A;Accession: T05702
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A;Reference number: S64499
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A;Cross-references: UNIPROT:O22118; EMBL:AB008543; PIDN:BAA23422.1
A;Experimental source: cultivar Akisengoku
C;Function:
                                                                                                                                                                                                                                                                        RESULT 30
T05702
phosphoenolpyruvate carboxylase (EC 4.1.1.31) - soybean (fragment)
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Pred. No. 5.5e+02;
1; Mismatches 3; Indels
               Indels
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A;Molecule type: mRNA
               Mismatches
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               <u>ب</u>
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               Conservative
                                                                                  3 YKRLFKKLKKF 13
                                                                                                                                                         FGRLFKMIKDY 55
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21 YRRIKLLKK 30
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Best Local Similarity
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A; Residues: 1-66 <PHI>
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               2
               Matches
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C;Accession: T07309

R;Waksaugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakasł Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997

A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlos A;Fitle: Complete nucleotide sequence of the chloroplast genome from the green alga Chlos A;Feterence number: Z15985, MUID:97303241; PMID:9159184

A;Accession: T07309

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-49 < WAK>
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A.; Anthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuma, S.; Galizzi, A.; Gallerc A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F., Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scror, A.; Althers, P.; Mipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wohlkawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tata, K.; Yoshida, K.; Yata, K.; Yata, K.; Yoshida, K.; Mreference number: Aseguence of the Gram-poslive bacterium Bacillus subtilis.
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A;Experimental source: strain 168
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C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: H99537
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
A;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmc
A;Reference number: A99512; MUID:21267165; PMID:11353084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appendes: Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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Pred. No. 6.6e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 2; Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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KKRFKSLEEF
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                               A; Genome: chloroplast
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A,Gene: yrzI
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                                                                                                                                                                                                                                        RESULT 34

B97327

hypothetical protein CAC3479 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97327
R;Nolling, J, Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Batteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97127
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-38 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q97DJ8; GB:AE001437; PIDN:AAK81405.1; PID:g15026569; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
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H91081
hypottetical protein NWB1455 [imported] - Neisseria meningitidis (strain MC58 serogroup C; Species: Neisseria meningitidis
C; Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
R; Tettelin, H: Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; It, H:; Olin, H:; Vanathovan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vanathors: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUD:20175755; PMID:10710307
A; Moscols type: DNA
A; Residues: 1-39 <-TET>
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strain MC58
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C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 5.3e+02;
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Pred. No. 5.2e+02;
1; Mismatches 5;
         Pred. No. 4.8e+02;
                                   Mismatches
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A;Experimental source: serogroup B,
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62.5%;
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50.0%;
      50.0%;
                                   Conservative
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Matches 5; Conservative
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KRIFSKLE 30
                                                                                          5 RLFKKLKK 12
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KIFKKIEK 10
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   Best Local Similarity
Matches 4; Conserv
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Les 6; Conserv
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A,Gene: CAC3479
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A;Gene: NMB1455
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Best Local S
Matches 6
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T07309
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Reference number: A01768
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Residues: 27-61 <TES>
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Residues: 1-63 <TAN>
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Residues: 1-63 <KAT>
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A.Residues: 1-51 < DUN>
A.Crose-references: UNTROT.P03791
B.Crose-references: UNTROT.P03791
A.Mol. Biol. 148, 303-330, 1981
A.Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be A.Reference number: A92866; MUID:82078034; PMID:7310871
A.Accession: H43004
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(997149)

Hyporteid protein CAC2027 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J; Bacteriol. 183, 4823-4838, 2001
                                                                                 A;Molecule type: DNA,
M. Residues: 1-50 cKUR.
A;Residues: 1-50 cKUR.
A;Residues: 1-50 cKUR.
A;Cross-references: UNIPROT:Q98R02; GB:AL445566; PID:g14089621; PIDN:CAC13381.1; GSPDB:A;Experimental source: strain UAB CTIP
A;Experimental source: strain UAB CTIP
A;Geneties:
A;Genetic sode: SGC3
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A; Residues: 1-51 <DU2>
A; Residues: 1-51 <DU2>
A; Cross-references: GB:V01127; NID:g15498; PIDN:CAA24337.1; PID:g15509
A; Cross-references: GB:V01127; NID:g15498; PIDN:CAA24337.1; PID:g15509
B; Dunn, JJ.; Studier, F.W.
J. Mol. Biol. 166, 477-535, 1983
A; Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7
A; Reference number: S42283; MUID:83241725; PMID:6864790
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Q1BP47
G18P47
G196 1.4 protein - phage T7
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C196 1.4 protein - phage T7
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Pred. No. 6.7e+02;
0; Mismatches 3; Indels
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Pred. No. 6.8e+02;
2; Mismatches 1;
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C;Superfamily: phage T7 gene 1.4 protein
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Best Local Similarity
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A; Residues: 1-51 < DUW>
A;Accession: H90537
A;Status: preliminary
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A Status: preliminary
A Molecule type: DNA
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Biochem. Physiol. B 95, 551-554; 1990 homp. Biochem. Physiol. B 95, 551-56; 1990 hydrite: Isolation and structure of cecropins, inducible antibacterial peptides, from the hyperence number: A60524; MUID:90213568; PMID:2184991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Note: cecropin B1 has hydroxylated Lys-47; cecropin B2 does not c;Comment: Identical cecropin B precursors are encoded by at least two different genes. C;Comment: Cecropins are a family of basic peptides having lytic and antibacterial activ. C;Comment: This peptide was isolated from the body fluid of silkworms vaccinated with kills.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B cDNA clones from the silkworm,
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A,Note: sequence extracted from NCBI backbone (NCBIN:131941, NCBIP:131942)
R;Teshima, T.; Ueki, Y.; Nakai, T.; Shiba, T.
Tetrahedron 42, 829-834, 1986
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Keywords: amidated carboxyl end; antibacterial; hemolymph; hydroxylysine
F;1-22,Domain: signal sequence #status predicted <SIG>
F;23-26/Domain: propeptide #status predicted <PRO>
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',Readdues: 1-63 <YMA'
',Cross-references: UNIPROT: P04142; DDBJ:DJ7394
',Taniai, K.; Kato, Y.; Hirochika, H.; Yamakawa, M.
ijochim. Blophys. Acta 1132, 203-206, 1992
',Title: Isolation and nucleotide sequence of cecropin E.;
',Reference number: S28948; MUID:93003325; PMID:1390892
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Pred. No. 7.6e+02;
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Matches 5, Conservative
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Gaps

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C; Species: Sulfolobus solfataricus
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C; Jacession: 909502
C; Accession: 909503
C; Accession: 909503
R; Sho, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Vong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Parett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:097U44; GB:AE006641; NID:913816613; PIDN:AAK43278.1; GSPDB:Gr
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-68 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Methanococcus jannaschii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
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C;Superfamily: Methanococcus jannaschii hypothetical protein MJ0975
                                                                                                                                                                                                                                                                                                                                              Apothetical protein SS012127 [imported] - Sulfolobus solfataricus
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       Pred. No. 8.5e+02;
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ilarity 50.0%; Pred. No. 8.6e+02;
Conservative 1; Mismatches 5;
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                                   2; Mismatches
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Job time : 12.2069 secs
62.5%;
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                                   5; Conservative
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A;Accession: G90502
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AIYEKGVLKLKK
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Best Local Similarity
Matches 6; Conserv
Best Local Similarity
Matches 5; Conserv
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C.Species: Bscherichia coli
C.Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C.Accession: JV0033; D65127
R.Andrews, S.C.; Harrison, P.M.; Guest, J.R.
R.Andrews, S.C.; Harrison, P.M.; Guest, J.R.
A.Title: Cloning, sequencing, and mapping of the bacterioferritin gene (bfr) of Escheric
A.Reference number: JV0032; MUID:89291745; PMID:2661540
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A;Accession: JV0033
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cosa-references: UNIPROT:P13655, GB:M27176; NID:g145406; PIDN:AAC13986.1; PID:g145408
A;Experimental source: strain Kl2
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Experimental source: strain Madrid E
C;Genetics:
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A; Residues: 1-64 SLAT>
A; Cross-references: GB:AB000410; GB:U00096; NID:g1789734; PIDN:AAC76362.1; PID:g1789735; A; Experimental source: strain K-12, substrain MG1655
F;27-61/Product: cecropin B #status experimental <MAT>
F;47/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
F;61/Modified site: amidated carboxyl end (Ile) (amide in mature form from following gly
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(271652)

hypothetical protein RP488 - Rickettsia prowazekii

C;Species: Rickettsia prowazekii

C;Species: Rickettsia prowazekii

C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C;Accession: C71652

R;Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998

A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893

A;Accession: C71652

A;Accession: C71654

A;Reterence number: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-64 <AND>
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                                                                                                                                     Query Match
43.1%; Score 28; DB 1; Length 63;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 4; Conservative 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 71.4 es 5; Conservative
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C;Superfamily: yheA protein
                                                                                                                                                                                                                                                                                 5 RLFKKLKK 12
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29 KIFKKIEK 36
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A;Gene: yheA

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Query Match

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

May 16, 2005, 08:21:21; Search time 54.8017 Seconds (without alignments) 121.475 Million cell updates/sec Run on:

1 ALYKRLFKKLKKF 13 US-09-648-816B-13 65 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

145419 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 74

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

|           | i,      |        | astasia lon | treponema d | white spot | variola vir | bacillus su | leptospira | borrelia bu | mycoplasma | homo sapien | desulfovibr | anthoceros | leptospira      | prochloroco | escherichia | thermoanaer | plasmodium | drosophila | methanosarc | malawimonas | plasmodium | xylella fas | plasmodium | brucella su | leptospira | vibrio chol | thermoanaer | bacteriopha | brassica na | archaeoglob |        |
|-----------|---------|--------|-------------|-------------|------------|-------------|-------------|------------|-------------|------------|-------------|-------------|------------|-----------------|-------------|-------------|-------------|------------|------------|-------------|-------------|------------|-------------|------------|-------------|------------|-------------|-------------|-------------|-------------|-------------|--------|
|           | , 100 C | 111000 | P34774      | 073ph2      | Q911d9     | 089619      | 034608      | Q8ex18     | 050991      | Q98qj6     | Q9uc64      | Q72b46      | Q85bu5     | Q8£8i9          | Q7vaa7      | Q8x7a7      | Q8r6y6      | Q7rrq4     | 046271     | Q8t183      | Q99891      | Q7rkx5     | Q9pgt0      | Q7reb3     | Q8fzj7      | Q8£286     | Q9kvh7      | Q8r9u0      | Q6wi99      | Q43403      | 028770      | 08tgr3 |
|           |         |        |             |             |            |             |             |            |             |            |             |             |            |                 |             |             |             |            |            |             |             |            |             |            |             |            |             |             |             |             |             |        |
| SUMMARIES | £       |        | YCX1_ASTLO  | Q73PH2      | Q91LD9     | 089619      | YDIN BACSU  | QBEXL8     | 050991      | Q98QJ6     | Q9UC64      | Q72B46      | YCX2 ANTFO | Q8F8 <u>T</u> 9 | Q7VAA7      | Q8X7A7      | QBR6Y6      | Q7RRQ4     | 046271     | QBTLS3      | Q9G891      | Q7RKX5     | Q9PGT0      | Q7REB3     | Q8FZJ7      | Q8F286     | Q9KVH7      | QBR9U0      | 06MI99      | Q43403      | YF02 ARCFU  | OBTGR3 |
|           | 0       | 9 :    | -           | N           | 7          | ~           | -           | ~          | 7           | ~          | 7           | ~           | ٦          | ~               | 7           | ~           | 0           | ~          | ~          | ~           | ~           | ~          | 7           | ~          | 7           | 7          | ~           | 7           | N           | ~           | -           | ~      |
|           | 1000    |        | 57          | 28          | 69         | 71          | 71          | 35         | 36          | 20         | 54          | 70          | 27         | 45              | 24          | 9           | 61          | 65         | 68         | 71          | 74          | 20         | 32          | 41         | 42          | 43         | 55          | 9           | 62          | 65          | 68          | 71     |
| ,         | Query   | March  | 63.1        | 56.9        | 56.9       | 55.4        | 53.8        | 52.3       | 52.3        | 52.3       | 52.3        | 52.3        | 50.8       | 50.8            | 50.8        | 50.8        | 8.05        | 50.8       | 50.8       | 50.8        | 50.8        | 50.0       | 49.2        | 49.2       | 49.2        | 49.2       | 49.2        | 49.2        | 49.2        | 49.2        | 49.2        | 49.2   |
|           | 9       | 30010  | 41          | 37          | 37         | 36          | 35          | 34         | 34          | 34         | 34          | 34          | 33         | 33              | 33          | 33          | 33          | 33         | 33         | 33          | 33          | 32.5       | 32          | 32         | 32          | 32         | 32          | 32          | 32          | 32          | 32          | 32     |
|           | Result  | į      | 7           | 7           | m          | 4           | s           | 9          | 7           | 80         | σ           | 10          | 11         | 12              | 13          | 14          | 15          | 16         | 17         | 18          | 19          | 20         | 21          | , 22       | 23          | 24         | 25          | 26          | 27          | 28          | 29          | 30     |

|        | Q9bxg9 homo sapien |        | Q7vkjl haemophilus | _      |        | •      | Q8dtm3 streptococc | O80135 bacteriopha | Q8yc17 brucella me | Q8£2g4 leptospira | -        | Q91fr7 chilo iride | O55728 chilo iride |
|--------|--------------------|--------|--------------------|--------|--------|--------|--------------------|--------------------|--------------------|-------------------|----------|--------------------|--------------------|
| Q9IBN4 | Q9BXG9             | Q7RI07 | Q7VKJ1             | Q47058 | Q6MLX1 | Q871T3 | QBDTM3             | 080135             | Q8YC17             | Q8F2G4            | 095317   | Q91FR7             | 055728             |
| N      | N                  | ~      | N                  | ~      | N      | ~      | N                  | N                  | N                  | N                 | N        | N                  | 7                  |
| 36     | 38                 | 39     | 39                 | 42     | 42     | 44     | 45                 | 23                 | 23                 | 23                | 29       | 29                 | 61                 |
| 47.7   | 47.7               | 47.7   | 47.7               | 47.7   | 47.7   | 47.7   | 47.7               | 47.7               | 47.7               | 47.7              | 47.7     | 47.7               | 47.7               |
| 31     | 31                 | 31     | 31                 | 31     | 31     | 31     | 31                 | 31                 | 31                 | 31                | 31       | 31                 | 31                 |
| 2      | . 23               | 4      | 'n                 | G      | 7      | 60     | 39                 | 0                  | 41                 | ~                 | <u>~</u> | 4                  | ιΩ                 |

### ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Hypothetical 7.2 kDa protein in rps2-rps9 intergenic region (ORF57)
Astaaia longa (Euglenophycean alga).
                                                                                                                                                                                                                [1] SEQUENCE FROM N.A.
SEQUENCE TROM N.A.
SEQUENCE TROM N.A.
MEDLINE=95163124; PubMed=7859309;
Gockel G., Hachtel W., Baier S., Fliss C., Henke M.;
"Genes for components of the chloroplast translational apparatus are conserved in the reduced 73-kb plastid DNA of the nonphotosynthetic euglenoid flagellate Astasia longa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CCAP 1204-17a;
MEDLINE=21080522; PubMed=11212895;
Gockel G., Hachrel W.;
"Complete gene map of the plastid genome of the nonphotosynthetic euglenoid flagellate Astasia longa.";
Protist 151:347-351(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 57;
Pred. No. 41;
3; Mismatches 2; Indels
                                                                                                                                                                         Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
NCBI_TaxID=3037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01CE152E60ED3B06 CRC64;
                                    57 AA.
                                    PRT;
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PIR; S38596; S38596.
Chloroplast; Hypothetical protein.
SEQUENCE 57 AA; 7156 MW; 01CE1
                                                                                                                                                                                                                                                                                                                                                           Curr. Genet. 26:256-262(1994).
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58.3%;
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Matches 7; Conservative
                                    STANDARD;
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P34774;
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RESULT 1
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RESULT Q73PH2

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Virology 277:100-110(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15064399; DOI=10.1073/pnas.0307639101;
Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F., Bodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H., Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F., Belengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F., Durkin S.A., Daugherry S.C., Shetry J., Shvartsbeyn A., Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B., Shateman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A., Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.; Meinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.; with other spirochete genomes of the oral pathogen Treponema denticola with other spirochete genomes ", park Paulsen Treponema denticola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21342572; PubMed=11448154; DOI=10.1006/viro.2001.1002; van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N., Tarchini R., Flers M., Sandbrink H., Lankhorst R.K., Vlak J.M.; "The white spot syndrome virus DNA genome sequence."; Virology 286:7-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 2; Length 58; Pred. No. 1.8e+02; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01A751BB0C81466F CRC64;
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                                                                                                Last sequence update)
Last annotation update)
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EMBL; AE017248; AAS11318.1; -.
   58 AA.
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                                                                   Created)
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[3]
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 35405 / DSM 14222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 AA; 6526 MW;
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Q91LD9;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                         (TrEMBLrel. 27, (TrEMBLrel. 27,
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14 IYKRLIQKLPK 24
                                                                                                                                                             Hypothetical protein.
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ORF105 (Wev205)
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                                                                05-JUL-2004
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JGR protein (A52R middle protein).
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ENBL; AR369029; AAK7774.1; -.
EMBL; AF33093; AAL33209.1; -.
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SEQUENCE 69 AA; 7843 MW;
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Hypothetical protein ydiN precursor.
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Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchl J., Sekowaka A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorowin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Vasarotti A., Vania A., Wandenbol M., Vannier P., Wasarotti A., Viari A., Wambutt R., Wadler E., Wedler F., Weltzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

"The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN=56601 / Serogroup Icterchaemorrhagiae / Serovar lai;
MEDLINE=22580143; PubMed=12712204; DOI=10.1038/nature01597;
MEDLINE-22580143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-G., Jia J., Tu Y.-F.,
Zhang Y., Zhu G.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35, DB 1; Length 71;
Pred. No. 4.5e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein ydin. D214FE34783FIF98 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z99107; CAB12424.1; -.
PIR; G69787; G69787.
Subrilist, BG12786; ydiN.
Complete proteome; Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.3%; Score 34; DB 2; L
46.2%; Pred. No. 3.4e+02;
tive 4; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB007637; BAA22749.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AA; 8405 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 53.8
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=LB189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YKRLFKKLKKF 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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SEQUENCE 35 AA;
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Mypulist, MYPU 3650; -.
Complete proteome; Hypothetical protein.
SEQUENCE 50 AA; 6163 MW; F39CA974CAD
                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Q72B46
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                                                                                                                                                                                                                                      STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
STRAIN=ATCC 35210 / B31;
MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K., Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
Richardson D.L., Harson M., van Vugt R., Palmer N., Adams M.D.,
Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
Artiach P., Bowman C., Garland S.A., Fujil C., Cotton M.D., Horst K.,
Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084; DOI=10.1093/nar/29.10.2145;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
MOSZER I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
                                                                                                                                                                                                    Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 36;
Pred. No. 3.5e+02;
-4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome, Hypothetical protein; Plasmid. SEQUENCE 36 AA; 4460 MW; 30032F5B00CBFEA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-JUN-2001 (TERMBLrel. 18, Created)
Ol-JUN-2003 (TERMBLrel. 18, Last sequence update)
Hypothetical protein MYPU 3550.
OrderedLocusNames=MYPU_3550;
Mycoplasma pulmonia
Bacteri.
                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence updat
01-JUN-2003 (TrEMBLrel. 24, Last annotation upc
Hypothetical protein BBB20.
GoderedLocusNames=BBB20;
Borrelia burgdorferi (Lyme disease spirochete).
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Nucled: Acids Res. 29:2145-2153(2001).
EMBL; AL445564; CAC13538.1; -.
PIR; B90557; E90557.
                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:580-586(1997).
EMBL; AE000792; AAC66341.1; -.
PIR; H70218; H70218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.3%;
            ALYKRLFKKLKKF 13
                          |:|:: ||: | |
15 AIYRKNFKETKYF 27
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Best Local Similarity 50.0°
                                                                                             PRELIMINARY;
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27 FKKFFEKIKK 36
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                                                                                                                                                                                            Plasmid cp26
                                                                                                                                                                                                                                                                                                                                                                                       burgdorferi.
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                                                                                                           050991;
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                                                                                              050991
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PubMed=15077118; DOI=10.1038/nbt959;

Heidelberg J.F., Seehadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,

Bougherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PF 4-derived endothelial cell growth inhibitor PEAK II (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=rpsU; CorderedLocusNames=DVU1792; ...
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                        Score 34; DB 2; Length bu; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Length 54;
Pred. No. 5.1e+02;
2; Mismatches 1; Indels
F39CA974CADFAC11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 AA; 6033 MW; COB560236BF1B14A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Ribosomal protein S11.
Name-rpsU; OrderedLocusNames=DVU1792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gupta S.K., Hassel T., Singh J.P.;
Proc. Natl. Acad. Sci. U.S.A. 92:7799-7803(1995)
HSSP; P02776; 1F9Q.
                                                                                                                                                                                                                                                                                                                                            54 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO, GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR002473; C-X-C/Interlkn 8.
InterPro; IPR001811; Chemokine_ILB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
MEDLINE=95372366; PubMed=7644496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PP00048; ILB; 1.
PRINTS; PR00436; INTERLEUKINB.
PRINTS; PR00437; SMALLCYTKCKC.
SMART; SM00199; SCY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.3%;
                                                   52.3%;
                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                        3 YKRLFKKLKK 12
                                                                                                                                                                                   3 YKKLYENIKK 12
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Length 27;

Score 33; DB 1; I Pred. No. 3.9e+02;

50.8%;

56FC003F1313179A CRC64;

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27 AA; 2955 MW;
                                                                                                                               2 LFKKISKF 9
                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prochlorococcus.
NCBI_TaxID=1219;
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                    Bacteria;
                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Q7VAA7
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                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Anthocerotophyta, Anthocerotales, Anthocerotaceae, Anthoceros.
WCBI_TaxID=48387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete nucleotide sequence of the hornwort (Anthoceros formosae) chloroplast genome: insight into the earliest land plants."; Nucleic Acids Res. 31:716-721(2003).
Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
"The genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.";
Nat. Blotechnol. 22:554-559(2004).
-! - SIMILARITY: Belongs to the $21P family of ribosomal proteins.
FMBL; AR017315; AAS96269.1; -.
                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINE=22598217; PubMed=12711687; DOI=10.1093/nar/gkg327;
Kugita M., Yamamoto Y., Fulikawa T., Matsumoto T., Yoshinaga K.;
"RNA editing in hornwort chloroplasts makes more than half the genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical 3.0 kDa protein in psbT-psbN intergenic region (ORF27)
Anthoceros formosae (Hornwort).
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Kugita M., Kaneko A., Yamamoto Y., Takeya Y., Matsumoto T.,
Yoshinaga K.;
                                                                                                                          TIGR; DVU1722...
GO; GO:0005440; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0003735; F:protein biosynthesis; IEA.
InterPro; IPR001911; Ribosomal S21.
                                                                                                                                                                                                                                                                                                              52.3%; Score 34; DB 2; Length 70; 58.3%; Pred. No. 6.48+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                PERNYS, PRO1165; Ribosomal S21, I.
PRINTS; PRO1056; RIBOSOMĀLS21.
PRODOM; PD005521; Ribosomal S21; 1.
TIGRFAMS; TIGRO0030; S21p; I.
PROSITE; PS01181; RIBOSOMAL S21; 1.
COMPLEE proteome; Ribonucleoprotein; Ribosomal protein.
SEQUENCE 70 AA; 8368 MW; SFAA4103D5E5FS09 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               functional.";
Nucleic Acids Res. 31:2417-2423(2003).
-1- SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AB086179; BACS5377.1; -.
EMBL, AB087463; BACS5474.1; -.
Chloroplast, Hypothetical protein.
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Les 7; Conservative
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55 AARKRLLKKIRK 66
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Q85BŪS;
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YCX2 ANTFO
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MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia, J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.;
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Gaps
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Nature 422:888-893(2003).
EMBL; AE011243; AAN4766.1; -.
COMPLETE proteome; Hypothetical protein.
SEQUENCE 45 AA; 5063 MW; D78B6526F2257B55 CRC64;
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Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
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1; Indels
                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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STRAIN=SARG / CCMP 1375 / SS120;
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01-0CT-2003 (TrEMBLrel. 25, Las
01-0CT-2003 (TrEMBLrel. 25, Las
Predicted protein family PM-19.
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MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302; MEDLINE=21992816; V. Xu X., Xuan Z., Hu S., Dong W., Yang J. Chen Y., Xu Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling I Tan H., Chen R., Wang J., Yu J., Yang H.; Manglete sequence of the T. tengcongensis genome."; Genome Res. 12:690270(2022).

EMBL, AR013205; AAM25766.1; -.
                                                                                 Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AA; 7136 MW; C4C768A74F8588BA CRC64;
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                        Thermoanaerobacteriaceae; Thermoanaerobacter
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50.0%;
                                                       OrderedLocusNames=TTE2647;
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Best Local Similarity 50.0
Matches 5; Conservative
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                          Hypothetical protein.
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                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21074935; PubMed=11206551; DOI=10.1038/35054089; Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evana P.S., Gregor J., Kirkpatrick H.A., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Melch                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                            Score 33; DB 2; Length 54;
Pred. No. 7.3e+02;
4; Mismatches 2; Indels
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Pred. No. 8e+02;
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                                                                                                           9E0F458D797F878D CRC64;
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0 AA; 7095 MW; 28F7CAFA76D70F61 CRC64;
a nearly minimal oxyphototrophic genome.";
Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
EMBL; AE017165; AAQ00601.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2002 (TrEMBLrel. 20, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative transposase (Hypothetical protein ECs1826)
EnderedLocusNames=ECs1826, z2563;
Escherichia roll Ottoren
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MEDLINE=21156231; PubMed=11258796;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                              6270 MW;
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                                                                                                                                                                                               Best Local Similarity 50.0
Matches 6; Conservative
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ALFIRLLKRLK 19
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PIR; B90857; B90857.
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tes 7; Conserv
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                                                                                       Complete proteome.
                                                                                                              54 AA;
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QBR6Y6
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AC QBR6Y
DT 01-JU
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Gaps

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Score 33; DB 2; Length bi, Pred. No. 8.1e+02;

4; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                  Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 65 AA; 7696 MW; 9AAEBD7D808AFCOF CRC64;
                                                         01-WAR-2004 (TrEWBLrel. 26, Created)
01-WAR-2004 (TrEWBLrel. 26, Last sequence update)
01-WAR-2004 (TrEWBLrel. 26, Last annotation update)
Hypothetical protein.
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65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=12368865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
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EMBL; AE010998; AAM06329.1; -.
InterPro; IPR011571; Wng hlx trns_reg.
ProDom; PD006327; Wing_hlx_tran_reg; 1.
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                       Name=orf74;
                                                                                                             Query Match
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Matches
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Q9G891
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MEDLINE=21971897; PubMed=11975337;
BAKER R.H., DeSalle R.;
"Multiple sources of character information and the phylogeny of Hawaiian drosophilide.";
Syst. Biol. 46:654-673(1997).
EMBL; U94206; AAC03432.1;
HSSP; P10807; 1B16.
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                                                                                                                                                                                                 Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=58310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanosarcina acetivorans.
Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales,
Methanosarcinaceae, Methanosarcina.
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Pred. No. 9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004022; F:alcohol dehydrogenase activity; IEA GO; GO:0008152; P:metabolism; IEA. InterPro; IPR002424; Insect_adh_fam. PRINTS; PR01167; INSADHFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 AA; 7544 MW; 80A8D98D37BA0D4F CRC64;
                                                                                                              (TrEMBLrel. 06, Last sequence update) (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
                                                          68 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                     046271;
01-JUN-1998 (TrEMBLrel. 06, Create
01-JUN-1998 (TrEMBLrel. 06, Last s
01-MAR-2004 (TrEMBLrel. 26, Last a
Alcohol dehydrogenase (Fragment).
                                                                                                                                                                                  Drosophila soonae (Fruit fly).
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Genome Res. 12:532-542(2002).
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity 60.0
Est Conservative
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                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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LYKTIFDKVK 21
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SEQUENCE
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                      RESULT 17
046271
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Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Koo H.L., Showay M.F., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR000307; Ribosomal_S16.
                                                                           Length 71;
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STRAIN=ATCC 50310;
Burger G., O'Kelly C.J., Gray W.M.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF295546; AAG13682.1; -
Complete proteome.
SEQUENCE 71 AA; 8391 MW; E09AF1F1F47205AD CRC64;
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Last annotation update)
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Last annotation update)
                                                                      50.8%; Score 33; DB 2; I 54.5%; Pred. No. 9.3e+02;
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Pred. No. 9.7e+02;
                                                                                                                          3; Mismatches
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Eukaryota, Malawimonadidae, Malawimonas.
NCBI_TaxID=136089;
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01-WAR-2004 (TrEMBLrel. 26, Last seq
01-WAR-2004 (TrEMBLrel. 26, Last smy
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Best Local Similarity 66.7
                                                                                                Local Similarity 54.5
Les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malawimonas jakobiformis.
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                         3 YKRLFKKLKKF 13
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18 FKKPIKKLQKF 28
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C27C898CD5A1D331 CRC64;

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32 AA; 3755 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=PY05152;
     SEQUENCE
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                                                   Query Match
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Matches
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                                                                                                                                                                                                                                                                         RESULT 22
                                                                                                                                                                                                                                                                                                Q7REB3
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                                                                                                      Carucci D.J.; "Genome sequence and comparative analysis of the model rodent malaria
Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janese C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                    parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bācteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                            Score 32.5; DB 2; Length 20;
Pred. No. 3.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
                                                                                                                                                                                                                                                                                                                                                 20 AA; 2477 MW; E649CBE384302759 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                  preliminary data.
EMBL; AABL01000770; EAA22261.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                    50.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
OrderedLocusNames=Xf0218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ALYKRLFKKLKK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|| |:||| ||
SLY-RIFKKKK 12
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                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xylella fastidiosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
tes 8; Conserv
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 2; Length 41;
Pred. No. 8.1e+02;
4; Mismatches 2; Indels
  Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 AA; 5126 MW; 09C75EFFDEA1EE16 CRC64;
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Last annotation update)
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Last annotation update)
Score 32; DB 2; 1 Pred. No. 6.5e+02;
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                                                                                                                                                                                                                                                                          41 AA.
                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=12368865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
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                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26, Last 01-MAR-2004 (TrEMBLrel. 26, Last Hypothetical protein (Fragment).
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  49.28;
                         46.28;
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                                                                                                 1 ALYKRLFKKLKKF 13
                                                                                                                                               4 AIWVKEIKKLKRF 16
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                                                   6; Conservative
                                                                                                                                                                                                                                                                          PRELIMINARY;
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5 YKLHYRKIKKY 15
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STRAIN=1330 / Biovar 1;
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Best Local Similarity
                         Local Similarity
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Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Yehen Y., Xue Y., Xu Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.; "A complete sequence of the T. tengcongensis genome.";
                                                                                                                         SEQUENCE FROM N.A.

STRAIN=E1 TOR NI6961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,

Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,

Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,

Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,

Mekalanos J.J., Venter J.C., Fraser C.M.;

"DNA sequence of both chromosomes of the cholera pathogen Vibrio
                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
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Pred. No. 1.1e+03;
1: Mismatches 0; Indels
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Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Hypothetical protein.
SEQUENCE 55 AA; 6538 MW; 83434DAF16132F3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AA; 7168 MW; 0191CF9A39065B7B CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seqn
01-OCT-2002 (TrEMBLrel. 22, Last anni
Hypothetical protein.
OrderedLocusNames=TTE1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , AE004107, AAF93345.1; -. G82355; G82355.
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EMBL; AE013107; AAM24714.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000)
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40 IFKKLKK 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIGR; VC0169; -.
  Vibrio cholerae.
                                                                                NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MB4;
                                                                                                                                                                                                                                                                                                                                                                                                                                 cholerae.
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MBDLINB=22588143; PubMed=12112204; DOI=10.1038/nature01597;

Ren S.-X., Pu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

Zhang Y., Zhu G.-P., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

Xu J.-G., Zhao G.-P.;
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                   Pauleen I.T., Seehadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A., Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                         "The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002),
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MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 2; Length 42;
Pred. No. 8.3e+02;
5; Mismatches 3; Indels
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Pred. No. 8.5e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                       42 AA; 5125 MW; 6CA2209E11F39E1D CRC64;
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01-0CT-2000 (TrEMBLrel. 15,
01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein vC0169,
OrderedLocusNames=VC0169;
                                                                                                                                                                                                                                                                                          EMBL; AE014443; AAN30395.1;
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OrderedLocusNames=LA2890;
Leptospira interrogans.
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32 IFWKLFKRLRK 42

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=98049343; PubMed=9389475; DOI=10.1038/37052;
A Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
A Kletchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
A Kirkness B.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
A Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
A Peterson S.N., Reich C.I., Wenkell L.K., Badger J.H., Glodek A.,
Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
A Utterback T.R., Cotton M.D., Spriggs T., Artiach P., Kaine B.P.,
Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
A Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
Moese C.R., Venter J.C.;
"The complete genome sequence of the hyperthermophilic, sulphaterachuring archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 1.3e+03;
2; Mismatches 2; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein YER158W-A.
                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypochetical protein AP1502.
OrderedLocusNames=AF1502;
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                                                                                                    68 AA.
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Complete proteome; Hypothetical protein.
SEQUENCE 68 AA; 8010 MW; 4A5474193EE
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
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                                                                                                    STANDARD;
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YF02_ARCFU
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DOI=10.1128/JB.185.17.5220-5233.2003;
Miller E., Heidelberg J., Eisen J., Nelson W., Durkin A., Ciecko A., Feldblyum T., Mitte O., Paulsen I., Nierman W., Lee J., Szczypinski B., Fraser C.; Ithe broad-host-range vibriophage KVP40: "Comparative genomics of a T4-related bacteriophage.";
J. Bacteriol. 185:5220-5233(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ross J.H.E., Murphy D.J.; "Charaterisation of anther-expressed genes encoding a major class of extracellular oleosin-like proteins in the pollen coat of
                                                                                                  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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Pred. No. 1.2e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Miller E., Lee J., Szczypinski B.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY283928; AAQ64123.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR006162; Ppantne S.
PROSTIE; PS00101; PHOSPHOPANTETHEINE; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 62 AA; 6832 MW; ACFCABB740AEA201 CRC64;
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MEDLINE=96237453; PubMed=8653113;
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Last
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EMBL, X95560; CAA64806.1; -.
PIR, T08133; T08133.
InterPro; IPR000136; Oleosin.
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                                      Hypothetical protein.
ORFNames=KVP40.0052;
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                                               ., Harrison P.M., Cheung K.H., Lan N., Echols N., Bertone P.,
                                                                                Miller P., Gerstein M.B., Snyder M.;
"An integrated approach for finding overlooked genes in yeast.";
Nat. Biotechnol. 20:58-63(2002).
EMBL; AF479922; AAL79235.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                            49.2%; Score 32; DB 2; Length 71; 50.0%; Pred. No. 1.3e+03;
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Bacteria, Pirmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 71 AA; 8775 MW; 8D6F7DD6D1EA8541 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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    MEDLINE=21624570; PubMed=11753363;
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58.3%;
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Matches 6; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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Q91BN4;
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STRAIN=subtype B; MEDLINE=91366314; PubMed=1890410; Parract A.M., Roff M.A., Amin T., Ball J., Parrett A.M., Battacharyya U., Booth J., Mansbrough-Jones M.H., Greenaway P.J.; Caracterisation of a series of human immunodeficiency virus isolates derived sequentially from a single patient."; Amed. Virol. 34:104-113(1991).
                                                                                                                                                                                                                                 STRAIN=subtype B; MEDLINE=20418939; PubMed=10954893; DOI=10.1089/088922200415027; MOVelli P., Vella C., Oxford J.S., Daniele R.S.; "Biological characterization of an infectious molecular clone of HIV
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 1e+03;
3; Mismatches 2; Indels
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Pred. No. 1.1e+03;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Park J.B.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databages.
EMBL; AR333001; AAK37514.1; -.
NON_TER 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vpu*.
D06A64136C2B0458 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VDUP protein (Framment).
Homo sapiens (Human).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                        Type 1GB8.";
AIDS Res. Hum. Retroviruses 16:1175-1178(2000).
EMBL; AJ271445; CAB92792.1; -.
GO; GO:0019076; P:viral release; IEA.
InterPro; IPR008197; Vpu.
Pfam; PF00559; Vpu; 1.
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01-MAR-2004 (TrEMBLrel. 26, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last sen
Hypothetical protein (Fragment).
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SEQUENCE 36 AA; 4120 MW;
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50.0%;
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Similarity 62.5%;
5; Conservative
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EMBL; V00260; CAA23509.1; -. HSSP; P04391; 1DUV.
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Best Local Similarity 58.3%;
Matches 7; Conservative
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6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   2 LYKRLFKKLKKF 13
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FKKNFKPLKK 16
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                                                                                                                                                                           K-12.";
Gene 16:119-132(1981)
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Best Local Similarity
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                                                            Escherichia coli
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SEQUENCE
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                                                                    Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                            parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002)
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pasteurellaceae, Haemophilus.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R., Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
"The complete genome sequence of Haemophilus ducreyi.";
Submitteed (JUN-2003) to the EMBL/Genbank/DDBJ databases.
EMBL; AE017156; AAP96636.1; -.
                                                                                                                                                                                                                                                                                                                                 Score 31; DB 2; Length 39;
Pred. No. 1.1e+03;
2; Mismatches 1; Indels
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Pred. No. 1.1e+03;
2; Mismatches 2; Indels
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Last annotation update)
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                                                             PubMed=12368865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                              preliminary data.
EMBL; AABL01001128; EAA15595.1; -.
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                                                                                                                                                                                                                                                                                                                                                53.3%;
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Matches 8; Conservative
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Best Local Similarity
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Q47058;
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Q47058
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Promoter and start of reading frame for E. coli gene argf. argf codes for ornithine carbamoyl transferase (E.C. 2.1.3.3.). (Fragment).
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Sockett R.E., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016743; F:carboxyl- and carbamoyltransferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:006520; P:amino acid metabolism; IEA. InterPro; IPR006132; OTCace_P. Transferase.
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bubhdel-H752164; DOI=0.1126/science.1093027;
Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
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Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
NCBI_TaxID=959;
                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Pred. No. 1.2e+03;
2; Mismatches 2; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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Pred. No. 1.2e+03;
1; Mismatches 4;
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NCBI_TaxID=562;
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Science 303:689-692(2004).
BMBL; BX842621; CAR79735.1; -.
COMPLETE PYCTEOME.
SEQUENCE 42 AA; 4891 MW; 67
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53 AA.

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(TrEMBLrel.
                                                                                             01-NOV-1998 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
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EMBL: Ap050805; BAC61866.1; Complete protecome; Hypothetical protein.

SEQUENCE 44 AA; 4783 MW; 33BIFCB71536E432 CRC64;
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STRAIN-UA159 / ATCC 700610 / Serotype c;
STRAIN-UA159 / ATCC 700610 / Serotype c;
MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
MADLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Adic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
Ferretti J.J.;
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Pred. No. 1.3e+03;
3; Mismatches 3; Indels
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                                                                                               Last sequence update)
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EMBL; AE014965; AANS8987.1; -.
                             44 AA.
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50.08;
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Best Local Similarity 50...
6; Conservative
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Matches 4; Conservative
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18 AMHKALYGKAKK 29
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                           PRELIMINARY;
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YSKIFRRLKQ 28
                                                                                                                                                                                                                                            Vibrionaceae; Vibrio.
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01-JUN-2003
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RESULT 40

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MEDLINE-20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
Delvecchio v. G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los Tranova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman Eselkov E., Blzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N.C., Overbeek R.;
The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
Proc. Natl. Acad. Sgi. U.S.A. 99:443-448(2002).

PIR, AC3599, AC3599.
                                                                                                                                                                               Bacteriophage bIL170.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=63118;
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Brucellaceae; Brucella.
NCBL_TaxID=29459;
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Pred. No. 1.5e+03;
2; Mismatches 2; Indels
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                           Last sequence update)
Last annotation update)
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EMBL; AY375285; AAR26450.1; -...
PIR; T03342; T03342.
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KELIKELEKF 13
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MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
Muller K., Tidona C.A., Bahr U., Darai G.;
"Identification of a thymidylate synthase gene within the genome
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Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
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the genome of insect tridescent virus type 6 between the genome
coordinates 0.310 and 0.347 (7990 bp).";
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NCB1_TaxID=10488;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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MEDLINE=86174607; Pubmed=3959991;
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Virus Genes 17:243-258(1998)
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MEDLINE-22598143; PubMed=12712204; DOI=10.1038/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-O., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-O., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Man M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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interrogans revealed by whole-genome sequencing.";
Nature 422:888-893(2003).
EMBL; AE011446; AANS0006.1; -.
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Winterce A.K., Fredholm M., Davies W.;
Submitted (ULL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z81181; CAB03557.1;
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Identification of genes encoding zinc finger proteins, non-histone chromosomal HMG protein homologue, and a putative GTP phosphohydrolase in the genome of Chilo iridescent virus.";
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iridovirus: coding strategy of the genome of Chilo iridescent virus.";
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the viral genome."
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MEDLINE=8907352; PubMed=3201750;
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"Identification and characterization of the repetitive DNA element in the genome of insect iridescent virus type 6.";
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SEQUENCE FROM N.A.
MEDLINE=21342589; PubMed=11448171; DOI=10.1006/viro.2001.0963;
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Pred. No. 1.6e+03;
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                                                                                                Med. Microbiol. Immunol. 175:43-53(1986)
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MEDLINE=93260401; PubMed=8492091;
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MEDLINE=94167241; PubMed=8121799;
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Virology 160:66-74(1987)
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Sonntag K.C., Darai G.;
"Characterization of the third origin of DNA replication of the genome
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Sonntag K.C., Schnitzler P., Koonin E.V., Darai G.;
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distinct family within the 'DEAD/H' superfamily: implications for the
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MEDILINE=84292065, PubMed=8021587;
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MEDLINE=99125223; PubMed=9926400; DOI=10.1023/A:1008017820941;
Muller K., Tidona C.A., Bahr U., Darai G.;
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Schnitzler P., Soltau J.B., Fischer M., Reisner H., Scholz J.,
Delius H., Darai G.;
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Sonntag K.C., Schnitzler P., Janssen W., Darai G.;
"Identification of the primary structure and the coding c the genome of insect integerent virus type 6 between the coordinates 0.310 and 0.347 (7990 bp).";
Intervirology 37:287-297 (1994).
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                                                                                                                                                                                                                                                                                                                                                           of insect iridescent virus type 6.";
Virus Genes 6:333-342(1992).
                                Created)
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MEDLINE=93118242; PubMed=1475907;
                                                                                                 Chilo iridescent virus (CIV)
                              01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                         Chilo iridescent virus.";
Virus Genes 17:243-258(1998)
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1; Indels

3; Mismatches

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Matches

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MEDLINE=92196996; PubMed=1549908;
Handermann M., Schnitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
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MEDLINE=92360401; PubMed=8492091;
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Schowsaser R., Raab K., Schnitzler P., Janssen W., Darai G.;
Identification of the gene encoding the major capsid protein of insect iridescent virus type 6 by polymerase chain reaction.";
J. Gen. Virol. 74:873-879(1993).
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MEDLINES-94167241; PubMed-8121799;
Schnitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
Delius H., Darai C.;
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Pred. No. 1.7e+03;
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EMBL, AF305141; AAB94439.1; -.
PIR; T03065; T03065.
SEQUENCE 61 AA; 7385 MW; 8F718A758C14AE0A CRC64;
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Virus Genes 18:243-264(1999)
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                                       the viral genome.";
Virology 160:66-74(1987).
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